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MORPHOLOGICAL CHARACTERIZATION AND DIVERSITY ANALYSIS OF FINGER MILLET (*Eleusine coracana* L. GAERTN.) GERMPLASM USING STANDARDIZED DUS DESCRIPTORS

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ABSTRACT

Finger millet (*Eleusine coracana* (L.) Gaertn.) is a climate-resilient and nutritionally important cereal crop whose effective genetic improvement depends on accurate characterization of available germplasm. The present study was undertaken to characterize 50 finger millet genotypes using fourteen standardized Distinctness, Uniformity and Stability (DUS) descriptors given by the Protection of Plant Varieties and Farmers' Rights Authority (PPV&FRA) and to assess morphological diversity among the evaluated genotypes. The experiment was conducted during the *kharif* 2023 season at the Agricultural Research Station, Muvaliya Farm, Anand Agricultural University, Dahod, Gujarat. Morphological observations were recorded for plant architecture, leaf, stem, inflorescence, finger and seed descriptors and hierarchical clustering was performed using Gower's distance and the unweighted pair-group method with arithmetic averages (UPGMA). Considerable variation was observed for most qualitative and quantitative descriptors. Erect growth habit (90%), absence of pigmentation at the leaf juncture (84%), leaf sheath pubescence (80%), long flag leaf blade length (80%), medium flag leaf blade width (90%), absence of culm branching (60%), medium peduncle length (68%), light green glume colour (54%), open ear shape (48%), absence of finger branching (68%), light brown seed colour (62%) and round seed shape (68%) were the predominant descriptor states. Finger multiple whorl was monomorphic, with all genotypes exhibiting absence of this trait. Hierarchical cluster analysis grouped the 50 genotypes into four major clusters, indicating substantial morphological diversity within the germplasm. The observed diversity and unique combinations of DUS descriptor states provide a reliable basis for varietal identification, germplasm documentation, plant variety protection under the PPV&FR Act and the selection of morphologically diverse parental lines for future finger millet breeding programmes.

Key words : *Eleusine coracana*, DUS descriptors, Morphological characterization, Germplasm diversity, UPGMA clustering, PPV&FR.

Introduction

Finger millet (*Eleusine coracana* (L.) Gaertn.) is an important small millet crop cultivated predominantly in the semi-arid and sub-humid regions of Asia and Africa. The crop is recognized for its exceptional adaptability to drought, low soil fertility and erratic rainfall conditions, making it highly suitable for climate-resilient agriculture.

In addition to its agronomic resilience, finger millet possesses superior nutritional quality, particularly its high calcium, iron, dietary fibre and polyphenol content, which has led to renewed interest in the crop for addressing food and nutritional security challenges. Recent reviews have emphasized the increasing importance of finger millet as a functional food crop and a promising component of sustainable farming systems (Gebreyohannes *et al.*, 2024;

Kaur *et al.*, 2024).

The effective utilization of finger millet germplasm in crop improvement programmes depends on accurate characterization and documentation of available genetic resources. In finger millet, traits associated with plant architecture, inflorescence structure, finger characteristics and seed attributes serve as important diagnostic features for distinguishing genotypes and assessing morphological diversity. Morphological characterization remains the primary and most economical approach for the preliminary assessment of germplasm diversity. Morphological descriptors, including qualitative and quantitative traits, provide an effective and economical approach for preliminary characterization and identification of genotypes. Such characterization facilitates the identification of unique accessions, elimination of duplicates, selection of parental lines, and efficient management of germplasm collections (Gebreyohannes *et al.*, 2024).

Distinctness, Uniformity and Stability (DUS) testing constitutes the cornerstone of varietal identification and registration under plant variety protection systems. In India, DUS testing is conducted under the provisions of the Protection of Plant Varieties and Farmers' Rights (PPV&FR) Act, which prescribes standardized morphological descriptors for evaluating candidate varieties. The use of uniform descriptor states enables reliable discrimination among genotypes and ensures consistency in varietal registration and protection. Despite the increasing application of molecular markers in crop characterization, morphological DUS descriptors continue to be the internationally accepted basis for testing distinctness, uniformity and stability of new varieties. Several studies have reported substantial phenotypic variability in finger millet for agronomic, nutritional and adaptive traits (Hansalia and Pali, 2024; Gebreyohannes *et al.*, 2024; Kaur *et al.*, 2024). However, comparatively fewer investigations have focused specifically on DUS based characterization, particularly in diverse Indian germplasm collections (Mishra *et al.*, 2025). Therefore, the present investigation was undertaken to characterize fifty finger millet genotypes using standardized DUS descriptors comprising qualitative and quantitative morphological traits, to assess the extent of phenotypic variability and to identify genotypes exhibiting distinct morphological attributes. The information generated from this study will contribute towards germplasm documentation, varietal identification, protection of plant varieties and selection of diverse parental materials for future finger millet improvement programmes.

Materials and Methods

Experimental material and site

The experimental material consisted of 50 finger millet genotypes (Table 1). The experiment was conducted during the *kharif* 2023 season at the Agricultural Research Station, Muvaliya Farm, Anand Agricultural University, Dahod, Gujarat, located at 22°83' N latitude, 74°26' E longitude, with an elevation of 286 m above mean sea level. The experimental site belongs to Agro-Climatic Zone III (Middle Gujarat) and is characterized by a semi-arid tropical climate. The region receives an average annual rainfall of approximately 786 mm, with the majority of precipitation occurring during the southwest monsoon. The soil at the site is predominantly deep to heavy black, characterized by low nitrogen availability and high moisture-holding capacity, making it well suited for the cultivation of rainfed crops.

DUS traits studied

During the crop growth period, observations were recorded for different morphological descriptors related to Distinctness, Uniformity and Stability (DUS) characterization. The traits evaluated included plant growth habit, pigmentation at leaf juncture, leaf sheath pubescence, glume colour, culm branching pattern, flag leaf blade length and width, peduncle length, ear shape, finger branching pattern, position of branching, occurrence of multiple whorls, seed colour and seed shape. The assessment of each genotype was carried out following standardized descriptor states and trait-specific guidelines prescribed by the Protection of Plant Varieties and Farmers' Rights Authority (PPV&FRA, 2015) for DUS testing. Morphological observations were recorded at appropriate crop growth stages, beginning from the seedling phase until maturity and harvesting, to ensure accurate characterization of the genotypes.

For certain traits, measurements were taken from an individual plant (MS) such as Flag leaf: Blade length (cm), Flag leaf: Blade width (cm) and Peduncle: Length (cm). Visual assessments by a single observation of a group of plants or parts of plants (VG) were conducted to evaluate traits including Plant: Growth Habit, Leaf Sheath Pubescence, Glume: Colour, Ear: Shape, Finger: Branching, Finger: Position of branching, Finger: Multiple whorl, Seed: Colour and Seed: Shape. Visual assessments by observations of individual plants or parts of plants (VS) were conducted to evaluate traits such as Plant: Pigmentation at leaf juncture and Stem: Culm branching.

Statistical analysis

To evaluate the genetic relationships and morphological diversity among the finger millet genotypes,

Table 1 : List of finger millet genotypes used in the experiment.

S. no.	Genotype	Source/Origin (State/Country)
1.	PCGF-4	AICRP, GKVK, Bengaluru
2.	PCGF-8	
3.	PCGF-9	
4.	PCGF-10	
5.	PCGF-12	
6.	PCGF-13	
7.	PCGF-15	
8.	PCGF-19	
9.	PCGF-21	
10.	PCGF-24	
11.	PCGF-27	
12.	PCGF-31	
13.	PCGF-32	
14.	PCGF-36	
15.	PCGF-37	
16.	PCGF-42	
17.	PCGF-43	
18.	PCGF-44	
19.	PCGF-45	
20.	PCGF-46	
21.	FMA-5	
22.	FMA-7	
23.	FMA-11	
24.	FMA-14	
25.	FMA-17	
26.	FMA-18	
27.	FMA-19	
28.	FMA-21	
29.	GN8	HMRS, NAU, Navsari
30.	FMA-23	AICRP, GKVK, Bengaluru
31.	CFMV 2	HMRS, NAU, Navsari
32.	FMA-25	AICRP, GKVK, Bengaluru
33.	FMA-26	
34.	FMA-29	
35.	FMA-33	
36.	FMA-34	
37.	FMA-35	

*Table 1 continued...***Table 1 continued...**

38.	FMA-36	
39.	FMA-37	
40.	FMA-40	
41.	FMA-41	
42.	FMA-42	
43.	FMA-43	
44.	FMA-45	
45.	FMA-47	
46.	FMA-48	
47.	FMA-54	
48.	FMA-55	
49.	FMA-59	
50.	FMA-60	

an unweighted pair-group method with arithmetic averages (UPGMA) cluster analysis was performed. Because the dataset comprised mixed data types (quantitative and qualitative traits), pairwise dissimilarity matrices were computed using Gower's general similarity coefficient (1 - similarity). Hierarchical agglomerative clustering via the UPGMA algorithm was subsequently applied to the Gower distance matrix. The extraction of hierarchical clustering results and visualization of the resulting dendrogram were conducted using the R package "factoextra" (Kassambara and Mundt, 2026) in the R environment using RStudio, running R version 4.6.1 software (Team RC, 2026).

Results

The fifty finger millet genotypes exhibited considerable variation for both qualitative and quantitative DUS descriptors, indicating the presence of substantial morphological diversity within the experimental material (Table 2). The standardized DUS descriptors enabled clear differentiation among genotypes based on plant architecture, leaf characteristics, inflorescence morphology, finger traits and seed attributes. Such variation is valuable for varietal identification, germplasm documentation and the selection of diverse parental lines in breeding programmes.

Plant architecture related descriptors

The descriptor plant growth habit exhibited variation among the fifty finger millet genotypes. The majority of the genotypes (45 genotypes) exhibited an erect growth habit, whereas 5 genotypes showed a decumbent growth habit. None of the genotypes were categorized under the prostrate growth habit (Table 2). Genotypes exhibiting

Table 2 : Frequency distribution of morphological and seed traits in finger millet genotypes as per DUS testing guidelines standardized by PPV&FR.

S. no.	Trait	Class	Score	Frequency	Percentage (%)	Name of genotypes
Plant architecture related descriptors						
1	Plant: Growth Habit	Erect	1	45	90	PCGF-4, PCGF-8, PCGF-10, PCGF-12, PCGF-13, PCGF-15, PCGF-21, PCGF-24, PCGF-27, PCGF-31, PCGF-32, PCGF-36, PCGF-37, PCGF-42, PCGF-43, PCGF-44, PCGF-45, PCGF-46, FMA-5, FMA-7, FMA-11, FMA-14, FMA-17, FMA-19, FMA-21, FMA-23, GN 8, FMA-25, FMA-26, FMA-29, FMA-33, FMA-34, FMA-35, FMA-36, FMA-37, FMA-40, FMA-41, FMA-42, FMA-43, FMA-45, FMA-47, FMA-54, FMA-55, FMA-59, FMA-60
		Decumbent	5	5	10	PCGF-9, PCGF-19, FMA-18, CFMV 2, FMA-48
		Prostrate	7	0	0	-
2	Plant: Pigmentation at leaf juncture	Absent	1	42	84	PCGF-9, PCGF-10, PCGF-12, PCGF-13, PCGF-19, PCGF-21, PCGF-27, PCGF-31, PCGF-32, PCGF-42, PCGF-43, PCGF-44, PCGF-45, PCGF-46, FMA-5, FMA-7, FMA-11, FMA-14, FMA-17, FMA-18, FMA-19, FMA-21, GN 8, CFMV 2, FMA-25, FMA-26, FMA-29, FMA-33, FMA-34, FMA-35, FMA-36, FMA-37, FMA-40, FMA-41, FMA-42, FMA-43, FMA-45, FMA-47, FMA-48, FMA-54, FMA-55, FMA-59
		Present	9	8	16	PCGF-4, PCGF-8, PCGF-15, PCGF-24, PCGF-36, PCGF-37, FMA-23, FMA-60
Leaf descriptors						
3	Leaf Sheath Pubescence	Absent	1	10	20	PCGF-42, PCGF-43, FMA-7, FMA-18, GN 8, CFMV 2, FMA-25, FMA-29, FMA-33, FMA-41
		Present	9	40	80	PCGF-4, PCGF-8, PCGF-9, PCGF-10, PCGF-12, PCGF-13, PCGF-15, PCGF-19, PCGF-21, PCGF-24, PCGF-27, PCGF-31, PCGF-32, PCGF-36, PCGF-37, PCGF-44, PCGF-45, PCGF-46, FMA-5, FMA-11, FMA-14, FMA-17, FMA-19, FMA-21, FMA-23, FMA-26, FMA-34, FMA-35, FMA-36, FMA-37, FMA-40, FMA-42, FMA-43, FMA-45, FMA-47, FMA-48, FMA-54, FMA-55, FMA-59, FMA-60
4	Flag leaf: Blade length (cm)	Short (<15)	1	0	0	-
		Medium (15.0-30.0)	3	10	20	PCGF-15, PCGF-36, PCGF-37, PCGF-43, FMA-7, FMA-11, GN 8, CFMV 2, FMA-25, FMA-60
		Long (30.1-45.0)	5	40	80	PCGF-4, PCGF-8, PCGF-9, PCGF-10, PCGF-12, PCGF-13, PCGF-19, PCGF-21, PCGF-24, PCGF-27, PCGF-31, PCGF-32, PCGF-42, PCGF-44, PCGF-45, PCGF-46, FMA-5, FMA-14, FMA-

Table 2 continued...

Table 2 continued...

						17, FMA-18, FMA-19, FMA-21, FMA-23, , FMA-26, FMA-29, FMA-33, FMA-34, FMA-35, FMA-36, FMA-37, FMA-40, FMA-41, FMA-42, FMA-43, FMA-45, FMA-47, FMA-48, FMA-54, FMA-55, FMA-59
		Very long (>45.0)	7	0	0	-
5	Flag leaf: Blade width (cm)	Narrow (<1.0)	3	5	10	PCGF-15, PCGF-37, PCGF-45, FMA-42, FMA-59
		Medium (1.0-2.0)	5	45	90	PCGF-4, PCGF-8, PCGF-9, PCGF-10, PCGF-12, PCGF-13, PCGF-19, PCGF-21, PCGF-24, PCGF-27, PCGF-31, PCGF-32, PCGF-36, PCGF-42, PCGF-43, PCGF-44, PCGF-46, FMA-5, FMA-7, FMA-11, FMA-14, FMA-17, FMA-18, FMA-19, FMA-21, GN 8, FMA-23, CFMV 2, FMA-25, FMA-26, FMA-29, FMA-33, FMA-34, FMA-35, FMA-36, FMA-37, FMA-40, FMA-41, FMA-43, FMA-45, FMA-47, FMA-48, FMA-54, FMA-55, FMA-60
		Wide (>2.0)	7	0	0	-
Stem descriptors						
6	Stem: Culm branching	Absent	1	30	60	PCGF-4, PCGF-8, PCGF-9, PCGF-12, PCGF-15, PCGF-19, PCGF-24, PCGF-32, PCGF-36, PCGF-42, PCGF-44, PCGF-45, FMA-5, FMA-7, FMA-14, FMA-21, GN 8, CFMV 2, FMA-25, FMA-26, FMA-29, FMA-34, FMA-37, FMA-40, FMA-41, FMA-43, FMA-45, FMA-48, FMA-55, FMA-60
		Present	9	20	40	PCGF-10, PCGF-13, PCGF-21, PCGF-27, PCGF-31, PCGF-37, PCGF-43, PCGF-46, FMA-11, FMA-17, FMA-18, FMA-19, FMA-23, FMA-33, FMA-35, FMA-36, FMA-42, FMA-47, FMA-54, FMA-59
7	Peduncle: Length (cm)	Very short (<10)	1	0	0	-
		Short(10.0-20)	3	16	32	PCGF-4, PCGF-8, PCGF-9, PCGF-31, FMA-7, FMA-21, GN 8, FMA-23, CFMV 2, FMA-26, FMA-34, FMA-35, FMA-37, FMA-45, FMA-48, FMA-54
		Medium (20.1-30)	5	34	68	PCGF-10, PCGF-12, PCGF-13, PCGF-15, PCGF-19, PCGF-21, PCGF-24, PCGF-27, PCGF-32, PCGF-36, PCGF-37, PCGF-42, PCGF-43, PCGF-44, PCGF-45, PCGF-46, FMA-5, FMA-11, FMA-14, FMA-17, FMA-18, FMA-19, FMA-25, FMA-29, FMA-33, FMA-36, FMA-40, FMA-41, FMA-42, FMA-43, FMA-47, FMA-55, FMA-59, FMA-60
		Long(30.1-40)	7	0	0	-
		Very long(>40)	9	0	0	-

Table 2 continued...

Table 2 continued...

Inflorescence descriptors						
8	Glume: Colour	White	1	0	0	-
		Light green	3	27	54	PCGF-4, PCGF-9, PCGF-10, PCGF-12, PCGF-21, PCGF-24, PCGF-42, PCGF-43, PCGF-44, PCGF-45, PCGF-46, FMA-5, FMA-14, FMA-17, FMA-19, FMA-21, GN 8, CFMV 2, FMA-29, FMA-33, FMA-34, FMA-37, FMA-41, FMA-48, FMA-54, FMA-55, FMA-59
		Dark green	5	0	0	-
		Light purple	7	22	44	PCGF-8, PCGF-13, PCGF-15, PCGF-19, PCGF-27, PCGF-31, PCGF-32, PCGF-36, FMA-7, FMA-11, FMA-18, FMA-23, FMA-25, FMA-26, FMA-35, FMA-36, FMA-40, FMA-42, FMA-43, FMA-45, FMA-47, FMA-60
		Dark purple	9	1	2	PCGF-37
9	Ear: Shape	Fist type	1	0	0	-
		Compact	3	4	8	PCGF-13, GN 8, FMA-33, FMA-34
		Semi compact	5	21	42	PCGF-8, PCGF-12, PCGF-15, PCGF-19, PCGF-21, PCGF-24, PCGF-32, PCGF-46, FMA-5, FMA-7, FMA-11, FMA-17, FMA-19, CFMV 2, FMA-29, FMA-41, FMA-42, FMA-48, FMA-54, FMA-59, FMA-60
		Open	7	24	48	PCGF-4, PCGF-9, PCGF-10, PCGF-31, PCGF-36, PCGF-37, PCGF-42, PCGF-43, PCGF-44, PCGF-45, FMA-14, FMA-18, FMA-21, FMA-23, FMA-25, FMA-26, FMA-35, FMA-36, FMA-37, FMA-40, FMA-43, FMA-45, FMA-47, FMA-55
		Droopy	9	1	2	PCGF-27
Finger descriptors						
10	Finger: Branching	Absent	1	34	68	PCGF-4, PCGF-8, PCGF-10, PCGF-13, PCGF-15, PCGF-19, PCGF-21, PCGF-27, PCGF-31, PCGF-36, PCGF-37, PCGF-42, PCGF-44, PCGF-45, PCGF-46, FMA-7, FMA-11, FMA-14, FMA-18, GN 8, FMA-23, CFMV 2, FMA-26, FMA-29, FMA-34, FMA-35, FMA-41, FMA-42, FMA-43, FMA-45, FMA-48, FMA-54, FMA-55, FMA-60
		Present	9	16	32	PCGF-9, PCGF-12, PCGF-24, PCGF-32, PCGF-43, FMA-5, FMA-17, FMA-19, FMA-21, FMA-25, FMA-33, FMA-36, FMA-37, FMA-40, FMA-47, FMA-59
11	Finger: Position of branching	In thumb finger	3	16	100	PCGF-9, PCGF-12, PCGF-24, PCGF-32, PCGF-43, FMA-5, FMA-17, FMA-19, FMA-21, FMA-25, FMA-33, FMA-36, FMA-37, FMA-40, FMA-47, FMA-59
		In all the fingers	5	0	0	-

Table 2 continued...

Table 2 continued...

12	Finger: Multiple whorl	Absent	1	50	100	PCGF-4, PCGF-8, PCGF-9, PCGF-10, PCGF-12, PCGF-13, PCGF-15, PCGF-19, PCGF-21, PCGF-24, PCGF-27, PCGF-31, PCGF-32, PCGF-36, PCGF-37, PCGF-42, PCGF-43, PCGF-44, PCGF-45, PCGF-46, FMA-5, FMA-7, FMA-11, FMA-14, FMA-17, FMA-18, FMA-19, FMA-21, GN 8, FMA-23, CFMV 2, FMA-25, FMA-26, FMA-29, FMA-33, FMA-34, FMA-35, FMA-36, FMA-37, FMA-40, FMA-41, FMA-42, FMA-43, FMA-45, FMA-47, FMA-48, FMA-54, FMA-55, FMA-59, FMA-60
		Present	9	0	0	-
Seed descriptors						
13	Seed: Colour	White	2	8	16	PCGF-21, PCGF-24, PCGF-27, PCGF-31, PCGF-37, FMA-35, FMA-42, FMA-43
		Light Brown	4	31	62	PCGF-4, PCGF-8, PCGF-9, PCGF-10, PCGF-12, PCGF-13, PCGF-15, PCGF-19, PCGF-32, PCGF-36, PCGF-42, PCGF-43, PCGF-44, PCGF-45, PCGF-46, FMA-5, FMA-7, FMA-14, FMA-17, FMA-18, FMA-19, FMA-21, FMA-23, FMA-25, FMA-26, FMA-29, FMA-36, FMA-45, FMA-48, FMA-54, FMA-59
		Copper Brown	6	8	16	FMA-11, CFMV 2, FMA-37, FMA-40, FMA-41, FMA-47, FMA-55, FMA-60
		Dark Brown	8	13	6	GN 8, FMA-33, FMA-34
14	Seed: Shape	Round	1	34	68	PCGF-13, PCGF-19, PCGF-21, PCGF-24, PCGF-27, PCGF-31, PCGF-32, PCGF-36, PCGF-37, PCGF-42, PCGF-43, PCGF-44, PCGF-46, FMA-5, FMA-7, FMA-11, FMA-17, FMA-18, FMA-19, FMA-21, GN 8, FMA-23, CFMV 2, FMA-26, FMA-33, FMA-35, FMA-37, FMA-40, FMA-41, FMA-43, FMA-47, FMA-55, FMA-59, FMA-60
		Reniform	3	0	0	-
		Ovoid	5	16	32	PCGF-4, PCGF-8, PCGF-9, PCGF-10, PCGF-12, PCGF-15, PCGF-45, FMA-14, FMA-25, FMA-29, FMA-34, FMA-36, FMA-42, FMA-45, FMA-48, FMA-54

erect growth habit may be preferred for facilitating better light interception and crop management, whereas decumbent types can serve as valuable genetic resources for broadening morphological diversity.

Variation was also observed for pigmentation at the leaf juncture, where two descriptor states were recorded (Fig. 1). The absence of pigmentation was predominant, observed in 42 genotypes (84%), whereas 8 genotypes (16%) showed the presence of pigmentation at the leaf juncture (Table 2). Presence of pigmentation at the leaf juncture represents a stable morphological marker that

can assist in genotype identification and selection of diverse parental combinations.

Leaf descriptors

The descriptor leaf sheath pubescence showed variation among the evaluated genotypes. Out of the fifty genotypes, 40 genotypes (80%) exhibited the presence of pubescence, whereas 10 genotypes (20%) showed absence of pubescence (Table 2). The predominance of pubescent leaf sheath among the germplasm indicates that this trait is a common morphological feature in the evaluated material. However, the contrasting non-

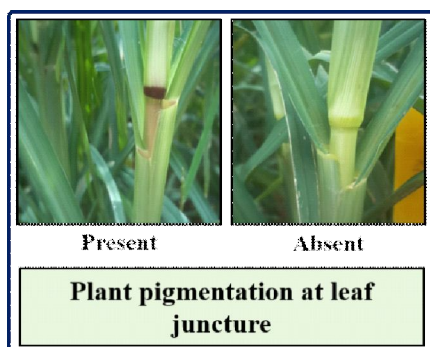


Fig. 1 : DUS descriptor states for plant pigmentation at leaf juncture in finger millet.

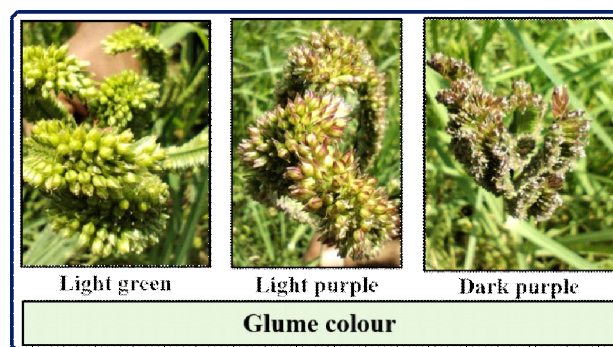


Fig. 2 : DUS descriptor states for glume colour in finger millet.

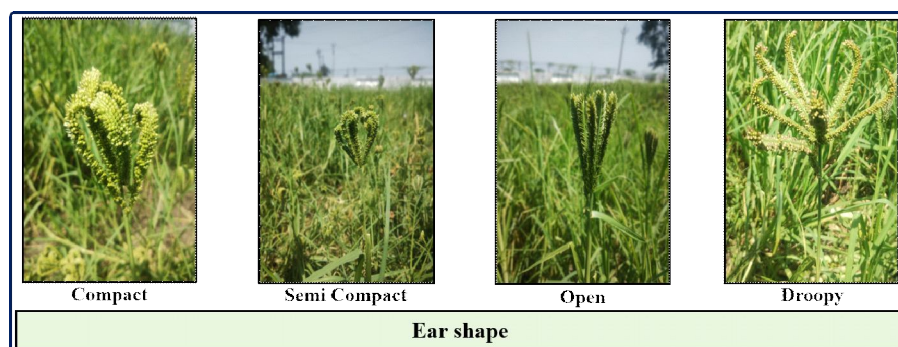


Fig. 3 : DUS descriptor states for ear shape in finger millet.

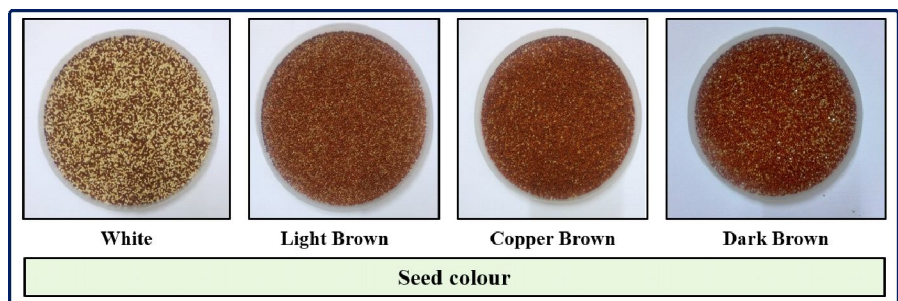


Fig. 4 : DUS descriptor states for seed colour in finger millet.

pubescent genotypes can serve as useful diagnostic materials for distinguishing varieties during DUS characterization.

Variation was also observed for flag leaf blade length, with genotypes distributed into different descriptor classes. A majority of the genotypes (40 genotypes) were categorized as having long flag leaf blades (30.1-45.0 cm), while 10 genotypes (20%) exhibited medium flag leaf blade length (15.0-30.0 cm). None of the genotypes were classified under short (<15 cm) or very long (>45 cm) categories (Table 2). The predominance of long flag leaves indicates limited variation for this descriptor within the studied germplasm; however, the available variation can still contribute to genotype identification and selection.

For flag leaf blade width, most of the genotypes (45; 90%) were grouped under the medium category (1.0-2.0 cm), whereas 5 genotypes (10%) possessed narrow flag

leaves (<1.0 cm). No genotype exhibited a wide flag leaf blade (>2.0 cm) (Table 2). The occurrence of narrow and medium leaf width categories indicates the presence of variability for leaf morphology among the evaluated genotypes.

Stem descriptors

The descriptor culm branching exhibited two distinct states among the evaluated genotypes. The absence of culm branching was observed in 30 genotypes (60%), whereas 20 genotypes (40%) exhibited culm branching (Table 2).

Variation was also observed for peduncle length, with the evaluated genotypes falling into two descriptor categories. The majority of the genotypes (34; 68%) possessed

medium peduncle length (20.1-30.0 cm), whereas 16 genotypes (32%) were classified as having short peduncle length (10.0-20.0 cm). None of the genotypes belonged to the very short (<10 cm), long (30.1-40.0 cm), or very long (>40.0 cm) categories (Table 2).

Inflorescence descriptors

The descriptor glume colour showed four distinct expression states among the evaluated genotypes (Fig. 2). Light green glumes (RHS No. 149A) were the most frequently observed, occurring in 27 genotypes (54%), followed by light purple glumes (RHS No. 59C) in 22 genotypes (44%). Only one genotype (2%) exhibited dark purple glumes (RHS No. 61C), while none of the genotypes possessed white (RHS No. NN155C) or dark green (RHS No. 141C) glumes (Table 2).

Substantial variability was also recorded for ear shape, with four descriptor states represented among the

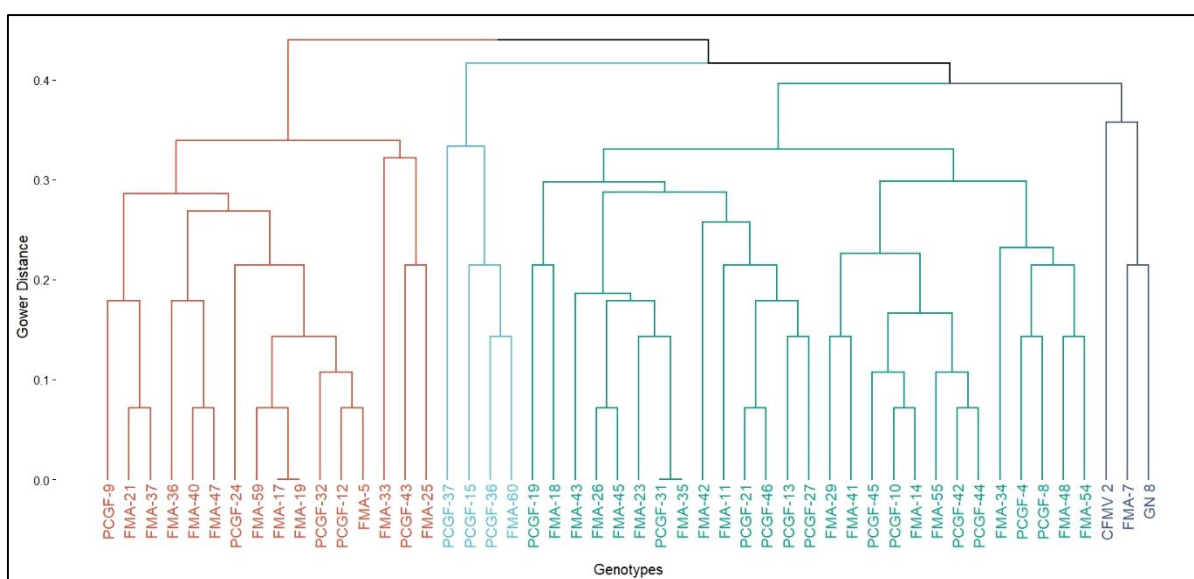


Fig. 5 : Hierarchical clustering (UPGMA) of finger millet genotypes using Gower's distance based on DUS descriptors.

studied germplasm (Fig. 3). The open ear type was the most common, observed in 24 genotypes (48%), followed by semi-compact ears in 21 genotypes (42%) and compact ears in 4 genotypes (8%). Only one genotype (2%) exhibited a droopy ear, whereas no genotype belonged to the fist type category (Table 2). The presence of diverse ear shapes reflects considerable morphological variation within the germplasm and provides an effective basis for varietal discrimination under DUS testing.

Finger descriptors

The descriptor finger branching displayed two expression states among the studied genotypes. The absence of finger branching was predominant and was recorded in 34 genotypes (68%), while 16 genotypes (32%) exhibited the presence of finger branching (Table 2).

Variation was also observed for the position of finger branching. Among the evaluated genotypes, 16 genotypes (32%) showed branching only in the thumb finger, whereas no genotype exhibited branching in all fingers. The remaining 34 genotypes (68%), which lacked finger branching, were not classified for the position of branching (Table 2). The restriction of branching to the thumb finger among branched genotypes highlights the limited but distinct variation available for this descriptor within the studied germplasm.

In contrast, the descriptor multiple whorls were uniform across all evaluated genotypes. All 50 genotypes (100%) were scored as absent for multiple whorls, and no genotype exhibited the presence of this trait (Table 2). The absence of variation indicates that this descriptor was monomorphic in the present set of germplasm and,

therefore, did not contribute to genotype differentiation.

Seed descriptors

The descriptor seed colour exhibited four expression states among the studied genotypes (Fig. 4). Light brown (RHS No. N172D) was the predominant seed colour, recorded in 31 genotypes (62%), followed by white (RHS No. NN155C) and copper brown (RHS No. N175A), each represented by 8 genotypes (16%). Only 3 genotypes (6%) possessed dark brown seeds (RHS No. N178A) (Table 2). The occurrence of multiple seed colour classes reflects appreciable diversity within the germplasm and enhances the effectiveness of seed colour as a distinguishing descriptor.

Cluster analysis

Hierarchical cluster analysis based on fourteen DUS descriptors grouped the fifty finger millet genotypes into four major clusters (Fig. 5), indicating the presence of appreciable morphological diversity among the evaluated germplasm. Cluster III was the largest, comprising 27 genotypes, followed by Cluster I with 16 genotypes. Cluster II contained 4 genotypes, while Cluster IV was the smallest and included only 3 genotypes. The unequal distribution of genotypes among clusters suggests differences in the extent of morphological similarity within the germplasm. Genotypes grouped within the same cluster shared similar combinations of DUS descriptor states, whereas those belonging to different clusters exhibited greater morphological divergence. The distinct grouping of a few genotypes into smaller clusters indicates the presence of unique morphological characteristics that differentiated them from the remaining accessions.

Discussion

Morphological characterization through DUS descriptors provides an effective approach for assessing genetic diversity, identifying distinct genotypes and documenting germplasm resources. In the present study, fifty finger millet genotypes exhibited considerable variation for plant, leaf, stem, inflorescence, finger and seed descriptors, indicating the presence of useful morphological diversity within the evaluated material. Plant architecture-related traits, particularly growth habit and pigmentation at the leaf juncture, showed distinct variation among genotypes. The predominance of erect growth habit reflects its common occurrence in cultivated finger millet, while less frequent growth forms contribute valuable diversity for genotype identification and parental selection. Similar variability for morphological traits has been reported in finger millet germplasm studies (Basavaraj *et al.*, 2021; Keerthana *et al.*, 2026). Leaf and stem descriptors such as leaf sheath pubescence, flag leaf dimensions, culm branching and peduncle length showed variation among genotypes. These traits are useful diagnostic characters for DUS testing and provide information on differences in plant architecture and adaptation. This is consistent with the findings of Kumar *et al.* (2019), Patil *et al.* (2019) and Singh *et al.* (2024). Inflorescence descriptors, particularly glume colour and ear shape, exhibited considerable polymorphism and were effective in differentiating genotypes. These visually distinguishable and relatively stable traits are valuable for varietal identification and protection. Similar results were reported by Louis *et al.* (2023) and Choudhary *et al.* (2025). Similarly, finger-related descriptors contributed to genotype discrimination, with variation observed for finger branching characteristics. Seed descriptors showed variation for seed colour and shape, which are important morphological markers due to their stability and ease of observation. This is consistent with the findings of Louis *et al.* (2023) and Keerthana *et al.* (2026). The occurrence of diverse seed colour classes and seed shapes provides useful resources for germplasm conservation and crop improvement programmes (Kaur *et al.*, 2024). The UPGMA clustering based on DUS descriptors revealed substantial morphological diversity among the evaluated finger millet genotypes by grouping them into four distinct clusters. Genotypes from widely separated clusters may serve as valuable parents for hybridization, while the clustering pattern supports efficient germplasm characterization, varietal identification and conservation (Ghimire *et al.*, 2023; Kanwer *et al.*, 2025; Hansalia *et al.*, 2026). Overall, the observed diversity among DUS descriptors demonstrates the usefulness of morphological

characterization for finger millet germplasm evaluation. The unique combinations of descriptor states identified in the present study can support varietal identification, plant variety protection, conservation of genetic resources and selection of diverse parents for future breeding programmes.

Conclusion

The present study demonstrated that standardized DUS descriptors are effective tools for the characterization and differentiation of finger millet germplasm. Considerable morphological variation was observed among the 50 genotypes for plant architecture, leaf, stem, inflorescence, finger and seed traits, whereas a few descriptors remained monomorphic, indicating their limited discriminatory value within the evaluated material. The hierarchical cluster analysis based on Gower's distance further revealed substantial phenotypic diversity by grouping the genotypes into four distinct clusters, highlighting the existence of morphologically diverse genetic resources. The unique combinations of descriptor states identified in the present investigation provide a reliable basis for genotype identification, germplasm documentation and varietal discrimination under DUS testing. These findings also contribute valuable baseline information for the protection of plant varieties under the PPV&FR Act and support the efficient management and conservation of finger millet genetic resources. Furthermore, genotypes belonging to morphologically distinct clusters and possessing unique qualitative traits can be utilized as potential parental materials in future breeding programmes to broaden the genetic base and develop improved cultivars. Overall, the study emphasizes the importance of standardized morphological characterization as a crucial first step in finger millet improvement and provides useful information for breeding, varietal registration and long-term germplasm conservation.

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