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ASSESSMENT OF GENETIC DIVERSITY IN CHICKPEA (*CICER ARIETANUM* L.) THROUGH MORPHOLOGICAL CHARACTERIZATION

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Abstract

Genetic diversity analysis of 40 Chickpea (*Cicer arietanum* L.) genotypes belonging to different geographical areas of India was conducted using Jaccard's similarity coefficient and dendrogram generated using Unweighted Pair Group Method with Arithmetic Average (UPGMA). Out of 20 morphological characters studied, eight characters were found to show distinctiveness among genotypes *viz*. ICC 1076, ICC 15854, ICC 15851, ICC 12646, ICC 10140, ICC 10953, ICC 16703 and GJG-3. UPGMA cluster analysis of morphological data distinguished the genotypes in to three clusters *viz*. A, B and C. However the genotypes *viz*. Pant G-186 and PKV *kabuli*-2 were found to be completely out rooted from the three clusters indicating their uniqueness and diversity.

Key words: Genetic Diversity, DUS and UPGMA

Introduction

Chickpea (*Cicer arietanum* L. 2x = 2n = 16) is the most important *rabi* season self-pollinated pulse crop. India is a premier chickpea growing country in the world, accounting 76 per cent of total area and production of the world. Two types of chickpeas are recognized, the white-seeded "*kabuli*" and the brown colored "*desi*" types. *Kabuli* chickpeas are relatively bigger in size having a thinner seed coat while the desi type seeds are relatively smaller in size having a thicker seed coat. The desi type chickpea contributes to around 80% and the *kabuli* type around 20% of the total production of chickpea in world.

The chickpea is tremendously diverse with respect to growth habit and morphology. The ability to distinguish and identify varieties of cultivated species is fundamental to the operation of crop improvement programme. Characterization based on the morphological characters or taxonomic characters is useful in their identification, because of the reliability of these attributes over environments. Efficient phenotyping can be very helpful to establish a clear identity or specificity to a genotype for further utilization in crop improvement programme. It is absolutely necessary to identify morphological descriptors for different chickpea genotypes and examine their consistency over the years by utilizing different genetic tools *in vogue*.

Therefore the present study was conducted to assess the genetic diversity existing in 40 chickpea germplasm accession belonging to different geographical areas based on morphological observations laid out in DUS guidelines.

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Methods and materials

Plant material and field experiment:

The experimental material for present investigation comprised of 40 chickpea genoty pes *viz*. 5683, 15304, 11347, 10135, 16016, 83755, 10537, 83816, 15894, 10584, 15041, 83687, 16019, 2144, 1546, 12646, 15097, 1747, 83289, 10140, 10192, 1026, 15607, 15682, 1076, 5888, 15854, 2116, 15551, 83393, 10953, 16703, 15898, 2380, 83323, 1515, were collected form IIPR Kanpur and GG-2, GJG-3, Pant G 186 and PKV *kabuli*-2 were obtained from AAU Arnej, AAU Anand, NDUAT Faizabad and NAU Navsari respectively. The experiment was carried out at Department of Seed Science and Technology, Anand Agricultural University Anand, during Rabi season 2014-2015 and 2015-2016. All the genotypes were grown

in a Randomized Complete Block design (RCBD) with three replications and 45 × 20 cm spacing. Before sowing, recommended dose (20 N, 20 P, 40 K kg/ha) was applied in the form of commercial fertilizers.

Morphological characterization of chickpea genotypes:

Twenty morphological characters as suggested by PPV & FR Authority, GOI, New Delhi were used for characterization chickpea genotypes. DUS guidelines were followed for recording observations. The observations were recorded on various phenotypic characters namely anthocyanin coloration of stem, stem height at initiation of first flower, time of flowering (50% of the plants with at least one open flower), growth habit of plant, colour foliage of plant, leaflet size (middle of the plant and middle of the leaf), leaf pattern, number of peduncle per flower, colour of flower, stripes on flower standard, length of peduncle, plant height, pod size (length), number of seeds per pod, colour of seed, seed size (weight of 100 seeds at 10% moisture content), shape of seed, testa texture of seed, ribbing of seed and type of seed.

Genotype diversity

Phenotypic data was transformed to binary form as described by Sneath and Sokal (1973). They demonstrated that, the data of quantitative traits having large number of genotypes can be expressed in binary form and used for accurate calculation and comparison of similarity coefficient.

Clustering was done using symmetric matrix of dissimilarity coefficient (DIST) and cluster obtained using Unweighted Pair

Table 1: Characterization based on morphological characters in Chickpea.

S. No.	Characteristics	State of expression	No of genotypes belonging to each class
1.	Plant : Height	Short (<45 cm)	12
		Medium (45-65 cm)	21
		Tall (>65 cm)	07
2.	Pod: Size(length)	Small (<15 mm)	03
		Medium (15-20 mm)	36
		Large (>20 mm)	01
3.	Pod: Number of seeds	One	00
		More than one	40
4.	Seed: Colour	Beige (*kabuli*)	01
		Creamy beige	00
		Green	00
		Yellow	00
		Orange	00
		Brown	19
		Dark brown	20
		Grey	00
		Black	00
5.	Seed: Size (weight of 100 seeds at 10% moisture content)	Very small (<20g)	01
		Small (20-25g)	10
		Medium (26-35g)	28
		Large (25-45g)	00
		Very large (>45g)	01
6.	Seed: Shape	Pea-shaped	00
		Owl's head	16
		Angular	24
7.	Seed: Testa texture	Rough	29
		Smooth	11
		Tuberculated	00
8.	Seed : Ribbing	Absent	01
		Present	39
9.	Seed: Type	Desi	39
		Kabuli	01
10.	Stem: Anthocyanin	Absent	29
		Present	11
11.	Stem: Height at initiation of first flower	Low (<8 nodes)	19
		Medium (8-15 nodes)	15
		High (>15 nodes)	06
12.	Time of flowering (50% of the plants with at least one open flower)	Extra early (<40 days)	00
		Early (40-60 days)	40
		Medium (61-80 days)	00
		Late (>80 days)	00
13.	Plant: Growth habit	Erect (0-150 from vertical)	11
		Semi-erect (16-600 from vertical)	21
		Spreading 61-800 from vertical)	08

continued ..... Table 1

continue ..... Table 1

S. No.	Characteristics	State of expression	No of genotypes belonging to each class
14.	Plant: Colour of foliage	Light green	06
		Medium green	25
		Dark green	15
		Greenish purple	04
15.	Leaflet : Size (middle of the plant and middle of the leaf)	Small (<10mm)	02
		Medium (10-15mm)	21
		Large (>15mm)	17
16.	Leaf: Pattern	Simple	38
		Compound	02
		Pinnate	02
17.	Flower: Number per peduncle	Single	40
		Twin	00
18.	Flower: Colour	White	01
		Pink	39
		Blue	00
19.	Flower : Stripes on standard	Absent	01
		Present	39
20.	Peduncle: Length	Short (<5mm)	04
		Medium (5-10mm)	11
		Long (>10mm)	25

Group Method with Arithmetic Average (UPGMA) using SAHN (Sequential, Heirarchilal Nested clustering method) modules of NTSYS-pc version 2.02i (Rohlf, 1998).

Result and Discussion

Morphological characterization

Assessment of genetic diversity is a prerequisite for formulating crop improvement strategies in any crop. Morphological characters, although succumb to environmental factors can be prove to be an indicator of variability resulting in the native population, if the crop genotypes are grown spatially and temporally. In the present study 20 morphological characters of 40 genotypes were examined for variability/diversity (table. 1). Genetic dissimilarities calculated from average taxonomic distance (E_{ij}) matrix among the 40 chickpea genotypes revealed that lowest value (0.11) was observed between the pairs *i.e.,* (ICC 83616 and ICC 10537), (ICC 83687 and ICC 15041), (ICC 1747 and ICC 10537), (ICC 17547 and ICC 83816), (GG-2 and ICC 15041), (GG-2 and ICC 83687), (ICC 10953 and ICC 12646), (ICC 10953 and ICC 10140), (ICC 15851 and ICC 1076), (ICC 15851 and ICC 15854) and (GG-3 and ICC 16703). Whereas, maximum value (7.45) was observed between the pair PKV *Kabuli*-2 and ICC-2144. Moreover, out of 20 characters' studies, 8 characters *viz.* plant growth habit (erect, semi erect and spreading; (fig 1), foliage colour of plant (light green, medium green, dark green; figure 2), stem anthocyanin colouration, flower colour, number of peduncle per flower, strip on standard, peduncle length of pod and leaf size (figure 3) were found to be critical in identifying distinctness. The results revealed that the genotypes are diverse representing a wide spectrum of variation observed in the native chickpea germplasm.

Genotype variability through cluster analysis:

The dendrogram constructed using data recorded from 20 morphological characters showed distribution of genotypes in to three clusters *viz.* A, B and C. Jaccard's similarity coefficients ranged from 0.56 to 1.00 with a mean genetic similarity of 0.78. (fig. 4) Cluster A consisted of 17 genotypes, among which ICC 1076, ICC 15854 and ICC 15851 were found to be very close with similarity co- efficient of 1.00. Similarly ICC 12646, ICC 10140 and ICC 10953 showed their proximity. The genotypes ICC 16703 & GG-3 also showed maximum similarity, which indicated the involvement of common parents in their genetic constitution.

Cluster B consisted of maximum (19) number of genotypes among which some genotypes showed a very close relationship within themselves such as *i.e.,* ICC-10537, ICC-83816 and ICC-1747 and ICC-15041, ICC-83687 and GG-2.

Cluster C was the smallest as compared to the other two clusters comprising only of two genotypes *viz.,* ICC 83393 & 15895 with similarity coefficient of 0.86%. However two genotypes *viz.* Pant G-186 and PKV *Kabuli*-2 out rooted from all the three clusters presumably due to their diverse morphological characteristics.

Crop improvement in chickpea is hampered due to the presence of narrow genetic base which need to be broadened so as to realize the genetic potential of this crop. Genetic diversity analysis through

Erect Semi-Erect Spreading

Fig.1: Plant growth habit of different chickpea genotypes.

Dark Green Medium Green

Light Green

Fig. 2: Foliage Colour of different chickpea genotypes

morphological, biochemical and molecular characterization should be the first step for identifying superior genotypes from the native and exotic gene pools. The UPGMA methods based on Jaccards similarity co-efficient applied in this study, can be an effective and simple method for assessing the latent diversity in the

Fig. 3: Stem anthocyanin colouration, flower colour, number of peduncle per flower, strip on standard, peduncle length of pod and leaflet size of different chickpea genotypes.

plant populations. Similar attempts were earlier made by other scientists also such as Sunil Kumar *et al*. (2014) Handi, S. (2010) and Temesgen *et al.* (2015).

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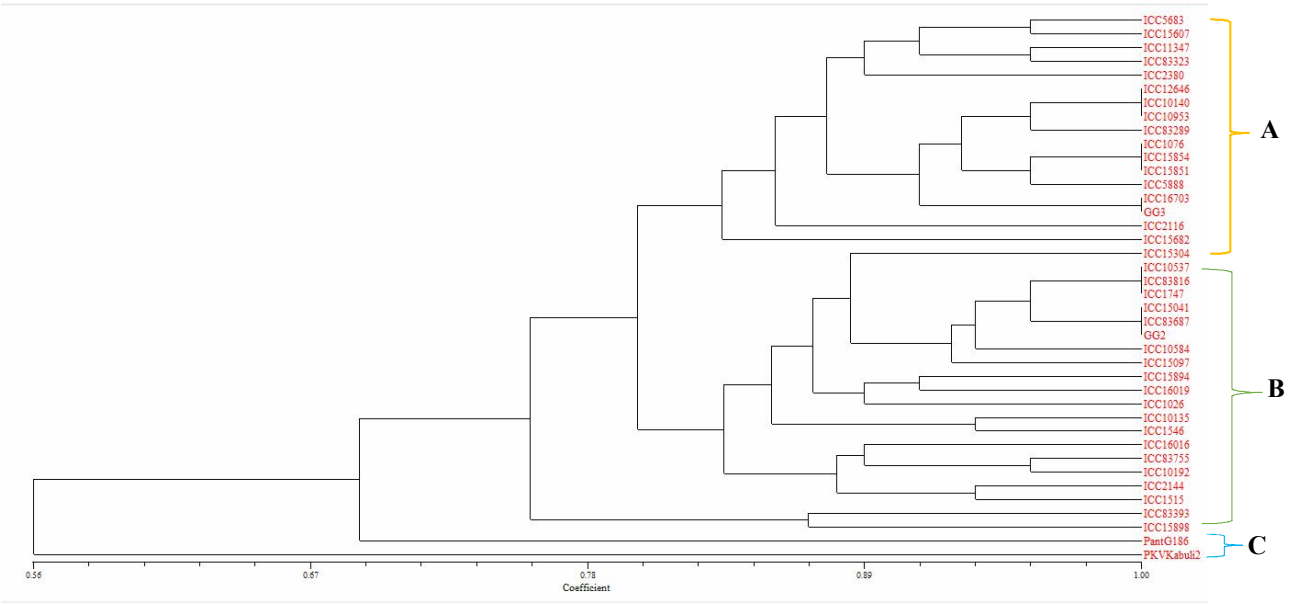

Fig. 4: Dendrogram of genetic relationship among 40 chickpea genotypes based on phenotypic traits

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