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Agro-morphological characterization of *desi* chickpea (*Cicer arietinum* L.) genotypes based on DUS descriptor

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Abstract
Varietal characterization, varietal identification and genetic purity are the most important aspect for seed certification officers and growers for maintaining the seed quality. One hundred ninety three *desi* chickpea genotypes were evaluated for twenty agro-morphological characters based on the guidelines for DUS descriptors on chickpea by PPV & FRA. The results indicated that the genotypes of chickpea can be distinguished and identified by plants and morphological characters. These differences are useful in identification of chickpea genotypes. The observations showed that the characters like anthocyanin coloration, days to 50% flowering, plant: growth habit, foliage colour, leaflet size, leaf pattern, peduncle length, plant height, pod: number of seed, seed colour, seed size, seed shape and seed texture, showed subsequent variations indicating polymorphic in nature as compared to the traits such as flower: number per peduncles, flower: strips, seed: ribbing and seed types, were found to be monomorphic.

Keywords: Chickpea, DUS, varietal identification, characterization

Introduction
Chickpea (*Cicer arietinum* L.), a winter annual crop belongs to the family Leguminosae/ Fabaceae. In India, chickpea is known by different names like chana or gram or bengal gram or chani in Haryana, Rajasthan, Uttarakhand, Uttar Pradesh, Madhya Pradesh, Chhattisgarh, Bihar, Jharkhand, chhole in Punjab, Jammu and Kashmir and Delhi; Chola in West Bengal; Harbara in Maharashtra; Boot in Orissa; Sanagulu in Andhra Pradesh; Kadale in Karnataka; Kadalai in Tamil Nadu; and Kadala in Kerala, indicating its wide spread cultivation and knowledge of utilization. Chromosome number in *Cicer* species can be generalized as 2n=2x= 16 (Bentham and Hooker, 1970) [3], although varying numbers both for chickpea (2n= 2x= 14, 16, 24, 32) and other wild Cicer species (2n=14, 16, 24) have been reported but could not be confirmed by other workers. The third most significant legume in the world after dry beans and dry peas is chickpea (*Cicer arietinum* L.), which has a high nutritional value and plays a big role in the evaluation of nitrogenous and phosphorus materials in deficient soil (Joshi *et al*., 2018) [6].
Chickpea is categorized into two major types based on distinct botanical or morphological traits as well as molecular diversity analysis: *desi* type and *kabuli* type the *desi* (microsperma) chickpea is distinguished by its small seeds, pods, leaflets, and plantlets. Despite this, considerable differences in flower and seed coat colour, as well as seed morphology, are typical. Characterization of morphological features has historically served as a foundation for categorizing, distinguishing, and cataloguing the germplasm the assessment of the descriptor is used to quantify germplasm. (Kumawat *et al*., 2020) [7].

Materials and Methods
One hundred ninety three germplasm accessions of *desi* chickpeas were used in the experiment for evaluation. The experiment was conducted in the *Rabi* season of 2021–2022 at the Instructional Farm, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.). The material was sown in four rows of 4.0m length with 30 x 10 cm spacing between and within each row, all of the genotypes were grown and evaluated in an Augmented Design with checks to raise the successful crop with prescribed agronomic and plant protection methods were used for the characterization and classification of chickpea genotypes, the observations were made on 5 randomly chosen plants of 193 germplasm lines for agro-morphological and seed traits at different crop growth stages according to the PPV & FRA, 2007, GOI guidelines for the conduct of the DUS test of chickpea (*Cicer arietinum* L.).

The lines have been observed, noted and measured during the vegetative and reproductive growing states for twenty agro-morphological characters on five consecutive plants of each entry.

The seed quality is estimated by varietal purity, be it physical or genetically. A cultivar can be clearly distinguished by morphological, physiological, cytological, and other and when reproduced (sexually/asexually). In practical, a variety must show distinct, uniform and stable (DUS) variations which will be useful in varietal identification. No cultivar/ variety can be identified or rejected by remaining only seed or morphological characters in the field. Thus stable visual diagnostic characters of seed and morphology are very essential (Lalitha, 2007) [8].

Table 1: List of 193 desi chickpea genotypes with their source.

S. No.	Country	State	No. of Lines
1	India	Exotic sp.	5
2	India	Andra Pradesh	7
3		Bihar	4
4		Gujarat	5
5		Haryana	2
6		Himachal Pradesh	1
7		Karnataka	3
8		Madhya Pradesh	27
9		Maharashtra	12
10		New Delhi	17
11		Orissa	2
12		Punjab	9
13		Rajasthan	10
14		Tamil Nadu	2
15		Uttar Pradesh	12
16		Uttrakhand	1
17		West Bengal	2
18	Syrian Arab Republic	-	1
19	Other	-	6
20	Unknown	-	29
		-	36
	Total		193

Results and Discussion

Chickpea crop improvement is restricted by a narrow genetic base, which needs to be expanded in order to utilize the genetic potential of these lines. Therefore, to determine the genetic diversity of a crop, it is necessary to before develop crop breeding strategies. Since, one of the most crucial prerequisites for the correct and logical use of working collections in upcoming breeding programs is the assessment of the genetic variability and characterization of primary genetic resource specimens.

Table 2: Agromorphological traits with DUS descriptor of chickpea

S. No.	Traits/ Characteristics	Classification/ States	Frequency distribution	Stages of observation	Variation
1.	Stem: Anthocyanin colouration	Absent,	133	Before flowering	Polymorphic
		Present	60		
2.	Stem: Height at initiation of first flower	Low (<8 nodes),		First flowering	Polymorphic
		Medium(8-15 nodes)			
		High (>15 nodes)			
3.	Time of flowering (50% of plants with at least one open flower)	Extra early (<40 days)	0	First flowering	Polymorphic
		Early (40-60 days)	114		
		Medium (61-80 days)	79		
		Late (>80 days)	0		
4.	Plant: Growth habit	Erect (0-150 from vertical)	26	50% flowering	Polymorphic
		Semi erect (16-600 from vertical)	167		
		Spreading (61-800 from vertical)	0		
5.	Plant: Colour of foliage	Light green	31	50% flowering	Polymorphic
		Medium green	156		
		Dark green,	03		
		Greenish purple	02		
		Green	02		
6.	Leaflet: size (middle of the plant and middle of the leaf)	Small (<10 mm),	180	50% flowering	Polymorphic
		Medium (10-15 mm)	11		
		Large (>15 mm)	02		
7.	Leaf Pattern	Simple,	02	50% flowering	Polymorphic
		Compound,	01		
		Pinnate	190		

8.	Flower: Number per peduncle	Single,	193	50% flowering	Monomorphic
		Twin	0		
9.	Flower: Colour	White,	01	50% flowering	Polymorphic
		Pink,	191		
		Blue	01		
10.	Flower: Stripes on standard	Absent,	0	50% flowering	Monomorphic
		Present	193		
11.	Peduncle length	Short (<5 mm),	20	Pod development	Polymorphic
		Medium (5-10 mm),	162		
		Long (>10 mm)	11		
12.	Plant: Height	Short (<45 cm)	181	Fully developed green pod	Polymorphic
		Medium (45-65 cm),	12		
		Tall (>65 cm)	0		
13.	Pod: Number of seeds	One,	187	Harvest maturity	Polymorphic
		More than one	06		
14.	Seed: Colour	Beige/Creamy beige	06	30 days after harvest	Polymorphic
		Green,	0		
		Yellow	32		
		Brown	90		
		Dark brown	59		
		Grey	06		
		Black	0		
15.	Seed: size(weight of 100seeds at 10% moisture content)	Very small (<20g),	174	30 days after harvest	Polymorphic
		Small (20-25g),	10		
		Medium (26-35g),	08		
		Large (36-45g),	01		
		Very large (>45g)	0		
16.	Seed: Shape	Pea-shaped,	04	30 days after harvest	Polymorphic
		Owl's head,	35		
		Angular	154		
17.	Seed: Testa texture	Rough,	140	30 days after harvest	Polymorphic
		Smooth,	29		
		Tuberculated	24		
18.	Seed: Ribbing	Absent,	193	30 days after harvest	Monomorphic
		Present	0		
19.	Seed: Type	Desi,	193	30 days after harvest	Monomorphic
		Kabuli	0		

Stem: Anthocyanin coloration, which is an important trait recorded before flowering was classified into two categories, i.e. presence and absence. Out of the 193 genotypes, 60 genotypes had anthocyanin pigmentation, while the remaining 133 genotype showed absence for the trait. The genotypes were divided into two groups based on the time of blooming, or the percentage of plants with at least one open flower, 114 genotypes flowered early (40–60 days), and 79 genotypes had medium flowering duration (61–80 days).

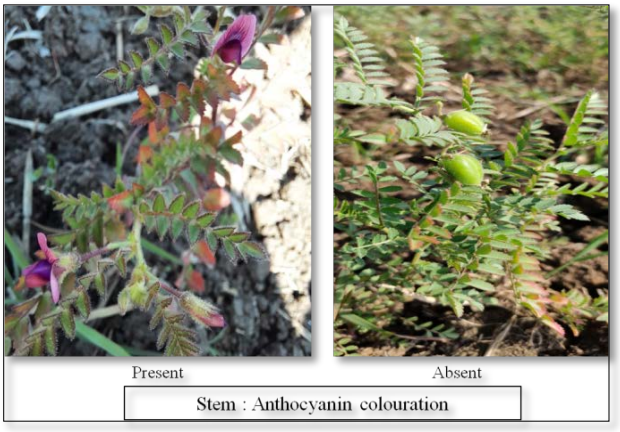
At 50% flowering stage the plants were observed for distinguishable morphological characters namely plant: growth habit, plant: colour of foliage, leaflet: size, leaf: pattern, flower: number per peduncle, flower: colour and flower: stripes on standard, contributing for identification and distinguishing the genotypes under observation. Based on variations in plant growth habit the genotypes were classified into two groups. 26 genotypes were erect type and 167 genotypes were classified into semi-erect type. Plant: colour of foliage which is an important distinguishing feature in plant characterization showed wide variation and grouped all the 193 genotypes into five categories i.e. light green (31), medium green (156), dark green (03), greenish purple(02) and green (01). Therefore, the study material comprised of 193 *desi* chickpea germplasm (Table 1). Variations were observed with respect to leaflet: size (i.e. length of leaflet from middle of the plant and middle of the leaf) and based on that, 180 genotypes were recorded with small leaflet size of less than 10 mm, 11 genotypes were recorded with medium leaflet size (10 mm – 15 mm) and 02 genotypes were recorded with large leaflet size (>15 mm). Variation was observed among the genotypes for leaf: pattern and among 193 genotypes, 190 genotypes had pinnate type of leaf pattern, 02 genotypes had simple type of leaf pattern and 01 genotype had compound type of leaf pattern. No variations were recorded in trait Flower: number per peduncle, all the genotypes had single flower per peduncle indicating the monomorphic traits.

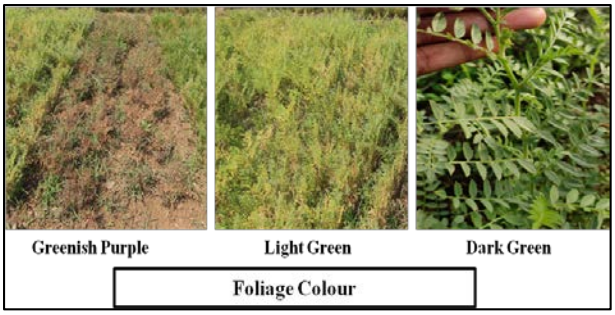
One of the most essential and easily detectable distinguishing visual feature is flower colour. Variation was found among the genotypes for flower: colour and out of 193, 190 genotypes had pink flowers, 02 genotypes had blue flowers and only one genotype recorded white flower colour. The genotypes were also examined for flower: stripes on standard and it was recorded that all 193 genotypes showed presence of stripes on standard petal of flower showing no differences. The study of peduncle: length at pod development stage revealed that the experimental material can be categorized into three group's i.e. short, medium and long peduncle genotypes. Amongst 193, 20 genotypes showed short peduncle length (<5 mm), 162 genotypes exhibited medium (5-10 mm) whereas, 11 genotypes exhibited long peduncle length (>10 mm). At fully developed green pod stage the genotypes were observed for plant: height and grouped the

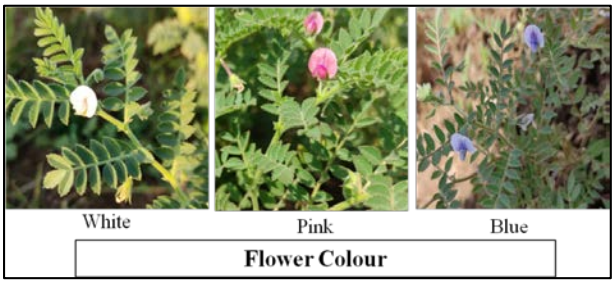
genotypes into two groups 181 genotypes were grouped as short (< 45 cm) and 12 genotypes were grouped as medium (45-65cm) plant height. Variations were also found in number of seeds per pod, 187 genotypes showed one seed per pod and remaining 06 genotypes found to have more than one seed per pod.

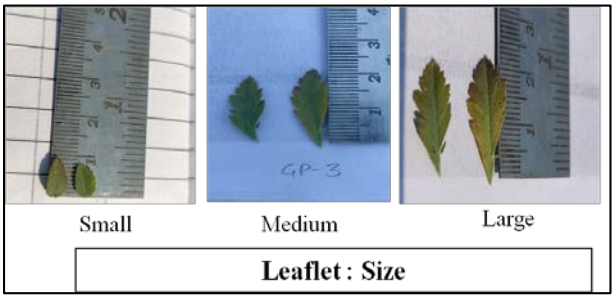
All the seed related traits *viz*., seed: colour, seed: size, seed: shape, seed: testa texture, seed: ribbing and seed: type were observed at 30 days after harvest. Among these seed traits, seed: colour and seed: size are proposed to be used for grouping chickpea varieties (Anon, 2007) [2] and these two traits are the most preferred traits by consumers as well as marketing traits (Solanki *et al*., 2019) [11]. Based on variations observed in seed: colour, the genotypes were classified into six colour groups which are, yellow(32), brown(90), dark brown(59) and grey (06), beige and creamy beige(06). Among these six colour groups, brown colour seeds were predominant. The seed: sizes in genotypes were recorded based on the 100 seed weight of each genotype at 10% moisture content. 174 genotypes exhibited very small size seeds (<20 g), 10 genotypes had small seed size ranging between 20-25 g, 08 genotypes showed medium seed size (26-35g) and 01 genotype showed large seed size with weight of 36-45g. This large seeded line would be considered as export purpose and can also be used in chickpea hybridization programme (Kumawat *et al*., 2020) [7]. Variations observed for seed: shape revealed that the angular type was predominant and exhibited by 154 genotypes, 35 genotypes had owl's head seed shape and only 04 genotypes had pea shaped seed shape. Based on wide variations observed in seed: testa texture three major groups were formed. Rough texture was observed in 140 genotypes, smooth texture (29) genotypes and tuberculated texture (24) genotypes. No variation was found in seed: ribbing and all the genotypes showed presence of seed ribbing and all the genotypes were *desi* type. Similar, genotype identification based on distinguishable morphological characters were carried out and reported by Janghel *et al*., 2020 [5]. A detailed morphological description of plants and seeds should therefore be assigned distinctive morphological profiles. Similar facts suggested by Solanki *et al*., (2019) [11], and Adem and Tesso (2019) [1].

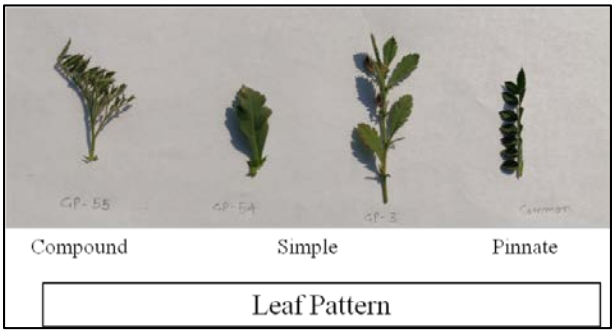
According to study findings, a plant breeder would find it most practical to choose genotypes at the field and seed level based on distinct morphological profiles. It would be beneficial to increase seed output if morphological characteristics were linked to increased seed yield or contributed significantly to yield. In order to produce a distinct profile of these lines, morphological characterization is therefore helpful. Therefore, comprehensive characterization promotes preferential selection and results in a more effective utilization of the material under consideration in the chickpea improvement program. The genotypes identification based on distinguishable morphological characters were reported by lalitha (2007) [8], Upadhyay *et al.* (2002) [12], Yadav and shrivastava (2002) [13], Gediya *et al*. (2018) [4], Nandedkar *et al.* (2021) [9] and Saxena *et al*. (2021) [10]

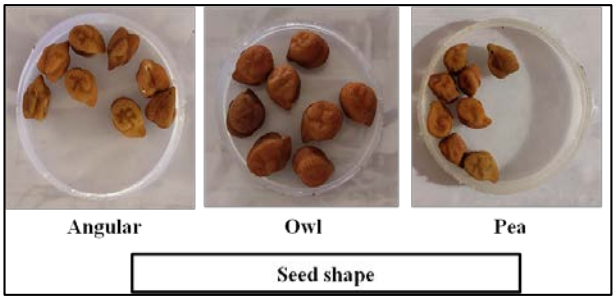


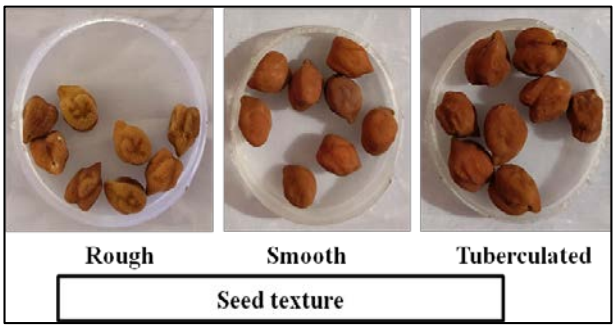












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