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Genetic Diversity Analysis for Yield and Yield Attributing Traits in Finger Millet (*Eleusine coracana* L.)

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Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

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ABSTRACT

The present investigation was carried out to assess the genetic variability, heritability, genetic advance, genetic diversity in 37 finger millet genotypes for 15 quantitative traits during *Kharif*, 2022 at Field Experimentation Centre, Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agricxulture Technology and Sciences, Uttar Pradesh in Randomized Block Design with 3 replications. The analysis of variance for mean sum of squares due to genotypes showed significant differences for all the 15 quantitative characters. The genotype, IE-184 followed by IE-195, IE-185, IE-191, IE-199, IE-180 exhibited highest grain Yield per Plant, while IE-111, IE-150, IE-169, IE-170, IE-175, IE-168 genotypes are early in maturity. Whereas, genotypic and phenotypic coefficient of variation were found high for flag leaf length, number of productive tillers, number of fingers per ear, finger length. High heritability and high Genetic advance were recorded in plant height, flag leaf length, ear width, number of fingers per ear, finger width. Clustering by Tocher's Method has grouped all 37 genotypes into 6 clusters, in

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which Cluster-I contains more (16) genotypes and Cluster-IV, Cluster-V, Cluster-VI contains less (1) genotypes. According to Mahalanobis Euclidean Distance (not to scale), the maximum Inter-Cluster distance is recorded between Cluster-I and Cluster-VI (10.52) followed by Cluster-II and Cluster-V (10.44), Cluster-II & Cluster-III (9.35), Cluster-II & Cluster-IV (9.21). Plant height followed by grain yield per plant and days to 50% flowering traits contributes the highest percentage towards the overall divergence among the genotypes. Hence the selection of genotypes based on the above-mentioned characters and Inter Cluster Distance will be useful for crop improvement in Finger Millet.

Keywords: Finger millet; genetic variability; correlation coefficient; path coefficient analysis.

1. INTRODUCTION

"Finger millet (*Eleusine coracana* Gaertn L.) is an important millet crop that belongs to the family: Poaceae, subfamily: Chloridoideae, with chromosome number 2n = 36. It is commonly known by various names such as ragi, nachani, and African millet. Finger millet is primarily cultivated in arid and semiarid regions of Africa and Asia, including countries like India, Uganda, Ethiopia, Nepal and Kenya. Finger millet is believed to have originated in East Africa, particularly in the highlands of Ethiopia and Uganda" [1]. "The origin of finger millet is traced back to the highlands of East Africa, specifically Ethiopia and Uganda" [2].

Finger millet is highly nutritious comprising of 328 Kcal of energy, 7.3g of protein, 72g of carbohydrates, 2.6g of crude fiber, 344mg of calcium, and 8.9mg of iron per 100 grams of Finger millet (Nutritive value of Indian food, NIN, ICMR, 2018) and offers various health benefits due to its composition of essential nutrients. "High in dietary fiber: Finger millet is a good source of dietary fiber, which aids in digestion, promotes satiety, and helps maintain healthy blood sugar levels) [3-6]. Finger millet is naturally gluten-free, making it a suitable alternative grain for individuals with gluten intolerance or celiac disease" [7,8,9,10].

D^2 analysis, also known as the Mahalanobis D^2 statistic, is an important tool in crop improvement for assessing genetic diversity and identifying superior genotypes. It quantifies the genetic variation within a crop population, allowing breeders to understand the extent and nature of genetic diversity [11-13]. This information is crucial for selecting parents in breeding programs, as genotypes with higher D^2 values indicate greater dissimilarity and genetic diversity, suggesting the presence of desirable traits. D^2 analysis helps prioritize traits for selection and guides breeders in making informed decisions during crop improvement [14-18]. Additionally, it helps in germplasm conservation by identifying unique or underrepresented genotypes that possess valuable traits for future breeding efforts [19,20].

1.1 Objectives

1. To assess the genetic diversity among Finger millet germplasm using D^2 analysis
2. To evaluate Finger millet genotype for yield and yield attributing traits
3. To estimate the genetic diversity for morphological characters
4. To identify the divergent parents for future hybridization

2. MATERIALS AND METHODS

The present investigation was carried out at the Field Experimentation Centre, Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, Uttar Pradesh during *Kharif*, 2022. The University is situated on the left side of Prayagraj-Rewa National Highway about 5km away from Prayagraj city. Prayagraj is located in South-eastern part of Uttar Pradesh state of India. The site of experiment is located at 25.57°N latitude, 81.56°E longitude and 98 meters above the mean sea level. The average precipitation is around 983mm annually with maximum concentration during July to October with few showers in winter. The crop was grown under *Kharif* season. The soil type of the experimental site was loamy mixed with pH ranging from 7.3 to 7.6.

The 37 genotypes of finger millet including one check variety is carried out to perform the experiment conducted in Randomized Block Design with three replications with spacing Row to Row spacing is 20 cm and Plant to Plant spacing is 10 cm. In each replication five

randomly selected best competitive plants are examined were recorded on following 15 quantitative traits *viz.,* Days to 50% flowering, Days to maturity, Plant height (cm), Flag leaf length (cm), Flag leaf width (cm), Number of productive tillers per plant, Number of fingers per Ear, Finger length (cm), Ear head length (cm), Ear head width (cm), Biological yield (gm), Harvest index (%), Test weight and Grain yield per plant (gm).

"The data were subjected to analysis of variance adopting standard statistical methods" (Panse and Sukhtme, 1985; Singh and Choudhary, 1979). "Additionally, the genetic parameters genotypic coefficient of variation (GCV), Phenotypic coefficient of varation (PCV), Heritability in the broad sense, Genetic advance as percent of mean and D^2 analysis was carried out by using the statistical methods. The additional components of variance include Phenotypic variance, Genotypic variance and Environmental Variance" [21].

The Software called Rstudio was used to perform the analysis mentioned above.

2.1 Experimental Material

The experimental materials for this research were obtained from the SHUATS, Department of Genetics and Plant Breeding in Prayagraj. The details of the experimental materials are mentioned below in Table 1.

Table 1. Experimental material

S.no	Genotypes	S.no	Genotypes
1	IE-177	**19**	IE-203
2	IE-179	**20**	IE-101
3	IE-180	**21**	IE-102
4	IE-181	**22**	IE-111
5	IE-183	**23**	IE-120
6	IE-184	**24**	IE-121
7	IE-185	**25**	IE-136
8	IE-186	**26**	IE-139
9	IE-187	**27**	IE-150
10	IE-189	**28**	IE-161
11	IE-190	**29**	IE-163
12	IE-191	**30**	IE-165
13	IE-195	**31**	IE-168
14	IE-196	**32**	IE-169
15	IE-197	**33**	IE-170
16	IE-198	**34**	IE-172
17	IE-199	**35**	IE-174
18	IE-200	**36**	IE-175
		37	FIN-7669 (Check)

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance

Analysis of Variance for all parameters recorded in 37 fingermillet genotypes is presented in Table 3 indicating the mean sum of squares due to replications, varieties, and error for thirteen characters studied. "The analysis of variance indicated the presence of ample variability in the experiment material and disclosed significant differences among the genotypes for all characters studied" [21].

Analysis of variance revealed that for all 15 quantitative traits shows genotype differences shows highly significant under study at 1% level of significance indicating the presence of genetic differences in the experimental material suggesting the importance of the genetic variability in order to identify the best genetic make-up provide better scope to selection.

On the basis of mean performance, the highest grain yield per plant was observed for fingermillet genotypes as IE-184 (4.2), IE-195 (4.2), IE-185 (4.1333), IE-191 (4.1333), IE-199 (4.1333), IE-180 (4), IE-190 (3.8667), IE-177 (3.5333), IE-179 (3.5333), IE-183 (3.5333), IE-189 (3.5333), IE-198 (3.5333), IE-186 (3.4667), IE-102 (3.3744), IE-111 (3.3744).

3.1.1 Phenotypic and genotypic variance

The variability estimates such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (h^2), genetic advance (GA), genetic advance of mean (GAM) for fifteen traits are explained under the following. For all the traits PCV was higher than GCV indicating that there is environment impact on genotypes. In the present study, Phenotypic coefficient of variation (PCV) was showing highest value for the character finger length (51.976), flag leaf width (40.737), number of productive tillers (33.153), flag leaf length (31.994), biological yield per plant (29.46), number of fingers per ear (24.771), plant height (22.546), finger width (22.286), ear width (22.135), ear length (20.723). While the Genotypic Coefficient of Variation (GCV) was showing highest value for character for flag leaf length (30.04), harvest index (28.2), number of productive tillers (24.804), biological yield per plant (22.9), days to maturity (22.79), plant height (22.078), number of fingers per ear (21.154), finger length (21).

Table 2. Analysis of variance (ANOVA) among 37 Fingermillet genotypes of 15 quantitative traits

S No.	Source of Variation	Mean Sum of Squares		
		Replication	Treatment	Error
	Degree of freedom	2	36	72
1	Days to 50% flowering	10.3	135.51**	13.17
2	Days to maturity	3.61	37.8*	6.55
3	Plant height	30.9	1674.55*	68.66
4	Flag leaf length	75.13	288.51**	34.16
5	Flag leaf width	0.13	0.37**	0.31
6	Number of fingers per ear	0.93	5.34**	1.45
7	Ear length	2.51	10.56*	3.72
8	Ear width	0.04	1.50**	0.3
9	Finger length	47.62	54.61*	45.7
10	Finger width	0.01	0.08**	0.03
11	Number of productive tillers	1.81	2.91**	1.28
12	Biological yield per Plant	372.93	235.44	92.82
13	Harvest index	556.3	418.41	107.92
14	Test weight	0.09	0.20**	0.115
15	Grain yield per plant	0.07	0.41**	0.05

*** indicates significance at 1% level of significance, * indicates significance at 5% level of significance*

Table 3. Genotypic parameters of 15 quantitative traits in fingermillet genotypes

S No.	Trait	GCV	PCV	h² (Broad Sense)	Genetic Advance 5%	Genetic Advance as % of Mean 5%
1	Days to 50% flowering	9.704	10.212	93.3	12.5	18.993
2	Days to Maturity	22.79	2.51	82.65	6.0444	0.04269
3	Plant Height	22.078	22.546	95.9	46.674	44.54
4	Flag leaf length	30.04	31.994	88.2	17.809	58.103
5	Flag leaf width	16.332	40.737	16.1	0.117	13.489
6	Number of fingers per Ear	21.154	24.771	72.9	2.005	37.214
7	Ear Length	16.675	20.723	64.7	2.503	27.64
8	Ear width	19.83	22.135	83.3	1.168	36.597
9	Finger Length	21	51.976	16.3	1.435	17.479
10	Finger width	17.931	22.286	64.7	0.224	29.721
11	Number of productive tillers	24.804	33.153	56.1	1.137	38.229
12	Biological Yield per Plant	22.9	29.46	60.57	11.0546	36.7595
13	Harvest Index	28.2	0.32748	74.2	18.053	56.0606
14	Test Weight	7.2	0.11136	42.7	0.2275	0.097
15	Grain yield per plant	10.114	10.79	87.8	0.668	19.527

GCV: *Genotypic Coefficient of Variation*, ***PCV:*** *Phenotypic Coefficient of Variation*, ***h^2:*** *Heritability*, ***GA% of Mean:*** *Genetic Advance as percent of mean*

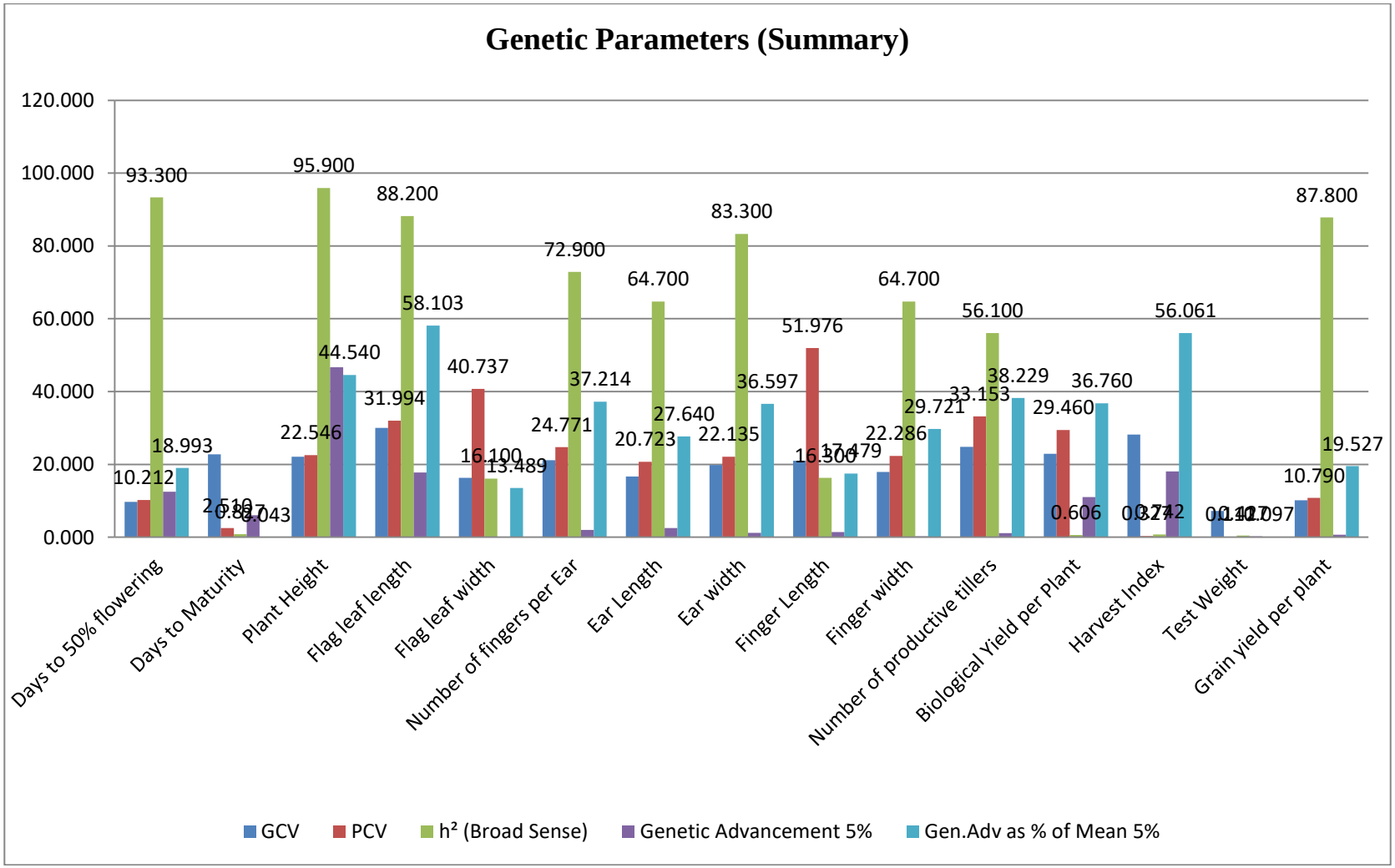

Fig. 1. Bar diagram depicting GCV, PCV, heritability and genetic advance for 15 quantitative characters in Fingermillet

3.2 Heritability

- "Heritability is showing moderate to high among the characters. These characters show no signs of low heritability. The high heritability and moderate heritability values for the traits under consideration in the current study indicated that they were less and moderate influenced by the environment and aided in the effective selection of features based on phenotypic expression utilising a simple selection approach" [21].
- The estimates of heritability (%) in the broad sense for 14 characters studied, which ranged from flag leaf width (16.1) to plant height (95.9). High heritability was recorded for plant height (95.9), days to 50% flowering (93.3), flag leaf length (88.2), grain yield per plant (87.8), ear width (83.3), days to maturity (82.65), harvest index (74.2), number of fingers per ear (72.9), ear length (64.7), finger width (64.7), biological yield per plant (60.57) Medium heritability was recorded for number of productive tillers (56.1), test weight (42.7), finger length (16.3), flag leaf width (16.1).

3.3 Genetic Advance

- Genetic advance for different traits revealed that it varied from 0.117 to 46.674. High genetic advance in plant height (46.674). Medium genetic advance was recorded for harvest index (18.053), flag leaf length (17.809), days to 50% flowering (12.5), biological yield per plant (11.0546). Low genetic advance was recorded for days to maturity (6.0444), ear length (2.503), number of fingers per ear (2.005), finger length (1.435), ear width (1.168), number of productive tillers (1.137), grain yield per plant (0.668), test weight (0.2275), finger width (0.224), flag leaf width (0.117).

3.4 Genetic Advance as Percentage of Mean

- In the present investigation, genetic advance as % of mean varied from 0.04269 to 58.103. High estimate of genetic advance as percent of mean was recorded in flag leaf length (58.103), harvest index (56.0606), plant height (44.54), number of productive tillers (38.229), number of fingers per ear (37.214), biological yield per plant (36.7595), ear width (36.597), finger width (29.721), ear length (27.64). Medium estimate of genetic advance as percent of mean was recorded in grain yield per plant (19.527), days to 50% flowering (18.993), finger length (17.479), flag leaf width (13.489). Low estimate of genetic advance as percent of mean was recorded in test weight (0.097), days to maturity (0.04269).

- "Many of the traits studied had a high heritability as well as a high genetic advance as a percentage mean, indicating that the characters are predominantly regulated by additive gene action. As a result of the accumulation of more additive genes leading to further improvement, simple selection would be effective of these traits based on phenotypic expression" [21,22-24].

3.5 D^2 Analysis

The cluster analysis revealed the grouping of genotypes into 6 distinct clusters. The presence of a large cluster, such as Cluster-1, indicates a higher degree of similarity among a significant number of genotypes (16). This could suggest the presence of a core group of genotypes with common ancestry or shared genetic background. On the other hand, the presence of smaller clusters or single genotypes in Clusters 2,3,4,5 and 6 indicates a higher level of distinctness or uniqueness in these genotypes.

Table 4. Cluster pattern of finger millet (*Eleusine coracana* L.) genotypes based on D^2 statistics

Cluster Group	No. of Genotypes	List of Genotypes
Cluster 1	16	IE-183, IE-186, IE-187, IE-189, IE-197, IE-198, IE-101, IE-102, IE-111, IE-120, IE-121, IE-136, IE-139, IE-161, IE-165, IE-169, IE-172, IE-174
Cluster 2	9	IE-184, IE-185, IE-195, IE-199, IE-177, IE-179, IE-180, IE-181
Cluster 3	9	IE-170, IE-175, IE-111, IE-150, IE-168, IE-203, IE-163, IE-196
Cluster 4	1	IE-191
Cluster 5	1	IE-190
Cluster 6	1	IE-200

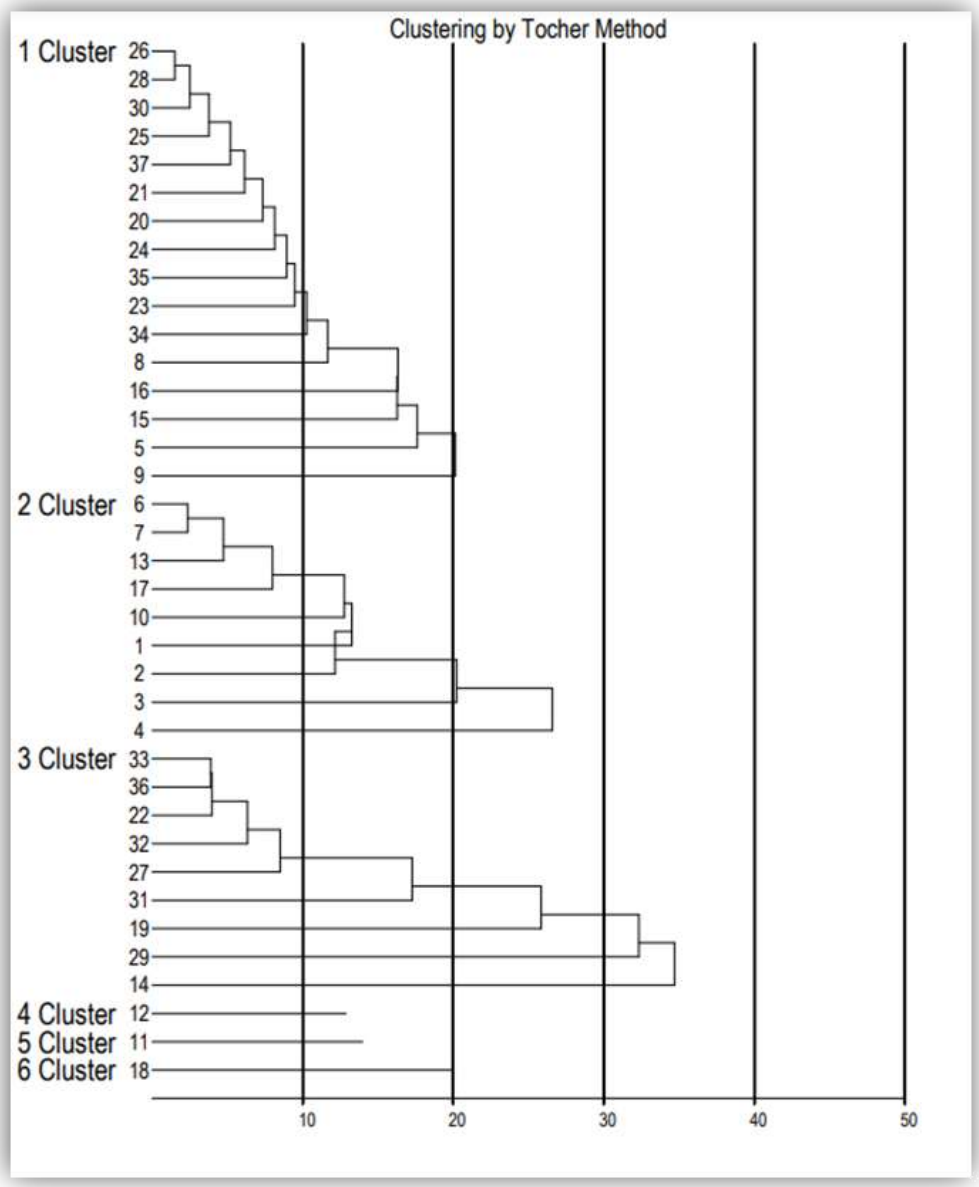

Fig. 2. Clustering by Tocher's method

Table 5. Mean intra and inter-cluster distances among six (6) clusters in Finger Millet (*Eleusine coracana* L.) by Tocher's method

S No.	Cluster Number	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6
1	**Cluster1**	4.68	6.6	7.44	5.61	7.29	8.3
2	**Cluster2**		4.57	9.35	9.21	10.44	6.89
3	**Cluster3**			4.93	8.36	7.21	7.58
4	**Cluster4**				0	5.94	10.52
5	**Cluster5**					0	9.15
6	**Cluster6**						0

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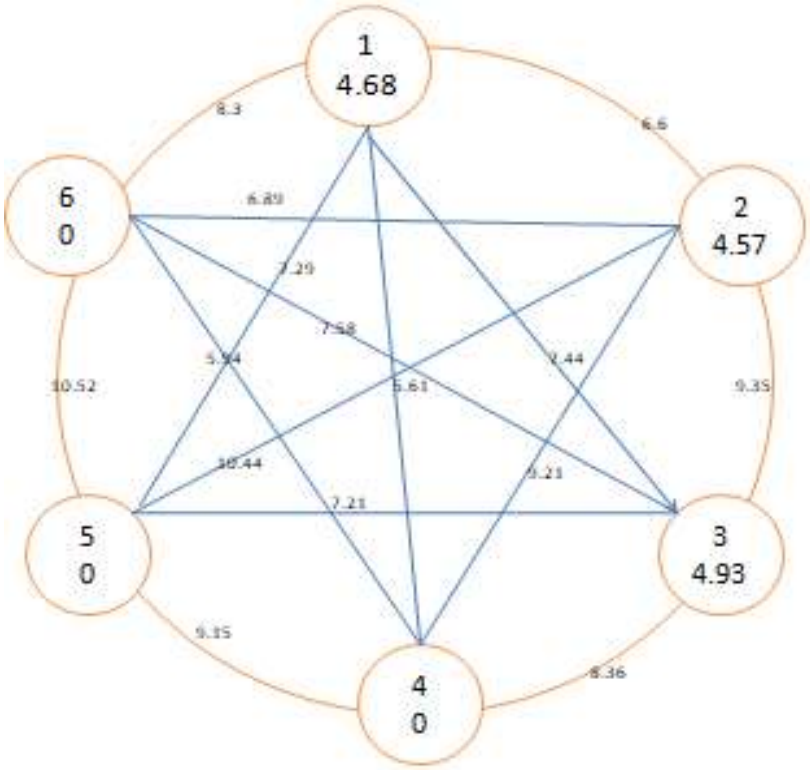

Fig. 3. Mahalanobis D^2 Tocher's method (not to scale)

The intra-cluster distance values ranged from 0.00 to 4.93, while the inter-cluster distance values ranged from 5.61 to 10.52. The intra-cluster distance is 0.00 in cluster-4, cluster-5, cluster-6 while 4.93 in cluster-3 followed by 4.68 in cluster-1 and 4.54 in cluster-2

The highest cluster mean value for days to 50% flowering was recorded in Cluster-6 (85), for days to pod setting was recorded in cluster-5(120), for days to maturity was recorded in cluster-3 (142), for plant height was recorded in cluster-3(71.53), for number of primary branches was recorded in cluster-4 (3.33), for number of secondary branches was recorded in cluster-3 (10.27), for number of pods per plant was recorded in cluster-4 (85.6), for number of seeds per plant was recorded in cluster-4 (103.2), for number of seeds per pod was recorded in cluster-4 , cluster-5 (2), for biological yield per plant was recorded in cluster-4 (30.87), for seed index was recorded in Cluster-2 (21.17), for harvest index was recorded in cluster-4 (45.23) and for seed yield per plant was recorded in cluster-4 (16.07).

The highest cluster mean value for days to 50% flowering was recorded in Cluster-3 (70.17), for days to maturity was recorded in Cluster-5 (130), for plant height was recorded in Cluster-1 (117.91), for flag leaf length was recorded in Cluster-5 (38.73), for flag leaf width was recorded in Cluster-6 (1.2), for number of fingers per ear was recorded in Cluster-3 (6.17), for ear length was recorded in Cluster-3 (10.33), for finger length was recorded in Cluster-3 (9.82), for biological yield per plant was recorded in Cluster-6 (5.11), for harvest index was recorded in Cluster-1 (34.32), for test weight was recorded in Cluster-6 (7.63) and for grain yield per plant was recorded in Cluster-2 (4.04).

4. CONCLUSION

Based on the work on 37 Genotypes of Finger Millet on 15 quantitative characters, it is concluded that all the studied genotypes have shown significant difference. The genotype, IE-184 followed by IE-195, IE-185, IE-191, IE-199, IE-180 exhibited highest grain Yield per Plant, while IE-111, IE-150, IE-169, IE-170, IE-175, IE-168 genotypes are early in maturity. Whereas, genotypic and phenotypic coefficient of variation were found high for flag leaf length, number of productive tillers, number of fingers per ear, finger length. High heritability and high Genetic advance were recorded in plant height, flag leaf length, ear width, number of fingers per ear, finger width. Clustering by Tocher's Method has

grouped all 37 genotypes into 6 clusters, in which Cluster-I contains more (16) genotypes and Cluster-IV, Cluster-V, Cluster-VI contains less (1) genotypes. According to Mahalanobis Euclidean Distance (not to scale), the maximum Inter-Cluster distance is recorded between Cluster-I and Cluster-VI (10.52) followed by Cluster-II and Cluster-V (10.44), Cluster-II & Cluster-III (9.35), Cluster-II & Cluster-IV (9.21). Plant height followed by grain yield per plant and days to 50% flowering traits contributes the highest percentage towards the overall divergence among the genotypes. Hence the selection of genotypes based on the above-mentioned characters and Inter Cluster Distance will be useful for crop improvement in Finger Millet.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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