Current Journal of Applied Science and Technology

Volume 42, Issue 40, Page 20-36, 2023; Article no.CJAST.108398
ISSN: 2457-1024
(Past name: British Journal of Applied Science & Technology, Past ISSN: 2231-0843, NLM ID: 101664541)

DUS-Based Morphological Profiling and Categorization of Chickpea (*Cicer arietinum* L.) Genotypes

Rakesh Kumar Yadav [a], Manoj Kumar Tripathi [a,b*], Sushma Tiwari [a,b], Ruchi Asati [a], Shailja Chauhan [a], Niraj Tripathi [c], R. S. Solanki [a], R. S. Sikarwar [a] and Mohammad Yasin [d]

[a] Department of Genetics and Plant Breeding, College of Agriculture, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior-474002, M.P., India.
[b] Department of Plant Molecular Biology and Biotechnology, College of Agriculture, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior-474002, M.P., India.
[c] Directorate of Research, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur-482004, M.P., India.
[d] RAK College of Agriculture, Sehore, Madhya Pradesh, India.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/CJAST/2023/v42i404259

Open Peer Review History:
This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: https://www.sdiarticle5.com/review-history/108398

Original Research Article

Received: 25/08/2023
Accepted: 31/10/2023
Published: 01/11/2023

ABSTRACT

In the realm of plant breeding, genetic diversity stands as a pivotal factor for advancing crop improvement initiatives. Morphological characterization assists as a critical role, allowing for the scrutiny of discernible traits in crop plants as this facilitates the identification, classification, and comprehension of genetic variations present among diverse genotypes. The objective of this

**Corresponding author: E-mail: drmanojtripathi64@gmail.com;*

investigation was to scrutinize the morphological traits of 71 chickpea genotypes, with a particular emphasis on 10 selected qualitative traits, in adherence to the DUS testing guidelines. The experimental design employed was the randomized complete block design (RCBD) with three replications at the Research Farm, Department of Genetics & Plant Breeding, College of Agriculture, RVSVV, Gwalior, Madhya Pradesh, India during *Rabi* 2021-22. Among the parameters investigated, three exhibited a consistent dimorphic phenotype, six displayed three distinct phenotypes (trimorphic), and only one trait manifested more than three phenotypic variations (polymorphic). The diverse chickpea genotypes showed a substantial amount of genetic variability, demonstrating the potential for assigning distinct morphological profiles for varietal identification and characterization. Remarkably, for traits such as the foliage and flower color and seed shape, a high level of diversity within the chickpea genotypes was investigated employing Shannon's diversity indices. This comprehensive morphological characterization not only contributes to the understanding of the genetic landscape of chickpea genotypes but also provides valuable insights for varietal identification and selection in breeding programmes in future.

Keywords: Chickpea; DUS characterization; genetic variation; Shannon's diversity index.

1. INTRODUCTION

Cicer arietinum L., stands as a prominent Rabi season annual legume crop recognized by various vernacular names such as Gram, Chana, Egyptian pea, Bengal gram, and Garbanzo bean. Taxonomically, it belongs to the genus Cicer within the family Fabaceae and the subfamily Papilionoidae. This diploid pulse crop is characterized by a chromosomal count of 2n=2x=16, possessing a genome size of 738 Mbp and encompassing approximately 28,269 genes, as documented by Varshney et al. [1]. It exhibits self-pollinating tendencies. Believed to have originated in South Eastern Turkey and traversed geographical boundaries through introductions to India and various other regions worldwide. Its cultivation is predominant in arid and semi-arid regions, spanning over 50 countries distributed across the Mediterranean basin, Central Asia, East Africa, Europe, Australia, and North and South America [2]. The global dissemination of chickpea attests to its adaptability and agricultural significance across diverse climatic zones.

Chickpea stands as a consequential botanical entity, proffering a vital source of nourishment for the burgeoning global population. This leguminous crop emerges as an exemplary reservoir of protein, surpassing cereal grains in this nutritional aspect [3]. Beyond protein, chickpea bestows dietary fiber, advantageous unsaturated fatty acids, an array of vitamins, and an assortment of macro and micro-nutrients [4], thereby imparting manifold health benefits to an ever-expanding world population [5]. In the larger dietary landscape, chickpea assumes a pivotal role, constituting a fundamental nutritional component for millions globally [6]. Its consumption contributes significantly to mitigating various health issues, including cardiovascular disease, type 2 diabetes, digestive disorders, and certain cancers [7,8]. Its intrinsic resilience to drought and heat, positioning it as an increasingly indispensable crop amidst the challenges posed by climate change [9]. Simultaneously, it prevails as the preeminent cool-season food legume cultivated under rainfed conditions, particularly in arid and semi-arid regions worldwide [10,11]. Currently, the global cultivation of chickpea spans an expanse of 15.004 million hectares, yielding a productivity of 1,057.8 kg per hectare and an annual production of 15.87 million metric tons worldwide [12]. India spearheads global chickpea cultivation, contributing a substantial 73.78% (10.943 million hectares) of the total global chickpea acreage and 73.45% (11.91 million metric tonnes) of production [13]. This underscores the pivotal role of India in sustaining global chickpea production and emphasizes the imperative to address challenges threatening its cultivation [14-17]. Despite its nutritional significance and adaptability, the cultivation of chickpea has encountered setbacks in recent times, marked by a decline in acreage and production [18-22]. This decline is attributed to an interplay of an array of biotic and abiotic factors [23-27].

In the pursuit of breaking the yield plateau and achieving sustainable gains, plant breeders are confronted with the necessity of incorporating diverse germplasm lines into their breeding programmes [28-39]. This imperative is underlined by the need for systematic characterization and evaluation of *Cicer* species,

with the aim of focusing target traits [40]. Morphological traits, serving as visual cues for identification and classification of germplasm, constitute a fundamental aspect of breeding endeavors [41-44]. Morphological studies, particularly through early and cost-effective morphological marker-based polymorphism analysis, provide a foundation for assessing diversity [41-44]. The elucidation of phylogenetic relationships among various germplasm lines through morphological characterization holds the potential to guide breeders in circumventing repetitive parentage [43]. This, in turn, aids in the development of improved varieties with a broader genetic base [41-44]. Within the framework of the General Agreement on Trade and Tariffs, the Government of India has established a sui generis system, the Protection of Plant Varieties and Farmers Rights Act [45]. This legislation emphasizes the importance of distinctiveness, uniformity, and stability (DUS) testing for providing protection to plant varieties, alongside novelty considerations. Under the PPV & FRA, the characterization of a variety becomes a prerequisite. Identification of plant varieties of common knowledge is essential for safeguarding new plant varieties. The DUS test serves as a mechanism to establish the uniqueness of a variety, requiring a comprehensive comparison with other varieties of common knowledge and the most closely related variety. Variety identification, especially concerning genetic purity, assumes paramount importance in national and international seed and breeding programmes. Characterization of variety is useful to identify and avoid duplication. Qualitative characters being more stable over generations [46], hence are reliable for characterization of varieties. Therefore, the present study is designed to systematically characterize 71 chickpea genotypes, with a focus on their qualitative traits, aligning with the imperative to ensure genetic diversity and the integrity of plant varieties within the regulatory framework.

2. MATERIALS AND METHODS

The present investigation transpired during the *Rabi* season of the 2021-2022 at the Research Farm, Department of Genetics & Plant Breeding, College of Agriculture, Rajmata Vijyaraje Scindia Krishi Vishwa Vidyalaya Gwalior, Madhya Pradesh, India. The experimental repertoire comprised 71 distinct chickpea genotypes. The assessment of these genotypes unfolded across three replications, employing a Randomized Complete Block Design (RCBD). Each genetic entry was systematically cultivated in four rows, extending 3.0 meters in length within every replication. The spacing between rows and within rows was meticulously maintained at 30×10 cm, respectively. The cultivation adhered to recommended agronomic practices and plant protection measures to optimize and safeguard the crop. The stringent application of these practices aimed to ensure the integrity of the experimental data and the successful cultivation of chickpea genotypes under controlled conditions.

The investigation encompassed the meticulous documentation of data corresponding to 10 distinct morphological descriptors including stem anthocyanin pigmentation, plant coloration, growth habit, flower color, flower stripes, plant height, seed color, seed shape, seed testa texture and seed ribbing. The data were systematically recorded on 10 randomly selected plants for each genotype, following to the guidelines outlined by the Protection of Plant Varieties and Farmers' Rights Authority, Government of India (PPV & FRA, 2018) [45] under the framework of Distinctness, Uniformity, and Stability (DUS).

2.1 Statistical Analysis

To quantify the diversity inherent within the chickpea genotypes, phenotypic frequencies of these morphological traits were harnessed. Subsequently, the Shannon-Weaver Diversity Index, denoted as H, was computed.

The calculation of this index followed the methodology delineated by Negassa et al*.* [47], employing the following formulae:

$$H = -\Sigma [pi \times \log(pi)],$$

Where pi signifies the proportion of the total numbers of entries belonging to the i^{th} class.

Furthermore, the clustering of genotypes based on their morphological attributes was executed through the application of the Unweighted Pair Group Method using the Arithmetic Averages (UPGMA) algorithm. This clustering analysis was conducted utilizing the NTSYS-pc 2.02i software, a tool for numerical taxonomy and multivariate analysis system [48]. The objective was to delineate relationships among genotypes based on their morphological profiles, contributing to a comprehensive understanding of the diversity present within the chickpea genotypes.

3. RESULTS AND DISCUSSION

Distinguishing traits associated with genetic purity and ensuring the authenticity of true-to-type cultivars hold paramount significance in the realm of crop improvement, maintenance breeding, and seed multiplication [41-42]. This imperative extends to the purview of plant breeders, seed certification agencies, and seed producers [43]. The integrity of genetic purity is susceptible to deterioration owing to various factors such as natural mutations, unintended outcrossing with off-types, and mechanical mixtures [44]. To counteract these challenges, diverse methods are employed under both field as well as laboratory settings to uphold the genetic purity of crops [35-36]. Characterization through morphological traits stands out as a pivotal approach, serving as a key component for the identification of genotypes or cultivars [41-44]. It is acknowledged that the identification of any cultivar cannot rely solely on a single trait. Instead, a comprehensive morphological description encompassing both plants and seeds becomes imperative [41-44]. In this context, the present investigation delves into various agro-morphological traits, revealing that, despite some lines sharing common qualitative features, they can be distinctly differentiated based on their monomorphic traits [43].

This observation accentuates the existence of discernible genetic variations present among the lines, even in instances where only a few characteristics exhibit divergence [43]. Particularly noteworthy is the acknowledgment that the genetic base has undergone narrowing due to the deliberate selection for yield improvement [49,41-42]. This study not only emphasizes the importance of detailed morphological characterization for maintaining genetic purity but also sheds light on the intricate genetic dynamics and variations within cultivated lines, necessitating a nuanced approach in crop breeding and conservation efforts.

3.1 Morphological Characterization

Morphological characterization serves as the initial phase in the comprehensive description and categorization of germplasm lines [35-38]. A profound comprehension of morphological attributes not only expedites the discernment and differentiation of plant varieties but also plays a pivotal role in the selection of desirable traits, formulation of new populations, and the strategic transfer of favorable genes into widely cultivated food legumes [43]. In this investigation, 71 genotypes were subjected to morphological characterization based on the criteria outlined in the DUS guidelines. Detailed findings presented in Table 1 and Fig. 1. A crucial morphological trait examined was the presence or absence of anthocyanin coloration in the stem before flowering. Among the 71 genotypes, 74.65% genotypes exhibited the presence of anthocyanin pigmentation, while 25.35% demonstrated the absence of this coloration. Notably, the observation of stem color variation aligns with the findings of Gediya et al. [50] in 58 chickpea genotypes. Plant growth habit, another pivotal trait, was scrutinized at the 50% flowering. Out of the 71 genotypes, 10 were categorized as erect types, 55 as semi-erect types, whereas the remaining six as spreading types. This variation in growth habit, also reported by Asati et al. [43], underlines the diverse nature of chickpea genotypes. The erect growth habit facilitates mechanical harvesting and supports increased plant population, potentially leading to enhanced yield. Conversely, spreading types may contribute to soil moisture conservation. These findings not only aid in identification but also lay the foundation for strategic breeding efforts geared towards developing crops with desirable and agronomically advantageous traits.

The investigation into plant foliage color, a fundamental trait in plant characterization, revealed extensive variation, categorizing them into three distinct groups: light green, medium green, and dark green. Among total genotypes, nine displayed a light green foliage color, 38 exhibited a medium green color and 24 exhibited a dark green foliage. Remarkably, the manifestation of greenish-purple foliage coloration was absent in this investigation, aligning with the findings of Nandedkar et al. [51]. Furthermore, the investigation scrutinized flower color variation, stratifying the genotypes into three groups. Twelve genotypes showed white flowers, 58 demonstrated pink flower pigmentation, whilst a singular genotype featured blue-colored flowers. One of the most essential and easily detectable distinguishing visual features is flower colour as it is commonly utilized as a marker gene in genetic studies and breeding [52]. A distinctive characteristic evaluated was the presence or absence of stripes on the standard of the flower. Among the 71 genotypes, 13 were devoid of stripes, while the remaining 58 exhibited distinct stripes on the standard of the petal. This observation contributes to the nuanced understanding of

floral morphology among the investigated genotypes. The study further encompassed an examination of plant height, revealing a spectrum of variation. Five genotypes displayed short plant stature (<45 cm), 60 genotypes were categorized as medium in height (45-65 cm), and the remaining six genotypes exhibited tall plant height (>65 cm). This variation in plant height is of particular significance, with potential implications for machine harvesting. Comparable findings of substantial variation in foliage and flower color, flower stripes, and plant height have also been reported by Thakur et al. [53] and Asati et al. [43].

Seed-related traits, encompassing seed colour, seed size, seed shape, seed testa texture, seed ribbing, and seed type, were meticulously examined approximately 30 days after harvesting. Among these traits, seed colour and seed size emerge as crucial parameters for the categorization of chickpea varieties. Moreover, these two traits hold significant sway as preferred characteristics among consumers and are essential in marketing strategies, as elucidated by Solanki et al. [54]. The observed considerable variation in seed color within the germplasm offers promising breeding material for varietal development programmes. This embraces specific significance, given the recognition of such variation in seed color for its association with elevated market prices and increased profitability to farmers. The diverse range of seed colors led to the classification of genotypes into eight distinct groups: brown (34), dark brown (7), black (2), creamy beige (14), green (4), orange (4), yellow (5), and gray (1). This categorization aligns with previous findings reported by Gediya et al. [50], Thakur et al. [53], and Asati et al. [43]. The identification and classification of genotypes based on seed color not only contribute to the understanding of genetic diversity within the germplasm but also bear significant implications for breeding programmes aimed at developing varieties with desirable seed characteristics.

Diverse seed morphologies were discerned, particularly in the dimension of seed shape, with the owl's head type prevailing in 48 genotypes, pea-shaped in 16 genotypes, and the angular type observed in only seven genotypes. Noteworthy variations were also noted in seed testa texture, where 17 genotypes exhibited a rough texture, 54 genotypes displayed a smooth texture, and tuberculated texture was conspicuously absent across all genotypes. Similar trends in seed ribbing were apparent, categorizing genotypes into two groups, with 52 genotypes lacking seed ribbing and the remaining 19 genotypes showcasing the presence of seed ribbing. These findings are in concordance with studies conducted by Solanki et al. [55], Gediya et al. [50], and Asati et al. [43]. Conspicuously, no discernible variation was detected in seed type, as all 71 genotypes classified as desi type. The surface texture of seeds emerged as a critical trait, with rough-textured seeds found in 17 genotypes, representing a potential deterrent for stored grain pests. Conversely, the smooth texture, exhibited by 54 genotypes, aligns with consumer preferences, contributing to enhanced market acceptance. Both rough and smooth-textured genotypes bear significance in further breeding agendas, as elucidated by Solanki et al. [54].

3.2 Shannon's Diversity Indices

In the context of hybridization endeavors, the acquisition of genetically diverse parental entities is paramount. The frequency distribution of diversity indices, specifically the H' index, was computed for ten qualitative traits as outlined in Table 2. Shannon's diversity indices, calculated for these morphological traits, ranged between 0.47 to 1.52. Remarkably, the trait of seed colour manifested the highest diversity index (1.52), signifying elevated diversity, whereas the trait flower stripes exhibited the lowest diversity index (0.47). These results align coherently with prior investigations, particularly those conducted by Mishra et al. [41], Sharma et al. [42], Thakur et al. [53] and Asati et al. [43]. These studies consistently emphasized that seed color stands out as a trait characterized by substantial diversity, whilst seed type exhibits comparably limited diversity. The computed diversity indices not only contribute quantitatively to the understanding of genetic diversity within the examined germplasm lines but also underpin the concept that certain morphological traits possess inherently higher variability than others. The knowledge derived from such diversity indices is crucial in formulating effective hybridization strategies, ensuring the inclusion of diverse genetic material, and ultimately enhancing the potential for successful breeding programmes.

Table 1. List of morphological traits with DUS descriptors as per PPV&FRA, 2018 [45]

S. No.	Descriptors	States	Stage of observation
1	Stem Anthocyanin pigmentation	Absent, Present	Before flowering
2	Plant: Growth habit	Semi erect (20-40° from vertical), semi spreading (40-60° from vertical) and spreading (60-80° from vertical)	50 % flowering
3	Plant: Colour of foliage	Light green, medium green and dark green	50 % flowering
4	Flower: colour	White, pink and blue	50 % flowering
5	Flower: stripes	Absent and present	50 % flowering
6	Plant: height	Short (<45 cm), medium (45-65 cm) and tall (>65 cm	Fully developed green pods
7	Seed colour	Beige, Creamy beige, Green, Yellow, Orange, Brown, Dark brown, Grey, Black	30 days after harvest
8	Seed shape	Pea shaped, owl's head and angular	30 days after harvest
9	Seed testa texture	Smooth, rough and tuberculated	30 days after harvest
10	Seed ribbing	Absent and present	30 days after harvest

Table 2. Frequency distribution and Shannon-weaver diversity index for various morphological traits

S. No.	Descriptors	Score	Genotype frequency	Percentage contribution (%)	Shannon's diversity index
1	**Stem Anthocyanin pigmentation**				0.56
	Absent	1	18	25.35	
	Present	9	53	74.65	
2	**Plant: Growth habit**				0.77
	Erect (20-40^{o} vertical)	3	10	14.08	
	Semi spreading (40-60^{o} vertical)	5	55	77.46	
	Spreading (60-80^{o} vertical)	7	6	8.45	
3	**Plant: Colour of foliage**				1.02
	Light green	1	9	12.67	
	Medium green	2	38	53.52	
	Dark green	3	24	33.80	
	Greenish purple	4	0	0	
4	**Flower: colour**				0.80
	White	1	12	16.90	
	Pink	2	58	81.69	
	Blue	3	1	1.40	
5	**Flower: stripes**				0.47
	Absent	1	13	18.30	
	Present	9	58	81.69	
6	**Plant: Height**				0.75
	Short (<45 cm)	3	5	7.04	
	Medium (45-65 cm)	5	60	84.50	
	Tall (>65 cm)	7	6	8.45	
7	**Seed colour**				1.52
	Beige	1	0	0	
	Creamy beige	2	14	19.69	
	Green	3	4	5.62	
	Yellow	4	5	7.03	
	Orange	5	4	5.62	

S. No.	Descriptors	Score	Genotype frequency	Percentage contribution (%)	Shannon's diversity index
	Brown	6	34	47.81	
	Dark brown	7	7	9.84	
	Grey	8	1	1.40	
	Black	9	2	2.81	
8	**Seed shape**				0.82
	Pea shaped	1	16	22.53	
	Owl's head	2	48	67.60	
	Angular	3	7	9.85	
9	**Seed: Testa texture**				0.55
	Rough	1	17	23.94	
	Smooth	2	54	76.06	
	Tuberculated	3	0		
10	**Seed: Ribbing**				0.58
	Absent	1	52	73.24	
	Present	9	19	26.76	

Table 3. Agro-morphological characterization of desi chickpea based on DUS descriptors

S. No.	Descriptors	Genotypes
1	**Stem anthocyanin pigmentation**	
	Absent	ICCV 201211, ICCV 201206, RVG 202, SAGL 22-116, SAGL 22-120, SAGL-152327, SAGL- 152238, SAGL- 152344, SAGL- 152227, SAGL-162364, SAGL- 152356, SAGL- 152337, SAGL- 153226, SAGL- 152222, SAGL- 152234, RVSSG 92, RVSSG 71, RVSSG 68
	Present	ICCV 201210, ICV 201109, ICCV 20116, ICGV 201115, ICCV 201214, ICCV 201205, ICCV 201104, ICCV 201117, ICCV 201207, Pant Gram-5, H12-55, SAGL 22-110, SAGL 22-116, SAGL 22-117, SAGL 22-118, SAGL 22-119, SAGL 22-121, SAGL 22-122, SAGL 22-123,SAGL 22-124, SAGL-152324, SAGL- 152237, SAGL- 152278, SAGL- 152250, SAGL- 152330, SAGL- 152405, SAGL- 152339, SAGL- 162299, SAGL- 162387, SAGL-162381, SAGL- 152336, SAGL- 152318, SAGL- 152258, SAGL- 152231, SAGL- 152223, SAGL- 152329, SAGL- 162376, SAGL- 162377, RVSSG 84, JG 315, RVSSG 74, JG 130, RVSSG 83, JAKI 9218, RVG 204, JG 6, ICC 4958, RVSSG 52, SAGL- 161024, SAGL- 163006, SAGL- 161025, SAGL- 163007, JG 62
2	**Plant: growth habit**	
	Erect (20-40^{o} vertical)	ICCV 201211, ICCV 20116, ICCV 201115, ICCV 201214, ICCV 201117, SAGL 22-116, SAGL- 152237, SAGL- 152329, RVG 204, JG 6
	Semi spreading (40-60^{o} vertical)	ICCV 201210, ICCV 201109, ICCV 201112, ICCV 201205, ICCV 201104, ICCV 201206, ICCV 201207, Pant Gram-5, H12-55, RVG 202, SAGL 22-110, SAGL 22-116, SAGL 22-117, SAGL 22-118, SAGL 22-120, SAGL 22-121, SAGL 22-122, SAGL 22-123, SAGL-152327, SAGL- 152324, SAGL- 152278, SAGL- 152250, SAGL- 152330, SAGL- 152238, SAGL-152405, SAGL- 152339, SAGL- 152344, SAGL- 152227, SAGL- 162381, SAGL- 162364, SAGL- 152356, SAGL- 152337, SAGL- 153226, SAGL-152336, SAGL- 152258, SAGL- 152231, SAGL- 152223, SAGL- 152234, SAGL- 162376, SAGL- 162377, RVSSG 84, JG 315, RVSSG 74, JG 130, RVSSG 83, JAKI 9218, RVSSG 92, ICC 4958, RVSSG 71, RVSSG 52, RVSSG 68, SAGL- 161024, SAGL- 163006, SAGL- 161025, JG 62
	Spreading (60-80^{o} vertical)	SAGL 22-119, SAGL- 162299, SAGL- 162387, SAGL- 152222, SAGL-152318, SAGL- 163007
3	**Plant: colour of foliage**	
	Light green	ICCV 20116, ICCV 201104, Pant Gram-5, SAGL 22-120, SAGL- 152238, SAGL- 152344, RVSSG 71, RVSSG 68, SAGL- 163007

S. No.	Descriptors	Genotypes
	Medium green	ICCV 201211, ICCV 201109, ICCV 201115, ICCV 201112, ICCV 201117, ICCV 201207, H12-55, SAGL 22-116, SAGL 22-117, SAGL 22-118, SAGL 22-119, SAGL 22-122, SAGL-152327, SAGL- 152324, SAGL- 152278, SAGL- 152330, SAGL- 162299, SAGL- 162381, SAGL- 162364, SAGL-152337, SAGL- 153226, SAGL- 152336, SAGL- 152227, SAGL- 152222, SAGL- 152318, SAGL- 162376, SAGL- 162377, RVSSG 84, RVSSG 74, JG 130, JAKI 9218, RVG 204, JG 6, RVSSG 92, SAGL- 161024, SAGL-163006, SAGL- 161025, JG 62
	Dark green	ICCV 201210, ICCV 201214, ICCV 201205, ICCV 201206, RVG 202, SAGL 22-110, SAGL 22-121, SAGL 22-123, SAGL 22-124, SAGL-152237, SAGL- 152250, SAGL- 152405, SAGL- 152339, SAGL- 162387, SAGL- 152356, SAGL- 152258, SAGL- 152231, SAGL- 152223, SAGL-152234, SAGL- 152329, JG 315, RVSSG 83, ICC 4958, RVSSG 52
	Greenish purple	-
4	**Flower colour**	
	White	SAGL 22-120, SAGL-152327, SAGL- 152238, SAGL- 152344, SAGL-152227, SAGL- 162364, SAGL- 152356, SAGL- 152337, SAGL- 153226, SAGL- 152234, RVSSG 92, RVSSG 71
	Pink	ICCV 201211, ICCV 201210, ICCV 201109, ICCV 20116, ICCV 201214, ICCV 201112, ICCV 201205, ICCV 201104, ICCV 201206, ICCV 201117, ICCV 201207, Pant Gram-5, H12-55, RVG 202, SAGL 22-110, SAGL 22-116, SAGL 22-117, SAGL 22-118, SAGL 22-119, SAGL 22-121, SAGL 22-122, SAGL 22-123, SAGL 22-124, SAGL- 152324, SAGL- 152237, SAGL- 152278, SAGL- 152250, SAGL- 152222, SAGL- 152330, , SAGL-152405, SAGL- 152339, SAGL- 162299, SAGL- 162387, SAGL- 162381, SAGL- 152336, SAGL- 152318, SAGL- 152258, SAGL- 152231, SAGL-152223, SAGL- 152329,, SAGL- 162376, SAGL- 162377, RVSSG 84, JG 315, RVSSG 74, JG 130, RVSSG 83, JAKI 9218, RVG 204, JG 6, ICC 4958, RVSSG 52, RVSSG 68, SAGL- 161024, SAGL- 163006, SAGL-161025, SAGL- 163007, JG 62
	Blue	ICCV 201115
5	**Flower stripes**	
	Absent	SAGL 22-120, SAGL-152327, SAGL- 152238, SAGL- 152344, SAGL-152227, SAGL- 162364, SAGL- 152356, SAGL- 152337, SAGL- 153226, SAGL- 152222, SAGL- 152234, RVSSG 92, RVSSG 92
	Present	ICCV 201211, ICCV 201210, ICCV 201109, ICCV 20116, ICCV 201214, ICCV 201112, ICCV 201205, ICCV 201104, ICCV 201206, ICCV 201117, ICCV 201207, Pant Gram-5, H12-55, RVG 202, SAGL 22-110, SAGL 22-116, SAGL 22-117, SAGL 22-118, SAGL 22-119, SAGL 22-121, SAGL 22-122, SAGL 22-123, SAGL 22-124, SAGL- 152324, SAGL- 152237, SAGL- 152278, SAGL- 152250, SAGL- 152330, SAGL- 152405, SAGL-152339, SAGL- 162299, SAGL- 162387, SAGL- 162381, SAGL- 152336, SAGL- 152318, SAGL- 152258, SAGL- 152231, SAGL- 152223, SAGL-152329,, SAGL- 162376, SAGL- 162377, RVSSG 84, JG 315, RVSSG 74, JG 130, RVSSG 83, JAKI 9218, RVG 204, JG 6, ICC 4958, RVSSG 71, RVSSG 52, RVSSG 68, SAGL- 161024, SAGL- 163006, SAGL- 161025, SAGL- 163007, JG 62
6	**Plant height**	
	Short (<45 cm)	H12-55, SAGL 22-110, H12-55, SAGL- 162364, SAGL- 152337
	Medium (45-65 cm)	ICCV 201210, ICCV 201109, ICCV 20116, ICCV 201214, ICCV 201112, ICCV 201206, ICCV 201117, ICCV 201207, Pant Gram-5, RVG 202, SAGL 22-116, SAGL 22-117, SAGL 22-118, SAGL 22-119, SAGL 22-120, SAGL 22-121, SAGL 22-122, SAGL 22-123, SAGL 22-124, SAGL-152327, SAGL- 152324, SAGL- 152237, SAGL- 152278, SAGL- 152250, SAGL- 152238, SAGL- 152339, SAGL- 152344, SAGL- 162299, SAGL-

S. No.	Descriptors	Genotypes
		162387, SAGL- 152227, SAGL- 162381, SAGL- 152356, SAGL- 153226, SAGL- 152336, SAGL- 152222, SAGL- 152318, SAGL- 152258, SAGL-152231, SAGL- 152223, SAGL- 152234, SAGL- 152329,, SAGL- 162376, SAGL- 162377, RVSSG 84, JG 315, RVSSG 74, JG 130, RVSSG 83, JAKI 9218, RVG 204, JG 6, RVSSG 92, ICC 4958, RVSSG 71, RVSSG 52, RVSSG 68, SAGL- 161024, SAGL- 163006, SAGL- 161025, SAGL-163007, JG 62
	Tall (>65 cm)	ICCV 201211, ICCV 201112, ICCV 201205, ICCV 201104, SAGL-152330, SAGL- 152405
7	**Seed colour**	
	Beige	-
	Creamy beige	SAGL 22-120, SAGL-152327, SAGL- 152344, SAGL- 152227, SAGL-162364, SAGL- 152356, SAGL- 152337, SAGL- 153226, SAGL- 152318, RVSSG 92, SAGL- 152234, SAGL- 162381, SAGL- 152238, RVSSG 71
	Green	SAGL 22-116, SAGL 22-122, RVSSG 68, SAGL- 161024
	Yellow	ICCV 201109, ICCV 201117, ICCV 201207, Pant Gram-5, H12-55
	Orange	SAGL- 152278, SAGL- 152250, SAGL- 152339, RVSSG 52
	Brown	ICCV 201211, ICCV 201210, ICCV 20116, ICCV 201214, ICCV 201112, ICCV 201205, ICCV 201104, ICCV 201206, ICCV 201115, RVG 202, SAGL 22-117, SAGL 22-121, SAGL 22-123, SAGL 22-124, SAGL-152324, SAGL- 152237, SAGL- 152330, SAGL- 152405, SAGL- 162387, SAGL- 152336, SAGL- 152258, SAGL- 152234, SAGL- 152329, SAGL-162376, SAGL- 162377, RVSSG 84, JG 315, RVSSG 74, JG 130, RVSSG 83, JAKI 9218, RVG 204, JG 6, ICC 4958, JG 62
	Dark brown	SAGL 22-110, SAGL 22-118, SAGL 22-119, SAGL- 162299, SAGL-152222, SAGL- 152231, SAGL- 152223
	Grey	SAGL- 161025
	Black	SAGL- 163006, SAGL- 163007
8	**Seed shape**	
	Pea shaped	SAGL-152327, SAGL- 152250, SAGL- 152238, SAGL- 152339, SAGL-152344, SAGL- 152227, SAGL- 162381, SAGL- 162364, SAGL- 152337, SAGL- 153226, SAGL- 152318, SAGL- 152258, SAGL- 152231, SAGL-152234, RVSSG 92, SAGL- 161025
	Owl's head	ICCV 201210, , ICCV 20116, ICCV 201214, ICCV 201112, ICCV 201104, ICCV 201206, ICCV 201117, Pant Gram-5, H12-55, RVG 202, SAGL 22-110, SAGL 22-116, SAGL 22-117, SAGL 22-118, SAGL 22-119, SAGL 22-120, SAGL 22-121, SAGL 22-122, SAGL 22-123, SAGL 22-124, SAGL- 152324, SAGL- 152237, SAGL- 152278, SAGL- 152330, SAGL-152405, SAGL- 162299, SAGL- 162387, SAGL- 152356, , SAGL- 152336, SAGL- 152222, SAGL- 152223, SAGL- 152234, SAGL- 162376, SAGL-162377, RVSSG 84, , RVSSG 74, JG 130, RVSSG 83, JAKI 9218, RVG 204, JG 6, ICC 4958, RVSSG 71, RVSSG 52, SAGL- 161024, SAGL-163006, SAGL- 163007, JG 62
	Angular	ICCV 201211, ICCV 201109, ICCV 201205, ICCV 201207, SAGL-152329, JG 315, RVSSG 68,
9	**Seed testa texture**	
	Rough	ICCV 201109, ICCV 201214, ICCV 201207, RVG 202, SAGL 22-118, SAGL 22-119, SAGL 22-121, SAGL 22-122, SAGL 22-123, SAGL 22-124, SAGL- 152330, SAGL- 152344, SAGL- 152223, , SAGL- 162377, RVSSG 84, RVSSG 52, SAGL- 161024
	Smooth	ICCV 201211, ICCV 201210, ICCV 20116, ICCV 20115, ICCV 201214, ICCV 201112, ICCV 201205, ICCV 201104, ICCV 201206, ICCV 201117, Pant Gram-5, H12-55, SAGL 22-110, SAGL 22-116, SAGL 22-117, SAGL 22-120, SAGL- 152324, SAGL- 152237, SAGL- 152278, SAGL- 152250, SAGL- 152238, SAGL- 152405, SAGL- 152339, SAGL- 162299, SAGL-

S. No.	Descriptors	Genotypes
		162387, SAGL- 152227, SAGL- 162381, SAGL- 162364, SAGL- 152356, SAGL- 152337, SAGL- 153226, SAGL- 152336, SAGL- 152222, SAGL-152318, SAGL- 152258, SAGL- 152231, , SAGL- 152234, SAGL- 152329, SAGL- 162376, JG 315, RVSSG 74, JG 130, RVSSG 83, JAKI 9218, RVG 204, JG 6, RVSSG 92, ICC 4958, RVSSG 71, RVSSG 68, SAGL-163006, SAGL- 161025, SAGL- 163007, JG 62
	Tuberculate	-
10	**Seed ribbing**	
	Absent	ICCV 201211, ICCV 201210, ICCV 201109, ICCV 20116, ICCV 201214, ICCV 201112, ICCV 201205, ICCV 201104, ICCV 201206, H12-55, RVG 202, SAGL 22-110, SAGL 22-118, SAGL 22-119, SAGL 22-120, SAGL 22-121, SAGL 22-122, SAGL 22-123, SAGL 22-124, SAGL-152327, SAGL- 152324, SAGL- 152237, SAGL- 152278, SAGL- 152250, SAGL-152330, SAGL- 152238, SAGL- 152405, SAGL- 152339, SAGL- 152344, SAGL- 152227, SAGL- 162381, SAGL- 162364, SAGL- 152337, SAGL-153226, SAGL- 152222, SAGL- 152318, SAGL- 152258, SAGL- 152231, SAGL- 162377, RVSSG 84, JG 315, RVSSG 83, JAKI 9218, RVG 204, RVSSG 92, ICC 4958, RVSSG 71, SAGL- 163006, SAGL- 161025, SAGL- 163007, JG 62
	Present	ICCV 201117, ICCV 201207, Pant Gram-5, SAGL 22-116, SAGL 22-117, SAGL- 162299, SAGL- 162387, SAGL- 152356, SAGL- 152336, SAGL-152223, SAGL- 152234, SAGL- 152329, SAGL- 162376, RVSSG 74, JG 130, JG 6, RVSSG 52, RVSSG 68, SAGL- 161024

Anthocyanin coloration absent

Anthocyanin coloration present

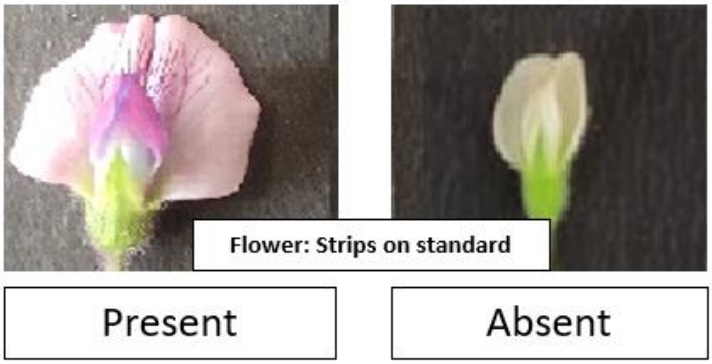
Erect

Semi erect

Spreading


Plant: Colour of foliage
Light green
Green
Dark green


Flower colour
Pink
Blue
White


Flower: Strips on standard
Present
Absent


Plant: Height
Tall
Medium
Short

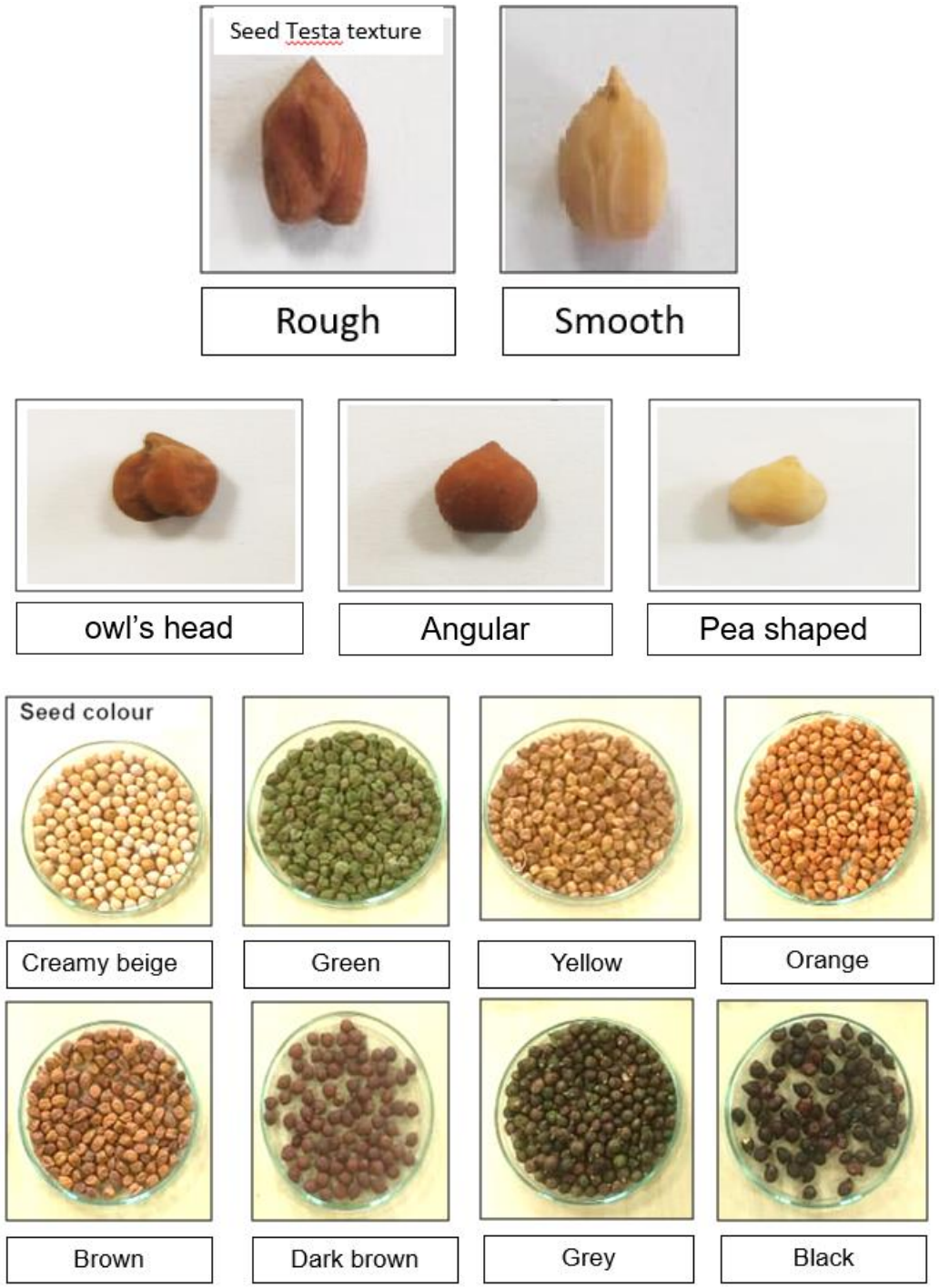


Fig. 1. Pictorial representation of agro-morphological traits in chickpea

3.3 Qualitative Cluster Analysis

A qualitative cluster analysis, employing the UPGMA algorithm implemented of 71 chickpea genotypes, considering 10 distinct qualitative traits (Table 3). The resultant dendrogram, depicted in Fig. 2, provides a visual representation of the relational similarities among the genotypes based on the measured qualitative variables. This dendrogram serves as an illustrative depiction of the efficacy of the methodological approach employed in this investigation for the systematic classification of chickpea genotypes. The hierarchical clustering analysis discerned two prominent clusters denoted as Cluster A and Cluster B. cluster A

encompasses 13 genotypes, whereas cluster B comprises a more extensive regiment of 58 genotypes. Remarkable internal structuring within cluster B is evident, leading to the delineation of two subgroups designated as 'b1' and 'b2'. Subgroup 'b1' is characterized by a minimal composition, encompassing only two genotypes, whereas subgroup 'b2' incorporates a more substantial contingent of 56 genotypes. The construction of a dendrogram with distinct clusters and subgroups attests to the efficacy of the functional methodology in effectively capturing and portraying the inherent diversity among chickpea genotypes. These delineated clusters and subgroups could potentially correspond to distinct genetic lineages or phenotypic variations within the germplasm lines. The findings of Asati et al. [43], who similarly employed dendrogram construction on a dataset of 78 chickpea genotypes across 17 qualitative traits, line up with and support the sturdiness of the clustering outcomes detected in present investigation. This analytical approach holds significance in facilitating the identification of genotypic patterns and relationships, thereby informing breeding strategies and germplasm management.

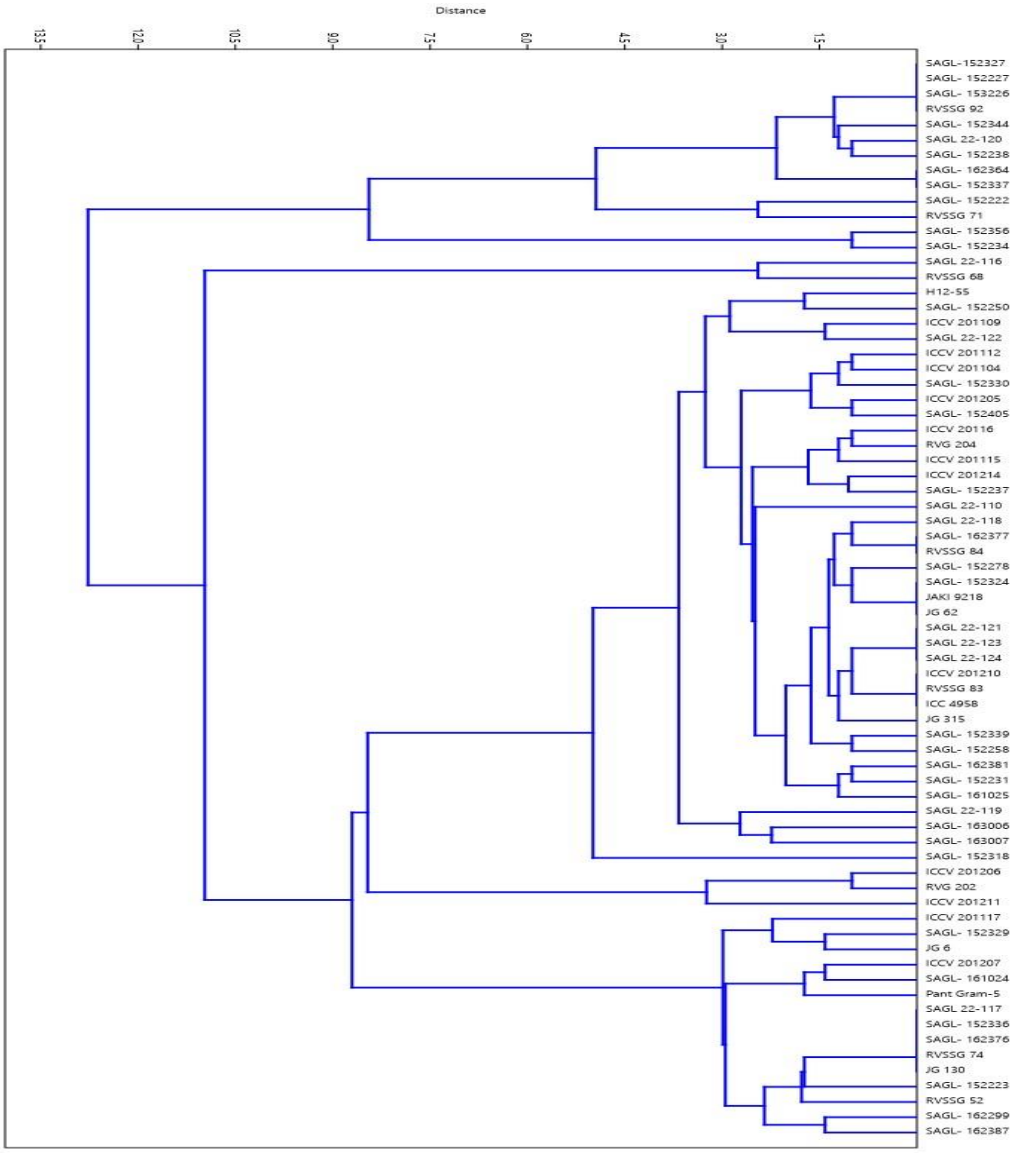


Fig. 2. UPGMA dendrogram based on morphological variability in qualitative traits of 71 Chickpea genotypes

4. CONCLUSION

In the comprehensive assessment of 10 distinct DUS traits within chickpea genotypes, it became evident that three traits exhibited a dimorphic pattern, six traits displayed a trimorphic pattern, whilst a single trait demonstrated polymorphic patterns with more than three phenotypic variations. This observation highlights the inherent morphological complexity and diversity within the evaluated germplasm lines. Conspicuously, traits such as seed color, foliage color, and seed shape showcased substantial diversity, implying their significance in shaping market dynamics and consumer preferences, thereby rendering them remarkable targets for enhancement through breeding programmes. The study's findings underscore the practical significance of a thorough morphological analysis for plant breeders, serving as a valuable tool for genotype selection under both in-field cultivation and seed management. The observed genetic variability present among the studied genotypes, coupled with distinctive morphological profiles derived from a combination of DUS traits, holds potential for varietal identification, characterization, and the strategic selection of diverse parental entities in hybridization programmes. This approach, aimed at eliciting a more heterotic response, is poised to yield superior segregants in the realm of chickpea breeding.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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