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Cultivar identification and diversity analysis based on morphological descriptors and image analysis in chickpea (*Cicer arietinum* L.)

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ABSTRACT

Thirty three genotypes of chickpea including 9 *kabuli* and 24 *desi* types were evaluated for distinctiveness based on 13 qualitative and 7 quantitative morphological DUS descriptors. In *desi* type, only 4 traits were polymorphic whereas, in *kabuli* type, only 3 were polymorphic. Identification profiles were generated on the basis of grouping and essential characters prescribed by DUS Guidelines of PPV & FR Authority. However, out of twenty four *desi* genotypes, distinct profiles could be created only for sixteen varieties and in *kabuli* type, only three out of nine genotypes could be singled out individually. Image analysis using scanned images of flowers of *desi* types successfully complemented the morphological descriptors to establish genotypic identity based on differences in the petal colour intensity and venation pattern. Genetic parameters for all the quantitative traits revealed less environmental influence on the characters expression thus, signifying their utility in the varietal characterization. Seven agro-morphological traits were used to assess the variability using Ward's Minimum Variance Cluster Analysis. Thirty three cultivars from both types were grouped into four cluster each, however, none of the clusters contained genotypes with all the desirable traits, which could be directly selected and utilized.

Key words: Chickpea, Distinctiveness, Essential characters, Grouping characters, Image analysis, Morphological descriptors.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is one of the most important and earliest cultivated legumes, approximately 7500 years old (Maiti and Ebeling, 2001). It ranks second among the world's food legumes in terms of area. India is the largest producer of chickpea (Bengal gram) which is highly rich in protein content and other essential nutrients. A variety of *desi* and *kabuli* chickpeas have been developed and the characteristics of these cultivars may vary depending on the producing region.

Morphological characters are successfully used in plant identification up to genus and species level but not to varietal level. As per the Protection of Plant Varieties and Farmer's Rights Act (Anon., 2001) 20 morphological DUS descriptors are used as a taxonomic tool for distinguishing chickpea at varietal level (Anonymous., 2007). Plant morphological characters have been recognized as the universally undisputed descriptors for DUS testing and varietal characterization of crop varieties. Use of morphological descriptors in sequential fashion is useful and convenient to discriminate the different varieties (Sarao *et al.*, 2009).

Keeping this in view, the study was taken up with the objective to determine the relative extent of distinctiveness of different morphological DUS descriptors for 9 *kabuli* and 24 *desi* genotypes. Since manual identification of varieties by specialized technicians is slow, has low reproducibility, and possesses a degree of subjectivity (Lootens *et al.*, 2007), image analysis studies were also carried out. To ascertain the variability level, the genetic parameters and diversity for these varieties was worked out using 7 agro-morphological traits.

MATERIALS AND METHODS

The research material consisted of 33 genotypes of chickpea; including nine of *kabuli* type and 24 of *desi* type. The genotypes were raised during *rabi* season 2014-15 and 2015-16 at the research farm of Division of Seed Science and Technology, ICAR-IARI, New Delhi. A plot size of 5 rows with each row of 5 meter length was maintained. Row to row and plant to plant spacing was maintained at 45cm x 20cm. The material was replicated thrice and all the agronomic practices were followed to raise a good crop. Ten competitive plants were randomly selected from each genotype in each replication to record the data. National DUS Test Guidelines (Anonymous, 2007) were followed beginning from the trial layout for recording of the last field-related observations.

Plant Morphological Traits: As per the DUS test guidelines, 20 agro-morphological characters were recorded in chickpea varieties /genotypes at different stages of plant growth. The data observation started before flowering which was observed for stem anthocyanin colouration (absent or

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present) and plants were examined for different morphological characters during different growth stages in the field. At the first flowering stage, quantitative traits like stem height and time of flowering were recorded. At 50% flowering stage, several traits were recorded *viz.* plant growth habit, colour of foliage, leaf pattern, and flower characters like number per peduncle, colour and stripes on standard. Quantitative character *viz.* leaflet size was also recorded at this stage. Other quantitative traits *viz.* peduncle length, plant height, pod size and number of seeds were recorded between pod development to harvest maturity stages. The seed characters *viz.* seed colour, seed size, seed shape, seed testa structure, ribbing and seed type were recorded after harvest.

Generation of distinct profiles/identification key: Since the major objective of cultivar characterization is to establish distinctness among the varieties, hence an attempt was made to study the utility of the observed characters in establishing distinctness. The characters were grouped on the basis of their ability to differentiate varieties *viz.* monomorphic, dimorphic and polymorphic traits. The DUS guidelines recognises four traits as grouping characters *viz.*, time of flowering, flower colour, seed colour and seed size. An identification key involving grouping and essential characters were developed for generating distinct varietal signatures for both *desi* and *kabuli* type.

Machine vision/image analysis: The machine vision studies were carried out on the flowers of *desi* chickpea varieties. Observations were recorded on ten flowers per variety and were replicated thrice. A flatbed scanner (Canon LiDE 110 version 1.2.00) was used for image acquisition. Images of all the flowers were grabbed at resolution of 600 dpi. All images were grabbed using identical settings. The images were stored in *.tif* format for further analysis. Image analysis was used to resolve the differentiation based on petal colour intensity and venation pattern of flowers of *desi* chickpea.

Diversity analysis: The year wise analysis of the metric traits was done to assess the extent of genetic variability. The estimates of genetic parameters, which included genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and the genetic advance, as a whole, give an idea of the mode of gene action in the expression of a character. The data was subjected for analysis of variance (Steel *et al.*, 1997). The genotypic and phenotypic correlations were calculated by Kwon and Torrie (1964) technique. The genetic advance was calculated by using Falconer (1989) formula.

$$\text{Genetic Variance } V_g = \frac{\text{Genotype Mean Square (GMS)} - \text{Error Mean Square (EMS)}}{\text{Number of replications (r)}}$$

Environmental Variance (Ve) = Error Mean Square (EMS)
Phenotypic Variance V_p = Genotypic Variance (V_g) + Environmental Variance (V_e) / r

Genotypic, Phenotypic and Environmental coefficient of Variation was calculated as

$GCV\ \% = \sqrt{Vg} / \bar{X} \times 100$, $PCV\% = \sqrt{Vp} / \bar{X} \times 100$, $ECV\% = = \sqrt{Vg} / \bar{X} \times 100$,

Where, GCV% = Genotypic Coefficient of variation; V*g* = Genotypic Variance; PCV % = Phenotypic Coefficient of variation; V*p* = Phenotypic Variance; ECV % = Environmental Coefficient of variation; V*e* = Environmental Variance.

Heritability (H^2) on Entry Mean Basis was calculated as

$$H^2 = \frac{Vp}{Vg}$$

The expected Genetic Advance for each trait was calculated as

$$GA = K \sqrt{Vp\ H^2}$$

Where, K = 1.40 at 20% selection intensity for trait; Vp = Phenotypic variance for trait; H^2 = Broad Sense Heritability of the trait; Genetic Advance as percentage of mean is calculated as,

$$GA\ \% = GA / X \times \overline{100}$$

The seven agro-morphological traits viz., stem height at initiation of first flower, time of flowering, leaflet size, peduncle length, plant height, pod size, and seed size were also used to assess the variability of these varieties in both the types using Ward's Minimum Variance Cluster analysis which helps in assessment of pattern and extent of variation in the germplasm. The cluster analysis was performed using Ward's Minimum Variance dendrogram clustering (Ward, 1963).

RESULTS AND DISCUSSION

Morphological characterization: The accurate description and identification of chickpea genotypes is crucial for DUS Testing. Hence, an attempt was made to establish the distinctive profiles of chickpea varieties by using a set of morphological characteristics prescribed in DUS Test Guidelines (Anonymous, 2007). The characters were grouped on the basis of their ability to differentiate varieties *viz.*, monomorphic, dimorphic and polymorphic traits. In d*esi* type chickpea, out of 13 qualitative traits, 7 traits *viz.* stem anthocyanin colouration, leaf pattern, flower colour, stripes on standard of flower, number of seeds/pod, seed ribbing and seed type were observed to be monomorphic, 2 traits *viz.* green colour intensity of foliage, and number of flower/peduncle were dimorphic and the rest 4 *viz.* growth habit, seed colour, seed shape and seed testa texture were polymorphic in nature. With respect to 7 quantitative traits, 6 traits (stem height at the initiation of first flower, leaflet size, peduncle length, plant height, pod size and seed size) were observed to be dimorphic in nature and only 1 (days to 50% of flowering) was monomorphic in nature.

In case of *kabuli* type chickpea, 7 qualitative traits were found to be monomorphic (anthocyanin coloration of stem, leaf pattern, number of flower/peduncle, flower colour, stripes on standard of flower, number of seeds/pod and seed type); 4 traits (growth habit, green colour intensity of foliage, seed shape and seed ribbing) were found to be dimorphic and only 2 traits (seed color and seed testa texture) were polymorphic. Out of 7 quantitative traits, 4 traits were found to be monomorphic (time of flowering i.e. 50% of the plants with at least one open flower, length of peduncle, plant height, pod size and seed size), 2 traits (stem height at the initiation of first flower and leaflet size) were dimorphic and only 1 trait (seed size) was polymorphic in nature. Furthermore, the expression of each character was found to be stable in both the seasons in all cultivars, thereby, emphasizing their consistency. Makanur *et al.* (2013) also reported similar polymorphism of traits in cowpea.

Generation of distinctive Profiles: Since the major objective of cultivar characterization is to establish distinctness among the varieties. Hence, an attempt was made to study the utility of the observed characters in establishing distinctness. The DUS guidelines recognises four traits as grouping characters *viz.*, time of flowering, flower colour, seed colour and seed size. The two plant morphological traits *viz.*, time of flowering and flower colour were monomorphic in nature for both the groups since all were observed to flower late (> 80 days) and all *desi* genotypes had pink flowers while all *kabuli* genotypes had white flower. Hence, distinctive profiles could not be generated on the basis of grouping characters alone. Therefore, essential characters were used to establish the individual identity by preparing an identification key for all the genotypes in both the groups. However, no single trait could identify the genotypes individually, but was used in combinations. Similar results were also reported by Sarao *et al.* (2009) in chickpea. The expression of the qualitative traits in all the genotypes was similar for both the seasons, confirming the stability of genotypes.

Anthocyanin colouration of the stem was present in all the *desi* genotypes (Fig.1). Four genotypes viz. Pusa 372, JG 315, C 235 and Radhey had medium stem height (*first group*) whereas the remaining twenty genotypes had high height of stem at initiation of first flower (*second group*). The four genotypes of the first group with shorter height of stem could be individually identified on the basis of number of flower per peduncle, peduncle length and plant height. In the second group, JG 11 could be identified from the spreading nature of the plant. Genotypes RSG 143-1, BG 1103 and IPC 2009-198 were erect in nature and could be singled out on the basis of peduncle length for RSG 143-1 (medium) and plant height (medium for BG 1103 and tall for IPC 2009-198). The remaining genotypes were semi-erect in nature and traits like leaflet size, peduncle length, plant height, number of flowers per peduncle and pod size were used to establish identity. However, genotypes Pusa 256 and JG 14 could not be differentiated on this basis. Similarly, H 00-108 BG 362 were found to be similar. PDG 84-16, PG 96006, KGD 1168 AND BGD 72 also fell in the same group and could not be individually differentiated.

All the *kabuli* genotypes lacked anthocyanin pigmentation on the stem (Fig.2). Four traits *viz.* height of stem at initiation of first flower, plant growth habit, foliage colour and leaflet size was found to be of utility to resolve distinctness. However, genotypes *viz.* Pusa 1108 and PG95333; Pusa 1088 and L550; BG 2085 and Pusa 1053 could not be differentiated from each other.

Image analysis studies: Given the large number of varieties in *desi* chickpea, it seems morphological descriptors alone did not sufficient to establish DUS criteria. Hence, some other markers/descriptors can be considered for complementing the morphological DUS descriptors for establishing distinctiveness of closely related varieties. In *desi* chickpea genotypes, it was observed that flower colour for all the varieties was pink. Since flower colour is listed as a grouping character in the DUS guidelines, hence an attempt was made to distinguish the *desi* varieties on the basis of visual differences observed in the petal colour intensity and venation pattern. The various floral images generated through machine vision i.e. scanner are depicted in Fig.3. These pictures for characterization are essential to display variability. They also provide a supplementary description of the descriptors by visual images. The morphological characterization revealed that out of twenty four desi genotypes, distinct profiles could be created only for sixteen varieties. Genotypes Pusa 256 and JG 14 were difficult to differentiate from each other. Similarly, H 00-108 and BG 362 were also identical for all observed traits. Genotypes PDG 84-16, PG 96006, KGD 1168 and BGD 72 could not also be individually differentiated.

Based on visual differences between floral images, it was observed that Pusa 256 had bright pink petals compared to dull pink petals of JG 14. Further, the venation pattern was more prominent in the latter as compared to the former. In Pusa 256, petal width was equal from top to bottom whereas for JG 14, the petals were broader at the middle. Similarly, H 00-108 and BG 362 could also be distinguished on the basis of floral morphology. H 00-108 had light pink, elliptical petals with veins prominent only near the centre, whereas BG 362 had dark pink, round petals with prominent venation pattern observed throughout the petal width. Genotypes PDG 84-16, PG 96006, KGD 1168 and BGD 72 could also be distinguished easily on the basis of visual differences between petal colour intensity and venation pattern. Hence, image analysis techniques can be used to complement the existing DUS morphological descriptors, since it is also a cost-effective technology wherein a scanner

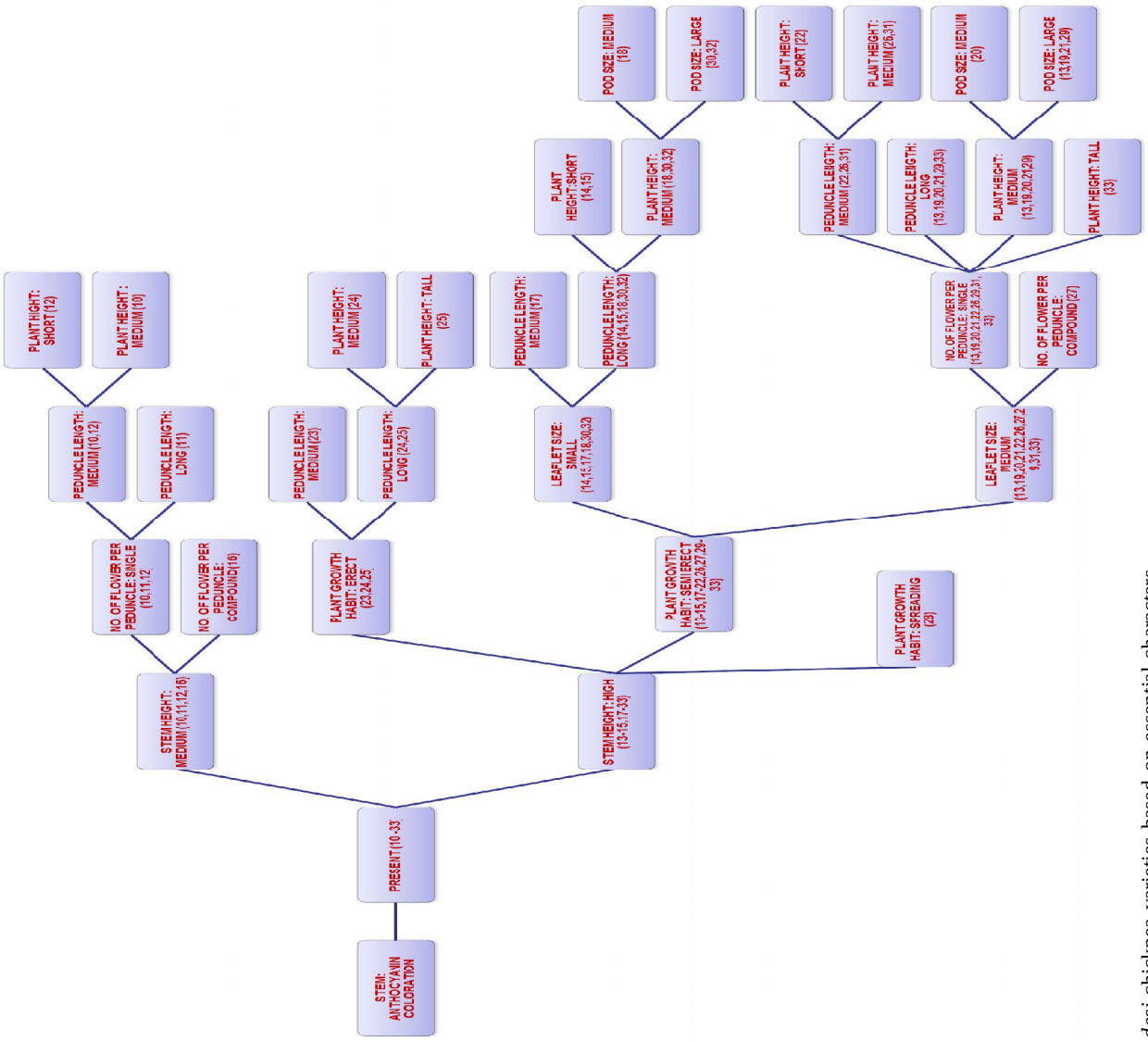

Fig 1: Identification key for *desi* chickpea varieties based on essential characters.

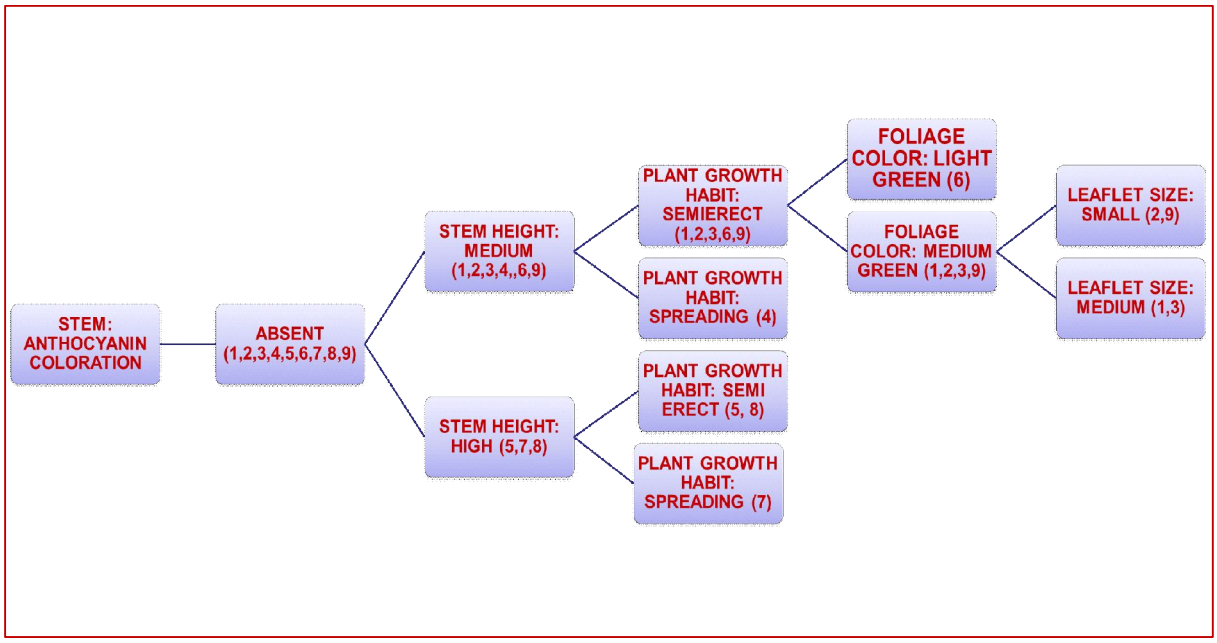

Fig 2: Identification key for kabuli chickpea varieties based on essential characters.

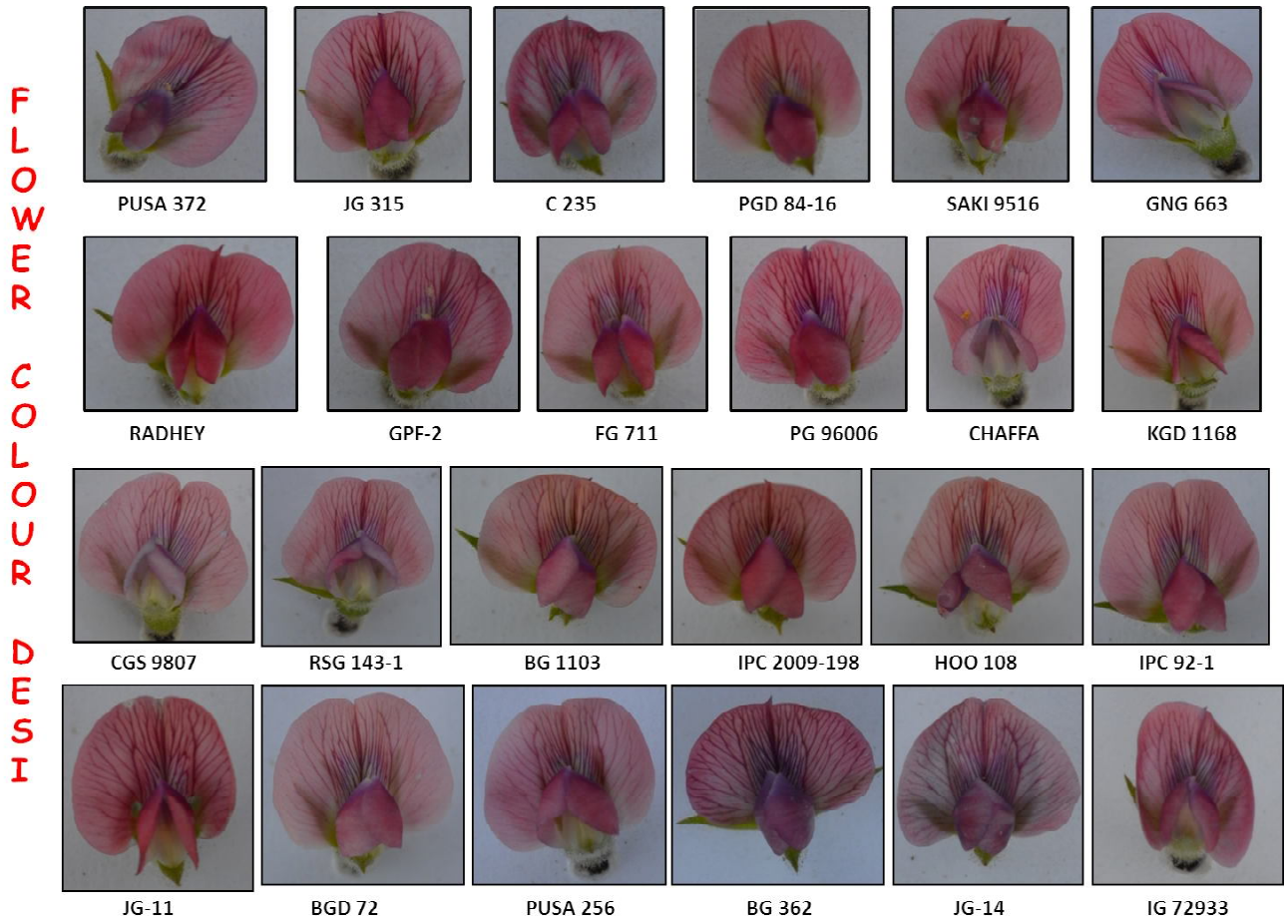

Fig 3: Image of *Desi* type flower by scanner.

can also detect the visual differences. Lootens *et al.* (2007) reported that image analysis is helpful to evaluate all colours present in given material and is stable as it is referenced against standard colour charts. Besides the use of this method for DUS testing, the derived quantitative colour data can be applied to quantitative genetics for inheritance studies. Duan *et al.* (2011), Maheshwari *et al.* (2013) and Birla *et al.* (2015) also suggested machine vision as an alternative for an automated, non-destructive and cost-effective technique to quantify the qualities of various rice varieties.

Genetic parameters: The quantitative data for the seven agro-morphological traits recorded in the present study is depicted in Table 1. Various genetic parameters, as detailed in Methodology part were elucidated from these traits for both kabuli and desi genotypes. The estimates of genetic parameters, which included genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and the genetic advance (Table 2), as a whole, give an idea of the mode of gene action in the expression of a character. High heritability accompanied with low level of

Table 1: Mean and variance values for agro-morphological traits recorded for *kabuli* and *desi* chickpea.

Genotypes			Height of insertion of first flower (cm)	Time of flowering (days)	Leaflet: Size (cm)	Peduncle: Length (cm)	Plant : Height (cm)	Pod: Size (cm)	Seed : Size (wt. of 100 seeds; g)
	1	BG 2085	13.06	118	1.01	1.41	54.40	2.73	20.35
	2	PUSA 1088	14.65	109	1.24	1.46	55.84	2.64	15.96
	3	PUSA 1053	14.50	102	1.07	1.33	55.38	2.95	25.91
	4	PUSA 5023	14.23	102	1.03	1.52	61.26	2.66	21.35
Kabuli	5	PUSA 1108	16.23	107	1.01	1.58	62.62	2.73	21.76
chickpea	6	ICC 17109	11.73	107	1.10	1.29	53.00	2.71	38.18
	7	IPCK 00-112	15.30	105	1.02	1.49	56.22	2.67	16.08
	8	PG 95333	16.51	97	1.27	1.84	62.19	2.75	24.99
	9	L-550	14.66	103	0.89	1.17	52.39	2.11	13.86
	MEAN		14.54	105	1.07	1.45	57.03	2.66	22.05
	SE		0.49	1.96	0.04	0.06	1.32	0.08	2.44
	SD		1.48	5.88	0.12	0.19	3.96	0.23	7.31
	Variance		2.19	34.53	0.01	0.04	15.66	0.05	53.37
	1	PUSA 372	14.78	102	1.00	0.94	51.97	1.93	10.76
	2	JG 315	14.85	101	1.01	1.11	48.05	1.97	10.06
	3	C 235	13.00	102	0.98	0.97	50.02	1.97	10.47
	4	PDG 84-16	15.50	88	0.98	1.47	49.22	2.28	11.46
	5	SAKI 9516	15.30	103	0.93	1.25	50.02	2.01	12.86
	6	GNG 663	15.10	99	0.89	1.03	49.30	1.95	10.76
	7	RADHEY	13.50	104	0.97	0.90	46.15	2.12	14.28
	8	GPF-2	15.80	106	0.88	0.87	48.14	1.96	10.69
Desi	9	FG 711	15.80	109	0.91	1.06	50.67	1.96	19.34
chickpea	10	PG 96006	15.40	111	1.17	1.02	51.24	2.14	20.77
	11	CHAFFA	13.40	102	1.08	1.11	52.19	1.74	20.98
	12	KGD 1168	15.40	104	1.34	1.23	50.33	2.16	20.08
	13	CSG 9807	15.10	100	1.20	0.88	45.12	2.08	19.96
	14	RSG 143-1	15.30	113	1.27	0.82	48.82	2.21	22.19
	15	BG 1103	16.50	116	1.08	1.08	61.02	2.38	20.16
	16	IPC 2009-198	16.80	114	1.39	1.22	68.01	2.52	21.32
	17	H 00-108	16.40	110	1.45	0.98	63.65	2.36	20.18
	18	IPC 92-1	16.30	106	1.35	1.91	54.42	2.19	13.91
	19	JG- 11	15.70	109	1.55	1.51	50.21	1.86	13.43
	20	BGD 72	16.30	114	1.21	1.19	54.12	2.21	16.14
	21	PUSA 256	16.20	107	0.99	1.24	71.09	2.20	8.86
	22	BG 362	17.10	106	1.05	0.95	52.91	2.48	12.22
	23	JG- 14	16.05	111	0.99	1.05	51.82	2.27	11.70
	24	IG 72933	16.30	117	1.01	1.10	56.54	2.25	8.88
	Mean		15.50	106	1.11	1.12	53.13	2.13	15.06
	SE		0.21	1.33	0.04	0.05	1.34	0.04	0.95
	SD		1.04	6.52	0.19	0.24	6.57	0.20	4.66
	Variance		1.09	42.51	0.04	0.06	43.16	0.04	21.70

Table 2: Estimates of genetic parameters for different traits in chickpea.

Genetic parameters	Height of insertion of first flower (nodes) cm	Time of flowering (days)	Leaflet: Size (cm)	Peduncle: Length (cm)	Plant : Height (cm)	Pod: Size (cm)	Seed : Size (g)
h2%	93.75	99.1	82.01	98.1	91.1	98.25	98.1
GA	26.24	12.11	10.1	21.65	6.32	13.65	50.2
PCV	13.7	6.3	5.96	11.2	3.1	7.1	26.53
GCV	12.98	6.1	5.48	11.05	2.96	7	26.2

Where: **h2%** - Heritability, **GA**- Genetic advance, **PCV** – Phenotypic coefficient of variation, **GCV**- Genotypic coefficient of variation

magnitude between PCV and GCV for all the traits indicated less environmental influence in their expression, hence, can be used in establishing the distinctness of the genotypes in chickpea. These results were in close agreement with the findings of Noor *et al.* (2003) and Farshadfar *et al.* (2013). Mushtaq *et al.* (2013) reported maximum heritability estimates for days to flowering, days to maturity, pods per plant, total weight of plant, secondary branches per plant, plant height, 100-grains weight and grain yield per plant. High heritability coupled with genetic advance observed for seed size indicated presence of additive gene action for this trait (Patil and Phandis, 1997) whereas, high heritability coupled with low genetic advance as observed for plant height revealed the presence of non-additive gene action. Bicer and Sakar (2007) have also reported that plant height was moderate/low heritable, and environmental conditions played a major role on this trait.

Diversity analysis: The analysis of variance revealed the presence of significant variability among the genotypes for all the characters studied. Twenty-four genotypes of *desi* group were grouped into four clusters (Fig.4). Maximum number of genotypes (8) was included in cluster I (Table 3a). Cluster II and III had 6 genotypes each whereas cluster IV had 4 genotypes. A perusal of results on cluster means (Table 3b) revealed that the cluster I could be characterized by shorter height of stem at initiation of first flower (14.73 cm), early flowering (100.63), small leaflet size (0.96), medium plant height (49.11), small pod size (2.03) and the lowest seed size (11.42) as compared to genotypes of Cluster IV with tall height of stem at initiation of first

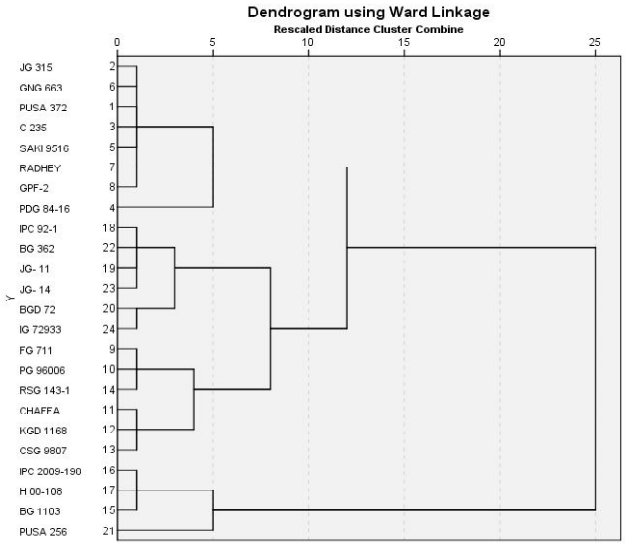

Fig 4: Dendrogram depicting clustering pattern of *desi* chickpea varieties.

Table 3 a: Clustering pattern for 28 *desi* chickpea genotypes.

Cluster	No. Of Genotypes	Varieties
I	8	JG 315, GNG 663, Pusa 372,C235, SAKI 9516, Radhey , GPF-2, PDG 84-16
II	6	IPC 92-1, BG 362, JG 11, JG 14, BGD 72, IG 72933
III	6	FG 711, PG 96006, RSG 143-1, Chaffa , KGD 1168, CSG 9807
IV	4	IPC 2009-198, H 00-108, BG 1103, PUSA 256

Table 3b: Cluster mean values for agro-morphological traits and their relative contribution to genetic divergence for *desi* type.

Character	Cluster I	Cluster II	Cluster III	Cluster IV
Stem: Height at initiation of first flower (cm)	14.73	16.29	15.07	16.48
Time of Flowering (day)	100.63	110.50	106.50	111.75
Leaflet: Size (cm)	0.96	1.19	1.16	1.23
Peduncle: Length (cm)	1.07	1.29	1.02	1.13
Plant: Height (cm)	49.11	53.33	49.73	65.94
Pod Size (Length) (cm)	2.03	2.21	2.05	2.37
Seed Size:(Wt .(g) of 100 seeds at 10% moisture content)	11.42	12.71	20.56	17.63

flower (16.48 cm), late flowering (111.75), large leaflet size (1.23), taller plant height (65.94 cm) and higher pod size (2.37 cm).

With respect to *kabuli* chickpea, the nine genotypes were grouped into four clusters as depicted in Fig.5. Maximum number of genotypes (4) was included in cluster III (Table 4a). Cluster I had 3 genotypes, while cluster II & IV had only 1 genotype each viz. BG 2085 and ICC 17109, respectively. Further, the overall composition of the clustering pattern showed that genotypes collected from the same geographic origin were distributed in different clusters. A perusal of results on *kabuli* type cluster means (Table 4b) revealed that the cluster I could be characterized by the smallest pod size (2.48) and lowest seed size (15.30), whereas cluster III was representative of larger pod size (2.78) and Cluster IV with the highest seed size (13.18) genotypes. Further, cluster III was found to have genotypes with the tallest stem height (15.37), early flowering (102.00), larger leaflet size (1.10), higher peduncle length (1.57) and the tallest plant height (60.36) compared to genotypes of cluster IV.

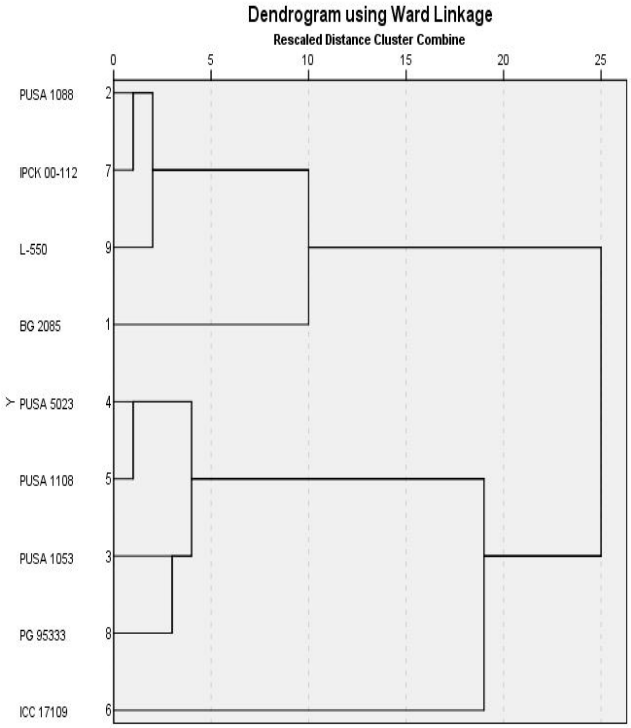

Fig 5: Dendrogram depicting clustering pattern of *kabuli* chickpea varieties.

Table 4a: Clustering pattern for 9 *kabuli* chickpea genotypes.

CLUSTER	No. OF GENOTYPES	VARIETIES
I	3	Pusa 1088, IPCK 00-112, L-550
II	1	BG 2085
III	4	Pusa 5023, Pusa 1108, Pusa 1053, PG 95333
IV	1	ICC 17109

Thus, a critical appraisal of the observations revealed that none of the clusters contained genotypes with all the desirable traits, which could be directly selected and utilized. Interestingly, all the minimum and maximum cluster mean values were distributed in relatively distant clusters. The results thus emphasise that hybridization between genotypes of different clusters is necessary for the development of desirable genotypes. Ahmad *et al*. (2012) studied the genetic diversity of 70 accessions of *Cicer arietinum* using morphological traits, seed protein and molecular markers and reported that the clustering pattern did not show any grouping that could be attributed to either the geographic distribution or the field performance. Similar findings were reported by Joshi *et al*. (2015) and Sanyal *et al*. (2016) while studying the genetic divergence of rice varieties. Hence, depending on the *per se* performance of the best genotypes within the clusters, they may be directly used for adaptation or may be used as parents in future hybridization programmes. The grouping of genotypes is of practical value to chickpea breeders in identifying the genotype with desired trait for utilization in breeding program for genetic improvement (Malik *et al*., 2014).

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Table 4b: Cluster mean values for agro-morphological traits and their relative contribution to genetic divergence for *kabuli* type.

Character	Cluster I	Cluster II	Cluster III	Cluster IV
Stem: Height at initiation of first flower (cm)	14.87	13.07	15.37	11.73
Time of Flowering (days)	105.67	118.00	102.00	107.00
Leaflet: Size (cm)	1.05	1.01	1.10	1.10
Peduncle: Length (cm)	1.38	1.42	1.57	1.30
Plant: Height (cm)	54.82	54.40	60.36	53.00
Pod Size (Length) (cm)	2.48	2.73	2.78	2.72
Seed Size :(Wt. (g). of 100 seeds at 10% moisture content)	15.30	20.36	23.50	38.18

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