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AGRO-MORPHOLOGICAL CHARACTERIZATION AND ASSESSMENT OF PHENOTYPIC DIVERSITY IN DESI CHICKPEA (*Cicer arietinum* L.) GERMPLASM USING DUS DESCRIPTORS

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ABSTRACT

Thirty-four chickpea (*Cicer arietinum* L.) genotypes were characterised for agro-morphological variability using 20 DUS descriptors as per PPV&FRA guidelines. Out of which, seven were monomorphic, seven dimorphic, four trimorphic and two were found to be polymorphic. Seed colour showed the highest level of polymorphism with six expression states, while foliage colour also showed good amount of variation. Gower dissimilarity based on 13 variable descriptors ranged from 0.000 to 0.846, with a mean value of 0.447, indicating substantial phenotypic variation among the genotypes. Hierarchical clustering grouped the genotypes into two major clusters, which was further supported by silhouette analysis, where the highest coefficient was observed at k = 2 (0.319). The first two coordinates of the Principal Coordinate Analysis totalled up to 47.09% of the total positive-eigenvalue variation and which also was comparable to the cluster analysis. The study showed that DUS descriptors, when combined with multivariate analyses, can effectively reveal phenotypic diversity and help in the identification and characterisation of chickpea germplasm. The identified contrasting genotypes can be further used formapping quantitative trait loci (QTLs), developing mapping populations and identifying diverse parents for hybridization to maximize genetic variability.

Key words : Chickpea, DUS descriptors, Gower dissimilarity, Silhouette analysis, PCoA.

Introduction

Chickpea (*Cicer arietinum* L.), commonly known as gram or chana in Northern India, is an important rabi-season pulse crop and the third most important pulse crop globally. It is a diploid species with 2n = 16 chromosomes and is believed to have originated in southeastern Turkey and Syria. Chickpea is nutritionally valuable, containing about 17–22% protein, 50–65% carbohydrates and 4–7% fat, besides essential minerals and bioactive compounds (Jukanti *et al*., 2012; Patil *et al*., 2024). It also improves soil fertility through biological nitrogen fixation. Chickpea is mainly adapted to cool and relatively dry environments. Chickpea remains one of the major pulse crops of India, occupying 9.66 million ha with an estimated production of 12.51 million tonnes and productivity of 1,295 kg ha^{-1} during 2025–26. In Chhattisgarh alone, the crop covered about 249.79 thousand ha, producing 246.29 thousand tonnes at an average productivity of 986 kg ha^{-1} (ICAR-IIPR, 2026). The substantial variation in chickpea productivity among states and production environments points to the importance of identifying well-adapted and phenotypically diverse germplasm. Systematic agro-morphological characterization therefore remains relevant for distinguishing genotypes, documenting useful variation and supporting the selection of material for breeding and varietal development.

The availability of diverse germplasm is essential for broadening the genetic base and developing improved varieties with desirable plant and seed characteristics. Agro-morphological characterization provides a simple and effective approach for identifying variation among

genotypes and establishing their distinctness. Distinctness, Uniformity and Stability (DUS) characterization is particularly useful for the identification and documentation of germplasm based on stable morphological descriptors (PPV&FRA, 2007). Traits related to plant architecture, foliage, flowering, pod and seed characteristics can provide valuable diagnostic features for differentiating genotypes (Nagavi *et al.*, 2024). In chickpea, morphological variation is also important for selecting plant types suitable for different production systems (Sanjay *et al.*, 2024). Therefore, systematic characterization of available germplasm is an important prerequisite for its effective conservation and utilization in crop improvement.

Chickpea (*Cicer arietinum* L.) is one of the most widely grown food legumes and remains especially important in South Asia, where it contributes both dietary protein and a range of micronutrients to predominantly cereal-based diets. Beyond its nutritional value, the crop is also well suited to relatively dry production environments and is therefore closely tied to the livelihood of farmers in rainfed regions. Much of that diversity is visible in fairly simple characters—plant architecture, foliage colour, flowering behaviour, pod morphology and, perhaps most strikingly, seed shape and colour (Koul *et al.*, 2022). Agro-morphological characterization therefore remains a useful starting point for germplasm evaluation, even in an era dominated by molecular markers and genomic tools. Morphological characters are inexpensive to record, directly observable in the field and often immediately relevant to breeders. Large-scale characterization of Indian chickpea germplasm has, in fact, revealed considerable variation for qualitative as well as quantitative traits, indicating that cultivated collections still contain substantial phenotypic diversity that can be exploited in crop improvement (Archak *et al.*, 2016).

Simply listing the expression states of DUS characters, however, gives only a partial picture of diversity. Multivariate approaches can reveal how those characters combine to separate genotypes and whether recognizable phenotypic groups are present. Gower's coefficient is particularly useful for this purpose because it can accommodate categorical and mixed-type variables without forcing nominal character states into an artificial numerical scale (Gower, 1971). Accordingly, the present investigation was undertaken to characterize 34 chickpea genotypes using 20 DUS descriptors and to examine their phenotypic relationships through frequency distribution, Gower dissimilarity, hierarchical clustering and principal coordinate analysis (PCoA). The broader aim was to identify distinctive and contrasting germplasm that could be useful for varietal characterization, germplasm management and the selection of diverse material for chickpea breeding.

Materials and Methods

The present investigation was conducted during the rabi season of 2025–26 at the Genetics and Plant Breeding Farm, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India. A total of 34 chickpea (*Cicer arietinum* L.) genotypes were evaluated for agro-morphological diversity. The experiment was laid out in a Randomized Block Design (RBD) with three replications under uniform agronomic conditions. Each plot comprised of 4 rows of 4m length in each replication. The row × row and plant × plant distance of 30 cm and 10 cm and net plot area was 4.8 m^2. Random five plants are selected from each of the plot to record morphological data.Morphological characterization of the genotypes was carried out using 20 distinctness, uniformity and stability (DUS) descriptors. Observations were recorded at the optimum stage of plant growth for assessment of each characteristic.The characters showing a single phenotypic expression were said to be monomorphic, those with two states as dimorphic, three states as trimorphic and traits exhibiting more than three expression states as polymorphic.

Gower dissimilarity analysis : Phenotypic dissimilarity among the genotypes was estimated using Gower's dissimilarity coefficient (Gower, 1971), which is suitable for datasets consisting of categorical and ordinal descriptors. The identical expression states between two genotypes were given a dissimilarity value of 0, whereas different states were given 1. The overall dissimilarity between a pair of genotypes was obtained as the average dissimilarity across all variable descriptors. A 34 × 34 pairwise dissimilarity matrix was generated for clustering and PCoA. Gower similarity was expressed as 1–D, where 'D' is the Gower dissimilarity coefficient.

Hierarchical cluster analysis: The Gower dissimilarity matrix was used to find outhierarchical agglomerative clustering using the unweighted pair-group method with arithmetic mean (UPGMA). The dendrogram obtained was used to visualise phenotypic relationships and grouping patterns among the 34 chickpea genotypes.To determine the number of clusters, silhouette analysis was performed (Rousseeuw, 1987).

Principal Coordinate analysis : Principal Coordinate Analysis (PCoA) was performed using the same Gower dissimilarity matrix to provide a graphical representation of the phenotypic relationships among the

genotypes in multidimensional space.The first two principal coordinates were used to construct the two-dimensional ordination plot and to examine the correspondence between the PCoA distribution and hierarchical cluster grouping.

Statistical analysis : All the analyses were carried out in R software [Version: 2026.05.0+218] using suitable packages for each analysis. Frequency and percentage distributions were worked out for all DUS traits, and the variable descriptors were further used to estimate Gower dissimilarity with the cluster package. Hierarchical clustering was carried out using the UPGMA method, while the optimum number of clusters was identified through silhouette analysis. PCoA was performed using the ape package to visualise the relationship among genotypes. Graphs were prepared using ggplot2, factoextra and corrplot, while readxl, dplyr and tidyr were used for data handling.

Results

Agro-morphological characterization of 34 chickpea (*Cicer arietinum* L.) genotypes was carried out using 20 distinctness, uniformity and stability (DUS) descriptors following PPVFRA guidelines. The genotypes exhibited considerable variation for several morphological characters, whereas some traits showed complete uniformity (Table 1, Figs. 1-12). Such morphological variation is useful for distinguishing, identifying and documenting chickpea germplasm.

Frequency distribution and polymorphism of DUS descriptors

Considerable agro-morphological variation was observed among the 34 chickpea genotypes for the 20 DUS descriptors evaluated. Of the 20 traits, seven were monomorphic, seven were dimorphic, four were trimorphic and two were polymorphic. Stem anthocyanin colouration, leaf pattern, flower colour, stripes on the standard, number of seeds per pod, seed ribbing and seed type showed monomorphic expression. All genotypes



(IC-554990) (IC-555133)

Fig. 1 : Stem: Anthocyanin colouration.



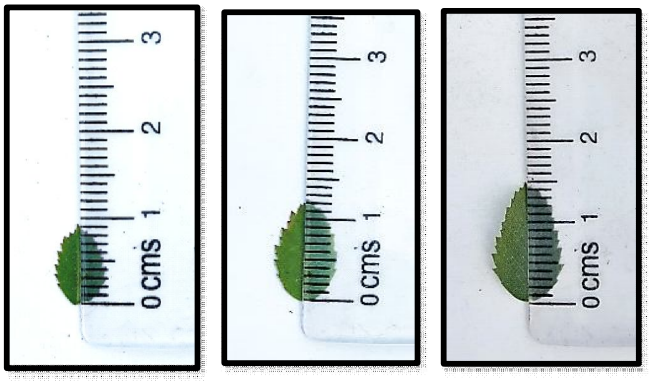
Medium (IC-555543) High (IC-273434)

Fig. 2 : Stem: Height at initiation of first flower.



Semi-Erect (IC-244463) Erect (IC-554990)

Fig. 3 : Plant: Growth habit.



Small (IC-486136) Medium (IC-305519) Large (IC-270936)

Fig. 4 : Leaflet: Size.



Light Green (PUSA-72) Medium Green (IC-83428) Dark Green (IC-305376) Greenish Purple (IC-506934)

Fig. 5 : Plant: Colour of foliage.

Table 1 : Agro-morphological characterization of chickpea genotypes based on DUS descriptors.

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
IC- 117657	p	medium	medium	semi erect	light green	medium	pinnate	s	pink	p	medium	short	large	>1	yellow	very small	angular	rough	p	desi
IC-486511	p	medium	early	semi erect	medium green	medium	pinnate	s	pink	p	medium	short	small	>1	brown	very small	owl's head	tuberculated	p	desi
IC-555543	p	medium	early	semi erect	dark green	small	pinnate	s	pink	p	medium	short	medium	>1	black	very small	angular	tuberculated	p	desi
IC- 487464	p	high	early	erect	medium green	medium	pinnate	s	pink	p	medium	medium	medium	>1	brown	medium	owl's head	rough	p	desi
IC-5525200	p	medium	early	erect	dark green	medium	pinnate	t	pink	p	long	medium	medium	>1	brown	very small	owl's head	smooth	p	desi
IC-328298	p	high	medium	semi erect	dark green	small	pinnate	s	pink	p	medium	short	medium	>1	orange	very small	angular	rough	p	desi
IC-468659	p	high	medium	semi erect	medium green	medium	pinnate	s	pink	p	medium	short	medium	>1	green	very small	angular	tuberculated	p	desi
IC-486136	p	medium	medium	semi erect	dark green	small	pinnate	s	pink	p	medium	medium	medium	>1	yellow	very small	angular	rough	p	desi
IC-273434	p	high	medium	semi erect	light green	small	pinnate	s	pink	p	medium	short	medium	>1	yellow	very small	angular	rough	p	desi
IC-407968	p	high	medium	erect	medium green	medium	pinnate	s	pink	p	medium	medium	medium	>1	green	very small	angular	rough	p	desi
IC-83428	p	high	early	semi erect	medium green	medium	pinnate	s	pink	p	medium	medium	medium	>1	green	very small	angular	rough	p	desi
IC-251695	p	medium	medium	semi erect	light green	medium	pinnate	s	pink	p	medium	short	medium	>1	dark brown	very small	owl's head	rough	p	desi
IC-209295	p	high	medium	semi erect	medium green	medium	pinnate	s	pink	p	medium	short	medium	>1	dark brown	very small	owl's head	rough	p	desi
IC-555133	p	high	early	semi erect	greenish purple	medium	pinnate	s	pink	p	medium	medium	large	>1	yellow	very small	angular	rough	p	desi
IC-83497	p	high	early	semi erect	light green	medium	pinnate	s	pink	p	long	medium	medium	>1	orange	very small	angular	tuberculated	p	desi
IC-348459	p	high	medium	semi erect	light green	medium	pinnate	s	pink	p	long	short	medium	>1	brown	very small	angular	tuberculated	p	desi
IC-275481	p	high	medium	semi erect	medium green	medium	pinnate	s	pink	p	medium	medium	medium	>1	green	very small	angular	rough	p	desi
IC-244463	p	high	early	semi erect	medium green	medium	pinnate	s	pink	p	medium	medium	medium	>1	brown	very small	owl's head	rough	p	desi
IC-554990	p	high	medium	erect	medium green	medium	pinnate	s	pink	p	medium	medium	medium	>1	green	very small	angular	rough	p	desi
IC-270936	p	high	medium	erect	light green	large	pinnate	s	pink	p	medium	medium	medium	>1	green	small	angular	tuberculated	p	desi
IC-305519	p	high	early	semi erect	medium green	medium	pinnate	s	pink	p	medium	short	medium	>1	orange	very small	angular	rough	p	desi
IC-83953	p	high	medium	semi erect	greenish purple	medium	pinnate	s	pink	p	medium	short	medium	>1	green	very small	angular	tuberculated	p	desi
IC-506934	p	high	early	semi erect	greenish purple	medium	pinnate	s	pink	p	medium	short	medium	>1	brown	very small	angular	rough	p	desi
IC-408182	p	medium	medium	semi erect	light green	medium	pinnate	s	pink	p	medium	short	medium	>1	green	very small	angular	tuberculate	p	desi
IC-305376	p	high	medium	semi erect	dark green	small	pinnate	s	pink	p	medium	short	medium	>1	orange	very small	angular	rough	p	desi
IC-555628	p	high	early	semi erect	medium green	medium	pinnate	s	pink	p	medium	medium	medium	>1	orange	very small	angular	rough	p	desi
IC-209237	p	high	medium	semi erect	greenish purple	small	pinnate	s	pink	p	long	medium	large	>1	green	very small	angular	tuberculated	p	desi
IC-555508	p	high	medium	erect	medium green	medium	pinnate	s	pink	p	long	medium	large	>1	brown	very small	owl's head	smooth	p	desi
Pusa-72	p	high	early	semi erect	light green	medium	pinnate	s	pink	p	medium	short	medium	>1	orange	very small	owl's head	smooth	p	desi
Pusa-547	p	high	early	erect	light green	medium	pinnate	s	pink	p	long	medium	medium	>1	yellow	small	owl's head	smooth	p	desi
Pusa-3043	p	medium	early	semi erect	medium green	medium	pinnate	s	pink	p	medium	medium	large	>1	brown	small	owl's head	rough	p	desi
Pusa-3062	p	medium	early	semi erect	medium green	medium	pinnate	s	pink	p	medium	medium	large	>1	brown	small	owl's head	rough	p	desi
Bhund Chana	p	medium	medium	semi erect	light green	medium	pinnate	s	pink	p	medium	medium	medium	>1	brown	very small	angular	rough	p	desi
Manjhola Chana	p	medium	early	erect	dark green	medium	pinnate	s	pink	p	long	medium	medium	>1	brown	small	owl's head	smooth	p	desi

p=present, s=single, t=twin

1= Accessions; 2= Stem: Anthocyanin colouration; 3= Stem: Height at initiation of first flower; 4= Time of flowering; 5= Plant: Growth habit; 6= Plant: Color of foliage; 7= Leaflet: Size; 8= Leaf: Pattern; 9= Flower: Number per peduncle; 10= Flower: Colour; 11= Flower: Stripes on standard; 12= Peduncle: Length; 13= Plant: Height; 14= Pod: Size; 15= Pod: Number of seeds; 16= Seed: colour; 17= Seed: Size; 18= Seed: Shape; 19= Seed: Testa texture; 20= Seed: Ribbing; 21= Seed: Type



Single(IC-273343) Twin (IC-5525200)

Fig. 6 : Flower: Number per peduncle.



(IC-273434) (IC-5525200)

Fig. 7 : Flower: Stripes on Standard.



Medium (IC-554990) Long (IC-348459)

Fig. 8 : Peduncle: Length.



V. Small (IC-348459)Small (IC-270936)Medium (IC-487464)

Fig. 9 : Seed:size.

possessed stem anthocyanin colouration, pinnate leaves, pink flowers, stripes on the standard, more than one seed per pod, seed ribbing and desi-type seeds. Among the



Small (IC-486511) Medium (IC-270936) Large (IC-209237)

Fig. 10 : Pod: Size (length).



Angular (IC-555133) Owl`s Head (IC-5525200)

Fig. 11 : Seed: shape.



Fig. 12 : Seed: colour.

dimorphic traits, high stem height at initiation of the first flower predominated (67.6%), while 52.9% of the genotypes showed medium flowering time. Semi-erect growth habit was predominant (76.5%), whereas erect growth habit occurred in 23.5% of the genotypes. Single flowers per peduncle were observed in 97.1% of the material, with only one genotype exhibiting twin flowers. Medium peduncle length was also predominant (79.4%), and 55.9% of the genotypes were classified as medium in plant height (Fig. 13).

Significant differences were observed for foliage and seed-related characters. Foliage colour was polymorphic,

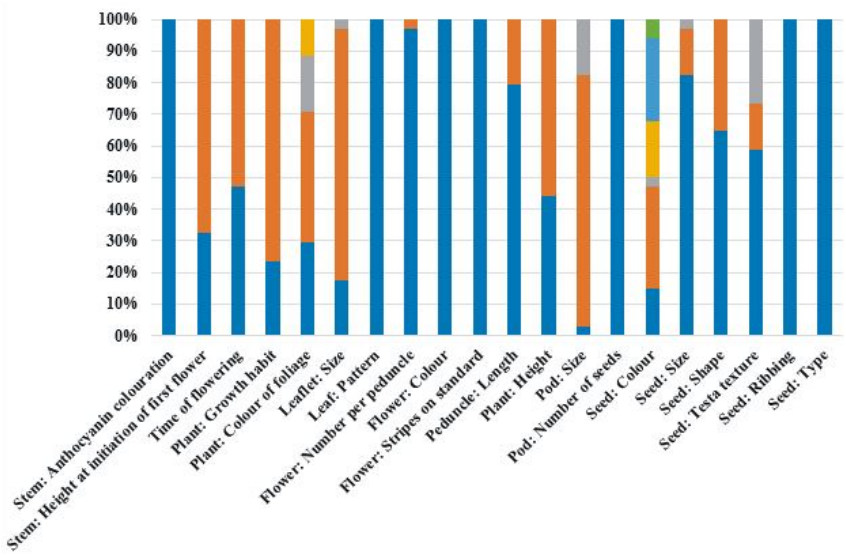


Fig. 13 : Frequency Distribution.

S. No.	DUS descriptor						
1	Stem: Anthocyanin colouration	Present: 34 (100.0%)					
2	Stem: Height at initiation of first flower	Medium: 11 (32.4%)	High: 23 (67.6%)				
3	Time of flowering	Early: 16 (47.1%)	Medium: 18 (52.9%)				
4	Plant: Growth habit	Erect: 8 (23.5%)	Semi-erect: 26 (76.5%)				
5	Plant: Colour of foliage	Light green: 10 (29.4%)	Medium green: 14 (41.2%)	Dark green: 6 (17.6%)	Greenish purple: 4 (11.8%)		
6	Leaflet: Size	Small: 6 (17.6%)	Medium: 27 (79.4%)	Large: 1 (2.9%)			
7	Leaf: Pattern	Pinnate: 34 (100.0%)					
8	Flower: Number per peduncle	Single: 33 (97.1%)	Twin: 1 (2.9%)				
9	Flower: Colour	Pink: 34 (100.0%)					
10	Flower: Stripes on standard	Present: 34 (100.0%)					
11	Peduncle: Length	Medium: 27 (79.4%)	Long: 7 (20.6%)				
12	Plant: Height	Short: 15 (44.1%)	Medium: 19 (55.9%)				
13	Pod: Size	Small: 1 (2.9%)	Medium: 27 (79.4%)	Large: 6 (17.6%)			

Fig. 13 : Frequency distribution of DUS Descriptors.

comprising medium green (41.2%), light green (29.4%), dark green (17.6%) and greenish-purple (11.8%) classes. Leaflet size was predominantly medium (79.4%), whereas small and large leaflets accounted for 17.6 and 2.9%, respectively. Pod size was also trimorphic, with medium-sized pods predominating (79.4%), followed by large (17.6%) and small (2.9%) pods. Seed colour was the most variable trait, displaying six expression states: brown (32.4%), green (26.5%), orange (17.6%), yellow (14.7%), dark brown (5.9%) and black (2.9%). Very small seeds predominated (82.4%), whereas small and medium seeds accounted for 14.7 and 2.9%, respectively. Angular seed shape occurred in 64.7% of the genotypes and owl's-head shape in 35.3%. Seed testa texture showed three states, with rough texture being most frequent (58.8%), followed by tuberculated (26.5%) and smooth (14.7%). Overall, the frequency distribution demonstrated that seed colour, foliage colour, testa texture, pod size and leaflet size contributed substantially to the observed phenotypic differentiation.

Shannon-Weaver Diversity indices

Shannon–Weaver diversity analysis revealed considerable variation among the 34 chickpea accessions for several morphological traits (Table 2). The diversity index ranged from 0.000 to 1.575, with the highest diversity observed for seed colour (H′ = 1.575), followed by foliage colour (H′ = 1.283) and seed testa texture (H′ = 0.946). Moderate diversity was recorded for time of flowering (H′ = 0.691), plant height (H′ = 0.686), seed shape (H′ = 0.649), height at initiation of first flower (H′ = 0.630), leaflet size and pod size (H′ = 0.593 each), and plant growth habit and seed size (H′ = 0.546 each). Peduncle length showed an H′ value of 0.508, whereas flower number per peduncle exhibited comparatively low diversity (H′ = 0.133). Seven traits, namely stem anthocyanin colouration, leaf pattern, flower colour, flower stripes on standard, pod number of seeds, seed

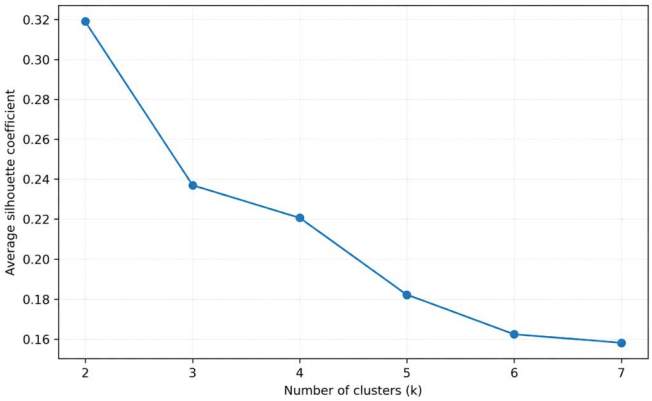


Fig. 14 : Silhouette Analysis.

diversity in seed colour, foliage colour and testa texture indicates their usefulness for distinguishing chickpea accessions and assessing phenotypic diversity.

Gower dissimilarity among genotypes

Gower dissimilarity index was analysed using the 13 variable DUS descriptors, and the seven monomorphic characters were excluded since they can't be used for discrimination. Pairwise Gower dissimilarity (range-0.0000 to 0.8462) had a mean of 0.4465 and median of 0.4615 showing good amount of phenotypic differentiation among the germplasm (Table 3). Whereas, pairwise similarity ranged from 0.1538 to 1.000.Three genotypic

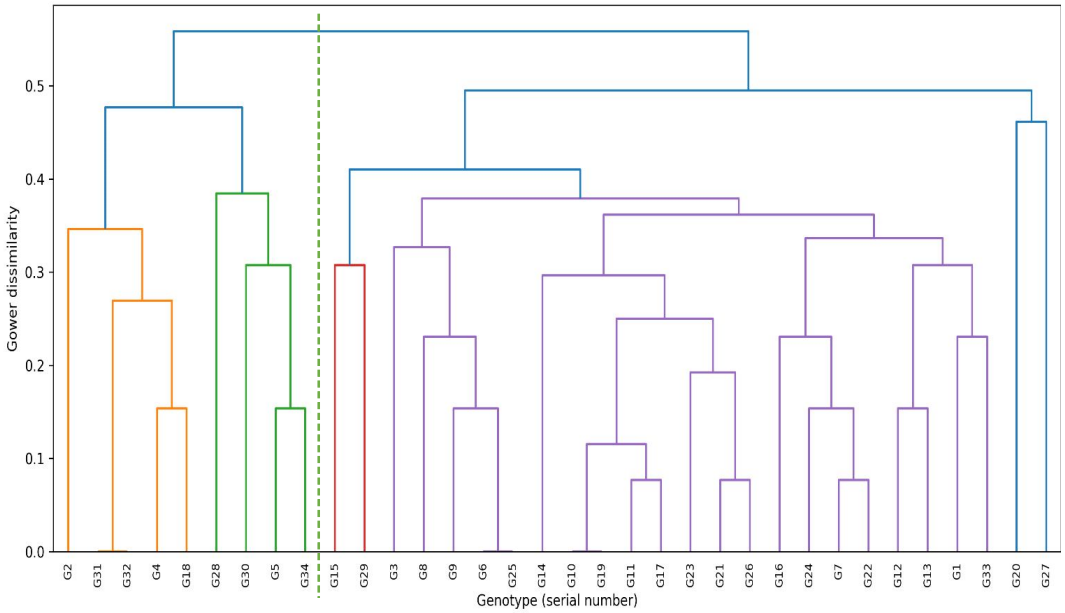


Fig. 15 : Dendrogram showing hierarchical clustering of 34 genotypes.

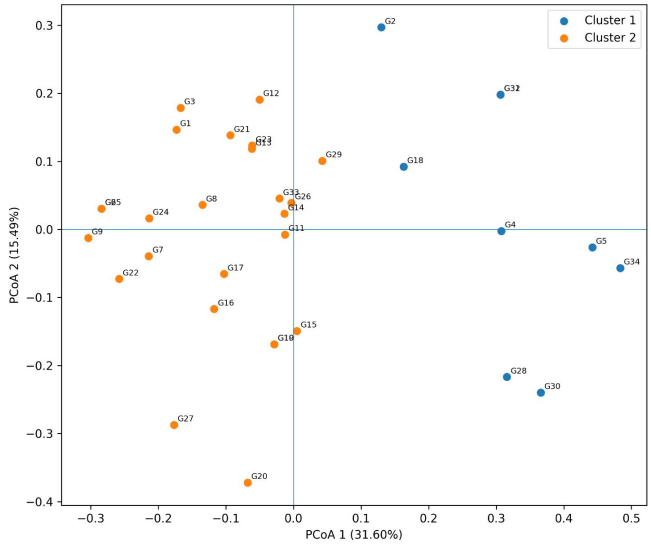


Fig. 16 : PCoA of chickpea genotypes based on Gower Dissimilarity.

ribbing and seed type, were monomorphic and therefore recorded an H′ value of zero. The predominance of

pairs, G6–G25, G10–G19 and G31–G32 recorded a Gower dissimilarity value of zero, indicating identical expression across all 13 variable DUS descriptors. In contrast, G3–G28, G5–G9 and G9–G34 recorded a maximum dissimilarity value of 0.8462, representing the most contrasting morphological germplasm lines.

Hierarchical clustering and silhouette analysis

Hierarchical clustering using the average-linkage or UPGMA procedure based on the Gower dissimilarity matrix revealed two principal phenotypic groups. Silhouette analysis performed for *k* values ranging from 2 to 7 supported *k* = 2 as the optimum solution, with the highest average silhouette coefficient of 0.319 (Fig. 14).

Cluster I comprised nine genotypes (G2, G4, G5, G18, G28, G30, G31, G32 and G34), whereas Cluster II contained the remaining 25 genotypes (Table 4, Fig. 5). Cluster I was characterized comparatively by a greater occurrence of early flowering, owl's-head seed shape and brown seed colour. Cluster II was larger and displayed

Table 2 : Shannon-weaver diversity index for various morphological traits.

Characteristics	Shannon's diversity index
Stem: Anthocyanin colouration	0.000
Stem: Height at initiation of first flower	0.630
Time of flowering (50% of the plants with at least one open flower)	0.691
Plant: Growth habit	0.546
Plant: colour of foliage	1.283
Leaflet: Size (length) (middle of the plant and middle of the leaf)	0.593
Leaf: Pattern	0.000
Flower: number per peduncle	0.133
Flower: colour	0.000
Flower: Stripes on standard	0.000
Peduncle: Length	0.508
Plant: Height	0.686
Pod: Size (length)	0.593
Pod: Number of seeds	0.000
Seed: colour	1.575
Seed: Size (weight of 100 seeds at 10% moisture content)	0.546
Seed: Shape	0.649
Seed: Testa texture	0.946
Seed: Ribbing	0.000
Seed: Type	0.000

Table 3 : Gower dissimilarity index.

Index	Value	Genotype-pairs
Minimum Gower dissimilarity	0.0000	G6–G25, G10–G19, G31–G32
Maximum Gower dissimilarity	0.8462	G3–G28, G5–G9, G9–G34
Mean Gower dissimilarity	0.4465	
Median Gower dissimilarity	0.4615	

greater heterogeneity for several descriptors, while semi-erect growth habit, angular seed shape and very small seed size were frequent. The moderate silhouette value further indicated that, although two major phenotypic groups were distinguishable, considerable overlap and within-cluster variation persisted among the chickpea genotypes.

Table 4 : Two Principal clusters.

Cluster	Genotypes	N=34
Cluster I	G2, G4, G5, G18, G28, G30, G31, G32, G34	**9**
Cluster II	G1, G3, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G19, G20, G21, G22, G23, G24, G25, G26, G27, G29, G33	**25**

Principal coordinate analysis

Principal coordinate analysis based on the Gower dissimilarity matrix provided a complementary visualization of phenotypic relationships among the 34 genotypes. The first principal coordinate accounted for 31.60% of the variation, while the second accounted for 15.49%. Together, the first two coordinates represented 47.09% of the positive-eigenvalue variation (Fig. 6). Genotypes assigned to the two principal clusters showed broad differentiation in the PCoA ordination, although partial overlap was evident, consistent with the moderate silhouette coefficient. Genotypes such as G28, G30 and G34 occupied comparatively distinct positions in the ordination, while several genotypes within the larger second cluster were positioned more closely together. The concordance between the PCoA and hierarchical clustering supported the presence of structured, but not sharply discrete, phenotypic diversity within the evaluated germplasm.

Discussion

The current investigation highlighted substantial agro-morphological variation among the 34 chickpea genotypes. Seed colour and foliage colour showed the greatest polymorphism, while leaflet size, pod size, seed size and testa texture also contributed substantially to genotype differentiation. Similar variability in seed, foliage, pod and plant architectural characters has been reported during DUS-based characterization of chickpea germplasm, highlighting the usefulness of these descriptors for varietal identification and germplasm characterization (Asati*et al*., 2023). In contrast, seven descriptors were monomorphic and therefore provided limited discriminatory information. Joshi *et al*. (2018) also reported that morphological DUS descriptors alone may be insufficient to distinguish some closely related chickpea cultivars, emphasizing the value of supplementary quantitative or molecular characterization.

Gower dissimilarity ranged from 0.000 to 0.846, with a mean of 0.447, demonstrating substantial phenotypic differentiation among the evaluated genotypes. Gower's coefficient is particularly suitable for categorical and mixed-variable datasets and has therefore been widely applied for assessing phenotypic diversity (Gower, 1971).

The identical profiles observed for G6–G25, G10–G19 and G31–G32 contrasted with the high divergence of G3–G28, G5–G9 and G9–G34, indicating the occurrence of both closely resembling and highly contrasting germplasm.

Hierarchical clustering separated the genotypes into two major groups, which was supported by silhouette analysis, where $k = 2$ produced the highest coefficient (0.319). The moderate silhouette value indicates that the two clusters were distinguishable but showed some degree of phenotypic overlap, consistent with the interpretation of Rousseeuw (1987). PCoA further supported the clustering pattern, with the first two coordinates accounting for 47.09% of the variation. Comparable multivariate characterization of chickpea germplasm has demonstrated that morphological diversity is distributed across several dimensions and can effectively reveal relationships among accessions (Archak *et al*., 2016). Overall, the combined DUS characterization, Gower dissimilarity, clustering and PCoA analyses effectively differentiated the chickpea germplasm and identified phenotypically contrasting genotypes that may be useful for varietal identification, germplasm management and selection of diverse parents in breeding programmes.

Conclusion

Agro-Morphological characterization and Assessment of Phenotypic Diversity in Chickpea (*Cicer arietinum* L.) germplasm used 13 DUS Descriptors, which showed variability, with seed colour and foliage colour contributing to the differentiation of genotypes. The Gower dissimilarity values also indicated a good level of phenotypic diversity in the germplasm lines. Based on hierarchical clustering and PCoA, the genotypes were broadly grouped into two major clusters, and the silhouette analysis also supported this pattern. A few meaningful associations were recorded among the observed traits related to growth habit, plant height and seed size. Overall, the findings show that DUS descriptors, when used along with multivariate statistical tools, provides a practical and reliable way to characterise chickpea germplasm.The diverse genotypes identified in this study offer significant utility for cultivar identification, germplasm preservation and the selection of parental lines with contrasting traits in future chickpea breeding programs.

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