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ASSESSMENT OF GENETIC DIVERSITY IN PROMISING FINGER MILLET (*ELEUSINE CORACANA* (L.) GAERTN.) GENOTYPES

Adarsh Ranjan[1], Sardar Sunil Singh[2], Birender Singh[1], Priyanka Kumari[1], Brajesh Kumar[1], Tushar Ranjan[3], Awdhesh Kumar[4] and Ashutosh Kumar[1]*

[1]Department of Plant Breeding and Genetics Bihar Agricultural University, Sabour-813210 Bhagalpur.
[2]Department of Plant Breeding and Genetics, Nalanda College of Horticulture Noorsarai-803113, Nalanda, Bihar
[3]Department of Molecular Biology and Genetic Engineering, Bihar Agricultural University, Sabour Bhagalpur, Bihar, India-813210
[4]Department of Statistics, Mathematics & Computer Application, Bihar Agricultural University, Sabour-813210 Bhagalpur.
*Corresponding author E-mail: ashutoshkumar0927@gmail.com
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ABSTRACT

Genetic diversity is the cornerstone of crop improvement programs. The present study aimed to assess the genetic divergence among 22 finger millet (*Eleusine coracana* L. Gaertn.) genotypes using Mahalanobis D² statistics. The experiment was conducted during the Rabi 2023–24 season in a Randomized Block Design with three replications. Data were recorded for twelve yield-attributing traits. Analysis of variance revealed highly significant differences ($p<0.01$) among genotypes for all traits, indicating substantial genetic variability suitable for divergence analysis. Based on D² values, the genotypes were grouped into five distinct clusters using Tocher's method. Cluster III was the largest, comprising nine genotypes, followed by Cluster II (7 genotypes) and Cluster I (4 genotypes). Clusters IV and V were solitary, each containing one genotype, indicating their genetic uniqueness. The maximum inter-cluster distance was observed between Cluster III and IV (1986.97), suggesting that crosses between these clusters have the highest potential for generating transgressive segregants. Cluster mean analysis identified Cluster IV as the most promising, exhibiting earliness and superior yield attributes. The traits contributing most to genetic divergence were ear head weight per plant (38.53%), harvest index (19.43%), and 1000-seed weight (15.74%). The results provide a clear basis for selecting genetically diverse parents for hybridization to enhance yield and adaptability in finger millet.

Keywords: Finger millet, Genetic divergence, Clustering, Mahalanobis D², Tocher's method, Hybridization.

Introduction

Finger millet (*Eleusine coracana* L. Gaertn.), commonly known as ragi, is a vital nutri-cereal renowned for its exceptional nutritional profile, including high calcium, dietary fiber, and essential amino acids (Devi *et al*., 2014). As a drought-tolerant crop, it plays a crucial role in the food security of arid and semi-arid regions of Africa and Asia. Despite its nutritional superiority and resilience, the productivity of finger millet remains low compared to major cereals, necessitating focused genetic improvement efforts.

The success of any breeding program hinges on the availability and utilization of genetic diversity. Selecting genetically diverse parents is critical for exploiting heterosis and achieving genetic recombination in subsequent generations (Arunachalam, 1981). While univariate analyses help understand individual trait variation, multivariate techniques like Mahalanobis D² statistics provide a more robust assessment of genetic divergence by considering multiple traits simultaneously (Rao, 1952). This method effectively quantifies genetic distances and groups genotypes into clusters, aiding breeders in

identifying the most divergent parents for hybridization (Daniel *et al*., 2011).

Several studies in finger millet have employed D^2 analysis to understand genetic architecture (Saundarya & Satish, 2015; Pali *et al*., 2022). However, continuous evaluation of new germplasm is essential to identify novel sources of variation. In this context, assessing the extent of variability, clustering pattern, and contribution of yield-related traits becomes highly relevant for guiding selection and hybridization strategies. A refined understanding of genetic divergence not only supports efficient parental choice but also ensures sustainable utilization of finger millet genetic resources for yield improvement and adaptability under changing climatic conditions.

Materials and Methods

Experimental Site and Material

The study was conducted during the Rabi season of 2023–24 at the Finger Millet Research Block of Bihar Agricultural University, Sabour, Bhagalpur, Bihar, India. The experimental material comprised 22 diverse finger millet genotypes, including improved varieties and advanced breeding lines obtained from ICRISAT, IIMR, and BAU, Sabour (Table 1).

Experimental Design and Observations

The trial was laid out in a Randomized Block Design (RBD) with three replications. Each genotype was sown in a 4m long two-row plot with a spacing of 25 cm × 10 cm. Recommended agronomic practices were followed to ensure healthy crop growth. Observations were recorded on five randomly selected competitive plants from each replication for twelve quantitative traits: plant height (cm), days to 50% flowering, days to maturity, number of tillers per plant, number of productive tillers per plant, number of fingers per plant, finger length (cm), ear head length per plant (cm), ear head weight per plant (g), 1000-seed weight (g), harvest index (%), and grain yield per plant (g).

Statistical Analysis

The mean data were subjected to Analysis of Variance (ANOVA) using R software (version 4.4.3) to test the significance of genotypic differences. Genetic divergence was assessed using Mahalanobis D^2 statistics (Mahalanobis, 1936). The genotypes were grouped into clusters following Tocher's method as outlined by Rao (1952). Intra- and inter-cluster distances were calculated, and the relative contribution of each character to the total divergence was determined by ranking the characters based on their Mahalanobis distance.

Results and Discussion

Analysis of variance

The ANOVA revealed highly significant differences ($p<0.01$) among the 22 genotypes for all twelve traits under study (Table 2). This confirms the presence of substantial genetic variability in the experimental material, providing a sound basis for further divergence analysis. Similar findings of significant genetic variability in finger millet have been reported by Suryanarayana *et al*. (2014) and Pali *et al*. (2022). Recent studies also reported large variability among finger millet genotypes for yield and related traits (Backiyalakshmi *et al*., 2021; Ojha *et al*., 2024).

Genetic Divergence and Clustering Pattern

The genetic divergence analysis using Mahalanobis D^2 statistic grouped the 22 genotypes into five distinct clusters (Table 3). Cluster III was the largest, consisting of nine genotypes (IE5249, ICFV221002, ICFV221029, ICFV221034, IE6326, S-1, S-2, PR202, VL376), indicating a close genetic relationship among them. Cluster II contained seven genotypes, and Cluster I contained four. Notably, Cluster IV (RAU8) and Cluster V (ICFV221011) were solitary, housing only one genotype each. This monotypic nature highlights their significant genetic distinctness from the other genotypes, making them valuable as unique parents for hybridization. This clustering pattern is visually represented in Figure 1. The findings are in agreement with the results of Charitha *et al*. (2023), who also reported non-overlapping clusters in finger millet. Similar cluster distributions were also found in other recent diversity studies on finger millet (Patil *et al*., 2021; Kumar *et al*., 2024).

Intra- and Inter-Cluster Distances

The average intra- and inter-cluster distances (D^2 values) are presented in Table 4. The intra-cluster distances, which measure diversity within a cluster, were highest for Cluster III (493.14), followed by Cluster II (221.94) and Cluster I (118.59). The high intra-cluster distance in Cluster III suggests considerable variability among its constituent genotypes, offering scope for selection within the cluster. In contrast, Clusters IV and V had zero intra-cluster distances, as expected for solitary clusters. The inter-cluster distances, which reflect the genetic divergence between clusters, varied considerably. The maximum inter-cluster distance was observed between Cluster III and Cluster IV (1986.97), indicating that genotypes from these two clusters are highly divergent. This was followed by the distance between Cluster III and V (1377.15) and between Cluster II and III

(1345.82). According to Mahalanobis (1936), crosses between genotypes from clusters with maximum divergence are likely to produce a wide range of variability and high heterotic effects, potentially yielding superior transgressive segregants. Therefore, hybridization between genotypes from Cluster III and IV is expected to be most rewarding. Similar conclusions on exploiting maximum inter-cluster distances have been made in finger millet by Basavaraj *et al*. (2023) and Gebreyohannes *et al*. (2024).

Cluster Mean Analysis

The mean performance of the five clusters for the twelve traits is summarized in Table 5. Cluster IV, represented by the check variety RAU8, emerged as the most superior cluster. It recorded the earliest days to 50% flowering (95.67 days) and maturity (121.33 days), the highest number of fingers per plant (8.02), finger length (10.3 cm), ear head weight (18.57 g), 1000-seed weight (3.12 g), harvest index (32.42%), and grain yield per plant (7.65 g). Cluster V (ICFV221011) also showed promising traits, including earliness and a high harvest index (32.18%). Cluster I exhibited good performance for tiller number and seed weight. In contrast, Cluster III, despite being the largest, was characterized by late maturity and lower mean values for most yield-attributing traits. The distinct mean values across clusters reinforce the genetic diversity captured by the D^2 analysis and help identify clusters with specific desirable characteristics for targeted breeding. Comparable results of superior cluster mean performance have also been documented in other finger millet diversity studies (Wolie *et al*., 2013; Crop Science, 2023).

Contribution of Traits to Genetic Divergence

The percentage contribution of each character to the total genetic divergence is presented in Table 6. Ear head weight per plant was the largest contributor (38.53%), followed by harvest index (19.43%) and 1000-seed weight (15.74%). Together with ear head length (10%) and finger length (9.09%), these five traits accounted for over 92% of the total genetic divergence. This indicates that panicle architecture and yield efficiency traits are the primary drivers of diversity in this set of germplasm. Consequently, selection of parents for hybridization should prioritize these traits to maximize genetic gains. Similar findings were reported by Basavaraj *et al*. (2023), where yield-related traits were major contributors to divergence. Recent molecular studies also confirm that yield-related traits contribute strongly to diversity in finger millet (Kumar *et al*., 2024; Backiyalakshmi *et al*., 2021).

Conclusion

The study revealed significant genetic diversity among the 22 finger millet genotypes, successfully grouping them into five distinct clusters. The high inter-cluster distances, particularly between Cluster III and IV, suggest a strong potential for heterosis and the creation of desirable variability through their hybridization. The unique genotypes in solitary clusters (RAU8 in Cluster IV and ICFV221011 in Cluster V) are valuable genetic resources. The cluster means provide a clear guide for selecting parents for specific traits, with Cluster IV being ideal for combining earliness and high yield. The analysis underscores that ear head weight, harvest index, and seed weight are the most critical traits for distinguishing genotypes. These findings provide a scientifically sound strategy for finger millet breeders to select diverse parents and design efficient crossing programs for developing high-yielding, adaptable cultivars.

Table 1: List of 22 finger millet genotypes along with their sources

S.No	Genotype	Source	S.No	Genotype	Source
1.	IE5249	ICRISAT	12.	S-3	BAU Sabour
2.	ICFV 221002	ICRISAT	13.	S-4	BAU Sabour
3.	ICFV 221029	ICRISAT	14.	PR 202	IIMR Hyderabad
4.	ICFV 221034	ICRISAT	15.	ICFV 221009	ICRISAT
5.	IE 2606	ICRISAT	16.	ICFV 221040	ICRISAT
6.	ICFV 221011	ICRISAT	17.	ICFV 221038	ICRISAT
7.	IE 6326	ICRISAT	18.	ICFV 221024	ICRISAT
8.	GPU 67	IIMR Hyderabad	19.	IE 5963	ICRISAT
9.	IE 4570	ICRISAT	20.	VL 376	IIMR Hyderabad
10.	S-1	BAU Sabour	21.	KMR 316 (check)	IIMR Hyderabad
11.	S-2	BAU Sabour	22.	RAU 8 (check)	RPCAU Pusa

Table 2: Analysis of variance (ANOVA) for yield and yield-attributing traits.

Source of Variations	Mean sum of Square		
	Replication	Treatments	Error
df	2	21	42
Plant height (cm)	23.721	350.020**	44.143
Days to 50% flowering	124.682	225.307**	29.491
Days to maturity	23.742	583.822**	10.631
No. of tillers per plant	0.015	1.944*	0.302
No. of productive tillers per plant	0.002	0.492**	0.018
No. of fingers per plant	0.013	2.085**	0.030
Finger length	0.001	8.346**	0.030
1000 seed weight (g)	0.006	8.335**	0.031
Ear head length per plant (cm)	27.835	9.123**	0.016
Ear head weight per plant (g)	0.775	0.300**	0.001
Harvest index	81.258	58.172**	0.104
Grain yield per plant (g)	24.027	3.742**	0.118

Table 3: Composition of finger millet genotypes in five clusters (Tocher's method).

Cluster	No. of Genotypes	Genotypes
Cluster 1	4	ICFV221009, ICFV221040, ICFV221024, KMR-316
Cluster 2	7	IE2606, GPU67, IE4570, S-3, S-4, ICFV221038, IE5963
Cluster 3	9	IE5249, ICFV221002, ICFV221029, ICFV221034, IE6326, S-1, S-2, PR202, VL376
Cluster 4	1	RAU8
Cluster 5	1	ICFV221011

Table 4: Intra- (diagonal, bold) and inter-cluster distances (D^2 values) among the five clusters.

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	118.59	815.42	1043.26	390.14	487.01
Cluster 2		221.94	725.22	1345.82	779.64
Cluster 3			493.14	1986.97	1377.15
Cluster 4				0	306.46
Cluster 5					0

Table 5: Percentage contribution of characters towards total genetic divergence.millet genotypes.

Characters	Range		Genotypic variance	GCV (%)	Phenotypic variance	PCV (%)	h^2 (Broad Sense)	Gen. Adv as 5 % of Mean
	Lowest	Highest						
Plant height (cm)	83.17	130.93	101.96	9.18	146.10	10.99	69.80	15.80
Days to 50% flowering	95.00	121.00	65.27	7.49	94.76	9.02	68.90	12.80
Days to maturity	118.00	162.00	191.06	9.90	201.70	10.18	94.70	19.86
No. of tillers per plant	6.00	8.00	0.06	3.71	0.37	8.89	17.50	3.20
No. of productive tillers per plant	4.00	6.00	0.16	7.93	0.18	8.38	89.70	15.48
No. of fingers per plant	5.00	8.00	0.69	13.38	0.72	13.67	95.80	26.99
Finger length	4.86	10.30	2.77	21.42	2.80	21.53	98.90	43.89
1000 seed weight (g)	4.87	10.30	2.77	21.41	2.80	21.53	98.90	43.86
Ear head length per plant (cm)	12.03	18.57	3.04	11.32	3.05	11.35	99.50	23.27
Ear head weight per plant (g)	2.01	3.12	0.10	12.38	0.10	12.41	99.50	25.43
Harvest index	17.76	37.31	19.36	16.78	19.46	16.83	99.50	34.48
Grain yield per plant (g)	4.20	8.50	1.21	17.21	1.33	18.03	91.10	33.83

Table 6 : Percentage contribution of characters to total genetic divergence.

Source	Times ranked 1st	Contribution %
Plant height (cm)	6	1.57 %
Days to 50% flowering	8	1.65 %
Days to maturity	2	0.78 %
No. of tillers per plant	3	1.0 %
No. of productive tillers per plant	1	0.43 %
No. of fingers per plant	4	1.3 %
Finger length	21	9.09 %
Ear head length per plant (cm)	24	10 %
Ear head weight per plant (g)	89	38.53 %
1000 seed weight (g)	34	15.74 %
Harvest index	45	19.43 %
Grain yield per plant (g)	1	0.43 %

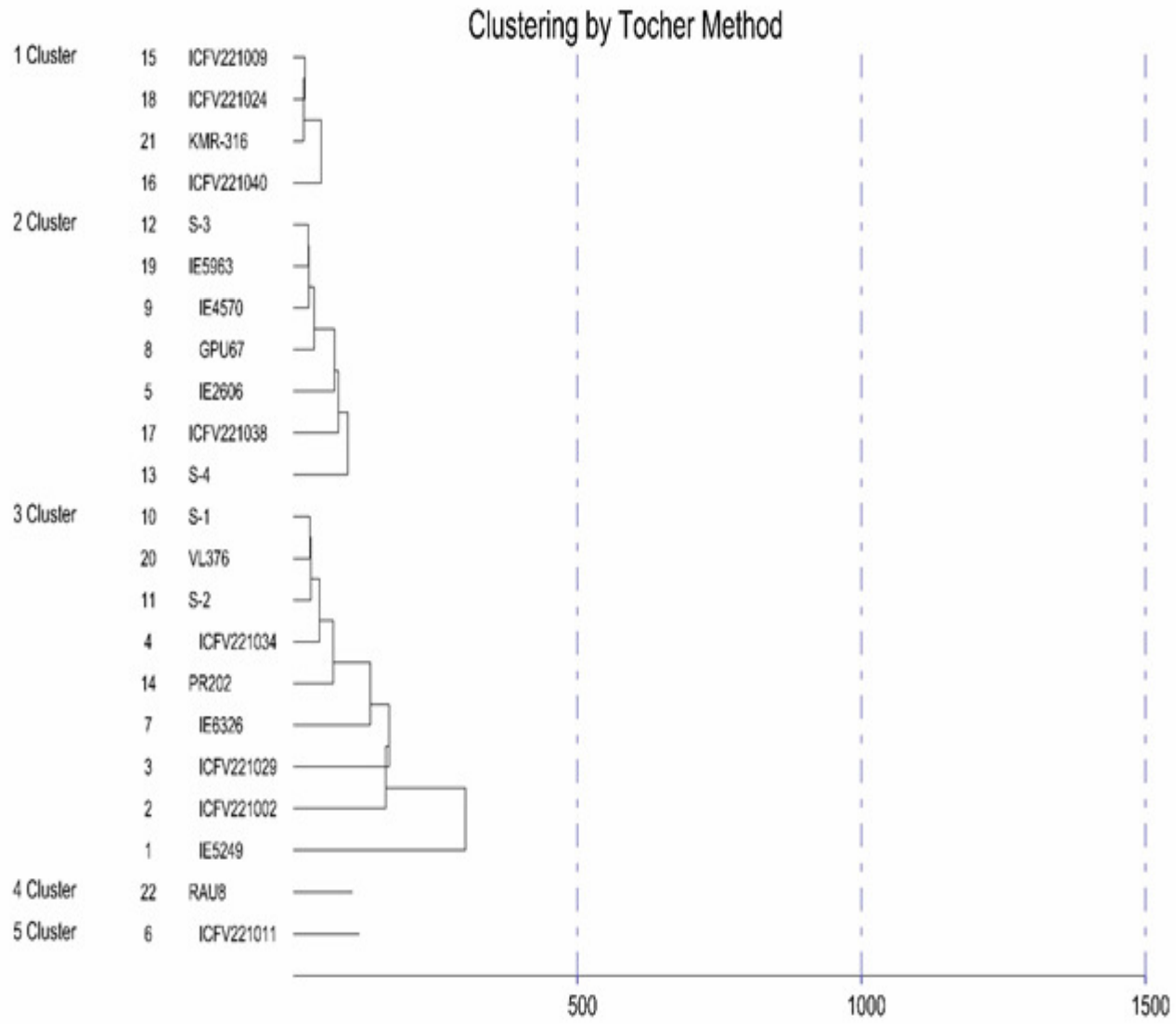

Fig. 1: Clustering pattern of 22 finger millet genotypes into five distinct groups using Tocher's method.

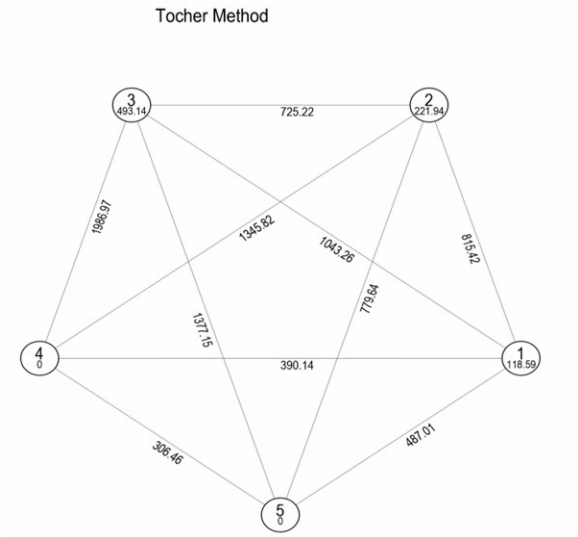

Fig. 2: Mahalanobis Euclidean distance using Tocher's method among 22 finger millet genotypes.

Author Contributions

Adarsh Ranjan: Conceptualization, Investigation, Data Curation. Sardar Sunil Singh: Supervision, Resources. Ashutosh Kumar: Writing - Original Draft, Formal Analysis, Visualization. Priyanka Kumari: Data Collection, Validation. Brajesh Kumar: Methodology. Birender Singh: Review & Editing. Tushar Ranjan: Software, Validation. Awdhesh Kumar: Statistical Analysis.

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Conflict of Interest

The authors declare no conflict of interest.

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