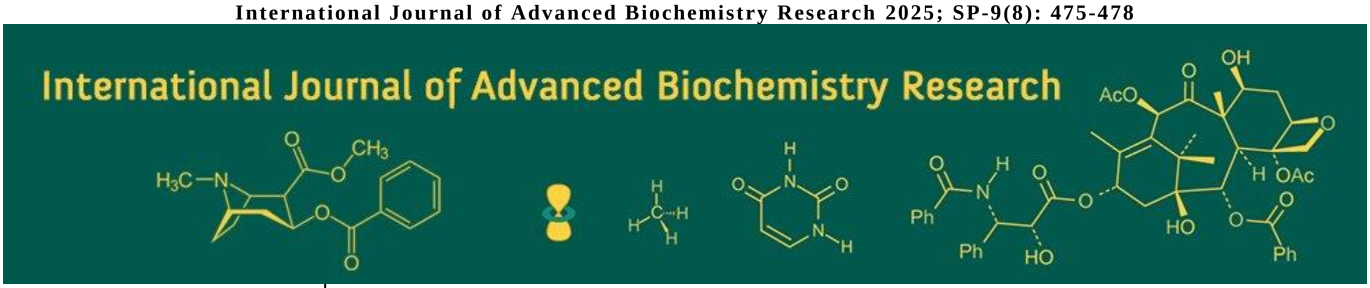

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Genetic divergence and cluster analysis of finger millet (*Eleusine coracana* L. Gaertn) genotypes based on multivariate traits

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Abstract

The present study assessed genetic divergence among 84 finger millet (*Eleusine coracana* L. Gaertn) genotypes using Mahalanobis' D^2 statistics, pooled over two years at Jagdalpur. The genotypes were grouped into six distinct clusters, indicating substantial genetic variability. Cluster IV had the highest number of genotypes (21), followed by Cluster II (19) and Cluster I and VI (12 each), suggesting a wide genetic base. The highest intra-cluster distance was observed in Cluster II (15.38), while the maximum inter-cluster divergence was between Cluster II and Cluster VI (40.87), highlighting their potential as parents for hybridization to exploit heterosis.Cluster mean analysis revealed that Cluster VI exhibited the highest grain yield (4.40 g/plant), along with superior performance in ear weight, biological yield, grain diameter, and harvest index, making it a promising group for yield improvement. Cluster II also recorded high grain yield (4.00 g), finger number, and harvest index. Cluster III showed the earliest maturity (100.47 days), indicating its suitability for breeding early-maturing varieties. Cluster IV stood out for tallest plants and longest fingers, while Cluster V had the highest number of fingers per ear and grain diameter. The observed inter-and intra-cluster diversity provides valuable insights for selecting genetically divergent parents to develop high-yielding, early-maturing, and nutritionally rich finger millet cultivars.

Keywords: Genetic divergence, cluster analysis, grain yield, heterosis, trait variability

Introduction

Finger millet (*Eleusine coracana* (L.) Gaertn.), commonly known as ragi in India and wimbi in East Africa, is a vital minor millet crop of the family Poaceae, subfamily Chloridoideae. It is an allotetraploid species (2n = 4x = 36) with the genomic constitution AABB, believed to have originated from its wild progenitor *Eleusine coracana* ssp. *africana* in the Ethiopian highlands (Mirza & Marla, 2020; Hittalmani *et al.*, 2004) [14, 9]. The crop was introduced to the Indian subcontinent over 3, 000 years ago and has since become an integral component of traditional farming systems, especially in rainfed and marginal lands.

Finger millet is highly adaptable, growing across a wide range of agro-climatic conditions, from sea level to elevations of 3, 000 meters, and thrives in areas with annual rainfall ranging from 350 to 1000 mm (Baath *et al.*, 2018) [3]. It follows the C_4 photosynthetic pathway, which enhances water-and nutrient-use efficiency, making it particularly suited for cultivation in drought-prone and low-input environments (Brutnell *et al.*, 2010; Warner & Edwards, 1988) [4, 21]. These traits underscore its potential as a climate-resilient crop, suitable for semi-arid regions in both Africa and Asia.

Nutritionally, finger millet surpasses many staple cereals. It is notably rich in calcium (~0.34%), dietary fiber (18%), protein (6-13%), along with essential micronutrients such as iron and zinc, and contains significant levels of bioactive compounds like polyphenols and phytates (Chandra *et al.*, 2016; Upadhyaya *et al.*, 2011) [6, 20]. Its consumption is associated with several health benefits, including anti-diabetic, anti-cancer, and cholesterol-lowering effects, and it contributes to the management of osteoporosis, anemia, and cardiovascular diseases (Devi *et al.*, 2011; Chandrasekara and Shahidi, 2011; Puranik *et al.*, 2017; Kumar *et al.*, 2021) [8, 7, 18, 11]. Owing to its impressive nutritional composition, the U.S. National Research Council (1996) [15] has recognized finger millet as a potential "super cereal" for the future.

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Despite these advantages, finger millet remains a neglected and underutilized crop, receiving limited attention in terms of genetic improvement, especially for traits like yield potential, stress tolerance, and nutritional enhancement. Nevertheless, considerable genetic diversity is present among traditional landraces, improved varieties, and wild relatives, offering immense opportunities for crop improvement (Ceasar and Ignacimuthu, 2011; Takan *et al.*, 2012) [5, 19].

In this context, the present study was undertaken to evaluate the agronomic performance of a diverse set of finger millet genotypes under rainfed conditions. The objective was to identify genetically superior lines with potential for utilization in breeding strategies focused on enhancing productivity, stress resilience, and nutritional value, particularly in marginal agro-ecosystems.

Materials and Methods

The present investigation was carried out during the kharif seasons of 2019 and 2020 at the Research cum Instructional Farm, S.G. College of Agriculture and Research Station, Jagdalpur. A total of 84 diverse finger millet genotypes**,** including four standard checks, were evaluated using an Augmented Randomized Block Design (ARBD), consisting of eight blocks, each comprising 10 test entries and four replicated checks. Each genotype grown in two rows of 3 m length at 22.5 cm spacing under rainfed conditions, following standard agronomic practices. Data were recorded on a total of 14 traits, including (including days to 50% flowering, days to maturity, plant height, number of tillers, finger length, finger width, ear weight, number of fingers, grain density, test weight, fodder yield, biological yield, grain yield, and harvest index). Observations were made on competitive plants in each entry, and check varieties were used for environmental adjustment as per the augmented design analysis. The pooled data from both years were used to perform Mahalanobis D^2 cluster analysis to assess the genetic divergence among genotypes. Prior to clustering, quantitative data were standardized, and the analysis was based on the pooled means of genotypes across the two years.

Results and Discussion

The Mahalanobis' D^2 statistics pooled over two years grouped the 84 finger millet genotypes into six distinct clusters, indicating the presence of considerable genetic diversity among the evaluated materials (Table 1). Cluster IV contained the highest number of genotypes (21), followed by Cluster II with 19 genotypes and Cluster I with 12 genotypes. Cluster VI also comprised 12 genotypes, whereas Cluster V and Cluster III included 11 and 9 genotypes, respectively. The distribution of genotypes across clusters was non-random, suggesting a broad genetic base. Notably, Cluster IV, which held the maximum entries, included genotypes such as GEC 398, GEC 420, GEC 487, and C.G. Ragi-2*, several of which displayed superior performance for yield and nutritional traits. Cluster II, with 19 genotypes, was also diverse, including entries like GEC 415, GEC 496, and GPU-28*, indicating their genetic distinctiveness. Promising genotypes like GPU-67* and GEC 105, found in Cluster I, and GEC 144 and GEC 503 in Cluster III, showed potential for use in crossing programs due to their placement in genetically distinct clusters. The relatively smaller clusters (III and V) still represent valuable genetic diversity and could serve as potential parents in hybridization to exploit maximum heterosis. This clustering pattern provides important insights for the selection of genetically divergent parents to develop superior segregating populations and enhance genetic gain in finger millet improvement programs. Similar finding was reported by Negi *et al.*, (2017) [16]; Anteneh *et al.*, (2019) [1]

Inter-and Intra-Cluster Distance Analysis

The pooled Mahalanobis' D^2 distance values revealed substantial genetic divergence among the six clusters of finger millet genotypes (Table 2). The intra-cluster distances, represented along the diagonal, reflect the genetic variability within each cluster. These ranged from 11.02 (Cluster I) to 15.38 (Cluster II), indicating that Cluster II had the highest internal diversity, followed closely by Cluster IV (13.72) and Cluster VI (12.61), while Cluster I exhibited the least intra-cluster variability (11.02), implying a relatively homogeneous group. The inter-cluster distances were uniformly higher than the intra-cluster values, affirming that the clusters are genetically distinct. The maximum inter-cluster distance was recorded between Cluster II and Cluster VI (40.87), followed by Cluster III and Cluster IV (33.30), and Cluster III and Cluster VI (33.22). These larger distances indicate the presence of substantial genetic divergence and suggest that genotypes from these clusters may serve as ideal parents in hybridization programs to exploit heterosis. Moderate inter-cluster distances were observed between Cluster IV and Cluster V (28.17), Cluster I and Cluster IV (26.59), and Cluster II and Cluster IV (28.66), highlighting additional potential cross combinations for generating genetic variability. Conversely, the lowest inter-cluster distance was between Cluster I and Cluster III (16.67), suggesting relatively close genetic relatedness between these clusters. Overall, the results demonstrate that genotypes from highly divergent clusters, particularly Cluster II and Cluster VI, or Cluster III and Cluster IV, can be effectively utilized as parental lines to generate transgressive segregants with enhanced agronomic performance. The clear differentiation between clusters also confirms the reliability of the grouping obtained through cluster analysis. Similar finding was reported by Kandel *et al.*, (2020) [10]; Anuradha *et al.*, (2023) [2]

Cluster Mean Performance for Grain Yield and Yield Components (Pooled Data)

The pooled cluster mean analysis for grain yield and its related traits in finger millet revealed considerable variability among the six clusters (Table 3), reflecting the extent of genetic divergence and potential utility of different clusters for targeted trait improvement. Cluster VI exhibited the highest grain yield (4.40 g/plant), followed closely by Cluster II (4.00 g) and Cluster V (3.85 g). Cluster VI also showed superior performance for ear weight (7.58 g), biological yield (14.08 g), and grain diameter (88.72), indicating its overall superiority in yield-contributing traits. Furthermore, it recorded the highest harvest index (30.88%), making it a promising group for yield enhancement. Cluster II recorded the highest number of fingers per ear (5.08) and high harvest index (28.31%), suggesting it could be exploited for improving grain yield through improved partitioning efficiency. Similarly, Cluster V recorded the highest number of fingers per ear (5.79) and performed well in terms of grain diameter (89.57) and test weight (3.44 g), indicating potential for improving grain size and weight.

Cluster IV was characterized by tall plants (92.70 cm) and longest fingers (6.91 cm), along with high values for ear weight (7.47 g) and number of fingers per ear (5.50), suggesting suitability for improving panicle architecture and biomass traits. In contrast, Cluster III had the lowest days to flowering (68.88) and maturity (100.47), indicating its potential use for earliness and development of early-maturing varieties. However, it showed relatively lower performance for grain yield (3.44 g) and its contributing traits. Cluster I showed moderate performance across traits but had relatively low grain yield (3.36 g) and biological yield (13.15 g). This cluster may serve as a genetic reservoir for specific traits like early flowering and moderate plant height. Overall, the diversity in mean values across clusters suggests that crossing genotypes from high-yielding clusters (like VI and II) with those showing early maturity (Cluster III) or tall and vigorous growth (Cluster IV) could lead to transgressive segregants combining desirable traits. This information is crucial for selecting parents in hybridization programs aimed at improving multiple traits simultaneously. Similar findings was reported by Kumari and Singh (2015) [12]; Mahanthesha *et al.*, (2017) [13]; Pali *et al.* (2022) [17].

Table 1: Number of genotypes in each cluster based in Mahalanobis' D2 value in finger millet at Jagdalpur pooled

Clusters	Number of genotypes	Genotypes
I	12	IC0476541, IC0476864, IC0476299, IC0477195, IC0477963, IC0476378, GEC 362, GEC 105, GEC 350, IC0476913, GEC 85, GPU-67*
II	19	GEC 252, IC0476937, IC0477405, IC0477325, GEC 127, IC0476753, IC0477591, IC0587989, GEC 415, GEC 54, GEC 247, GEC 496, GEC 145, IC0476959-X, GEC 473, GEC 148, GEC 338, GEC 134, GPU-28*
III	9	GEC 144, GEC 260, GEC 503, GEC 319, GEC 58, GEC 161, GEC 170, GEC 446, GEC 112
IV	21	GEC 398, GEC 420, IC0477491, GEC 378, IC0477654, GEC 369, GEC 487, GEC 238, GEC 321, GEC 511, GEC 485, GEC 275, GEC 331, GEC 417, GEC 353, GEC 71, GEC 488, GEC 103, GEC 341, IR-1*, C.G. Ragi-2*
V	11	GEC 440, IC0587982, GEC 197, IC0587947, GEC 342, GEC 67, GEC 386, GEC 61, GEC 483, GEC 47, GEC 508
VI	12	IC0477632, IC0477681, IC0476921, GEC 174, IC0477951, IC0477604, GEC 421, GEC 432, GEC 396, GEC 469, GEC 27, GEC 414

Table 2: Pooled Mean inter and intra-cluster D2 value values in 6 clusters of fingers Millet

Clusters	I	II	III	IV	V	VI
I	11.02					
II	23.40	15.38				
III	16.67	25.24	11.04			
IV	26.59	28.66	33.30	13.72		
V	20.87	38.13	20.85	28.17	12.81	
VI	23.70	40.87	33.22	23.12	17.45	12.61

Table 3: Pooled Cluster mean component of grain yield and its components of finger millet at Jagdalpur

Cluster	DF	DM	PH	FL	FW	NTP	NFE	GD	EWT	BY	FY	HI	TW	GY
1	78.69	111.47	71.35	5.52	0.93	2.41	4.90	73.73	6.07	13.15	9.80	25.62	3.35	3.36
2	76.75	109.49	78.73	5.70	0.84	2.40	5.08	51.90	6.06	14.04	10.05	28.31	3.32	4.00
3	68.88	100.47	78.91	5.11	0.80	2.14	4.52	73.97	5.22	12.68	9.25	26.89	3.39	3.44
4	89.21	122.21	92.70	6.91	0.82	2.42	5.50	69.27	7.47	13.43	9.86	26.68	3.29	3.58
5	77.05	109.68	84.24	6.09	0.90	2.09	5.79	89.57	7.52	13.21	9.37	28.58	3.44	3.85
6	89.24	121.41	81.00	6.78	0.88	2.38	5.64	88.72	7.58	14.08	9.70	30.88	3.43	4.40

Conclusion

The present study clearly demonstrates substantial genetic diversity among 84 finger millet genotypes based on Mahalanobis' D^2 analysis, which grouped the genotypes into six distinct clusters. The wide range of intra-and inter-cluster distances confirms the existence of significant divergence, which can be effectively exploited for hybridization and genetic improvement. Clusters II and VI, which exhibited the highest inter-cluster distance (40.87), are particularly promising for developing heterotic hybrids due to their genetic distinctiveness. Cluster VI emerged as the most promising group for grain yield and associated traits, while Cluster III showed potential for breeding early-maturing varieties. Cluster IV and Cluster V exhibited superiority in plant height, finger length, and grain attributes, indicating their value in trait-specific improvement. The divergence in cluster mean performances suggests that strategic crossing between genotypes from high-yielding clusters (VI and II) and those possessing early maturity (Cluster III) or desirable morphological features (Cluster IV and V) could produce transgressive segregants with improved yield, adaptability, and maturity. These findings provide a valuable foundation for parent selection in finger millet breeding programs aimed at enhancing grain yield, stress tolerance, and phenological adaptation under rainfed conditions.

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