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Assessment of Genetic Diversity and its Associated Traits in Chickpea (*Cicer arietinum* L.)

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Authors' contributions

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

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ABSTRACT

In India, the rabi pulse Chickpea (*Cicer arietinum* L.) holds one of the most important position which is a member of Fabaceae family. Chickpea production accounts for 20% of the total pulse production in the world. The present investigation was carried out in Rabi-2019-2020 at Western Section of Birsa Agricultural University Research Farm, Kanke, Ranchi. Twenty six genotypes of chickpea comprising four checks *viz.,* BG 372, KWR 108, KPG 59 and Birsa Chana 3 were taken for the present investigation. Observations were recorded on eleven quantitative traits and three qualitative traits in this study. Mahalanobis D^2 statistics revealed five clusters. Among the five clusters, cluster I (23 genotypes) consisted of maximum genotypes followed by cluster II (4 genotypes) and cluster III, IV, V were mono-genotypic. Based on inter-cluster distances and mean

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performances of clusters for different traits, the advanced breeding lines among the genotypes belonging to cluster I and IV are expected to produce yield and other yield-related traits.Based on inter-cluster distance and cluster mean genotypes such as GNG1958, GCP105, JG14, BAUG15, BAUG107, BAUG108, BAUG109, BAUG115, BAUG121, BAUG123, BAUG124 and BAUG129 were found suitable for their utilization in hybridization programme. The observations for qualitative characterization on flower colour, seed colour and seed testa texture of thirty chickpea genotypes were recorded as per the guidelines of conduct of test for DUS approved by the Protection of Plant Varieties and Farmers' Rights Authority (PPV&FRA).

Keywords: Chickpea; genetic diversity; genetic stocks; hybridization programs.

1. INTRODUCTION

Chickpea (*Cicer arietinum* L.) is an annual rabi leguminous crop belonging to the family Fabaceae, subfamily Fabiodeae. Chickpea (*Cicer arietinum* L.) with a genome size of 732 Mbp is a self-pollinated with cleistogamy flower, diploid (2n = 2x = 16) in nature. Genetic enhancement in yield components of chickpeas is required to address the issues of low productivity. To develop improved high yielding chickpea varieties, it has been crucial to understand the genetic basis of yield, yield components, and associated agronomic traits (Kakaei & Farshadfar, 2025; Shahnaz et al., 2025).

Chickpea has played a major role in the realization of the Pulse Revolution in India making the country near self-sufficiency in Pulses. There is a more than129% increase in production (11.02MT) and 32% increase in productivity (1067 kg/ha) of chickpeas during 2017-20 as compared to those during 2000-02. This has resulted in an average chickpea availability of 10.90 MT in the country during 2017-19 which signifies a more than 80% jump over that during 2000- 02. In 2018 – 19, the total area under chickpea cultivation in the country was 9.44 mha, whereas production was 10.13 mt with a productivity of 1073 kg/ha.

Assessing the genetic diversity of farmed crop plants is vital for selecting relevant genotypes for a hybridization program. To developing new genetic stocks, each breeding effort must involve genetically diverse parents. D2 statistics is a technique that helps in the recognition of genetically distinct parents for use in hybridization programs. This technique evaluates the force of differentiation at the intra-cluster and inter-cluster levels, which aids in the selection of genetically dissimilar parents for their reuse in hybridization programs.

It is important to define morphological descriptors for different genotypes of chickpea and to analyze their consistency over the years using various genetic tools (Singh et al., 2018). Plant morphological characteristics have long been acknowledged as the unquestionable descriptors for DUS testing and varietal classification of crop varieties (Joshi et al., 2018).

2. MATERIALS AND METHODS

The field experiment was conducted at Department of genetics and Plant Breeding, a Western section of Birsa Agricultural University, Kanke, Ranchi located at an elevation of 634 meter above mean sea level with 85°18'48.3"East longitude and 23°25'47.3"North latitude during Rabi 2019-2020. Thirty genotypes including four checks *viz.,*BG 372, KPG 59, KWR 108 and Birsa Chana 3 were used to study the genetic diversity. The genotypes were planted in a Randomized Block Design with three replications during Rabi 2019- 2020. Each genotype was sown in three rows in each replication with a row length of 3m and spacing between row to row and plant to plant was 30 cm and 10cm respectively. The data was recorded on five randomly selected plants from each replication for the characters such as Germination Percentage, Days to 50% flowering, Days to maturity, Plant height, Number of primary branches per plant, Number of pods per plant, Number of seeds per pod, Number of seeds per plant, 100 – seed weight and Yield per plant. The analysis for divergence was done by following Mahalanobis (1936) D2 statistic. Tocher´s method as described by Rao (1952) was followed for cluster formation. The observations for qualitative characterization on flower colour, seed colour and seed testa texture of thirty chickpea genotypes were recorded as per the guidelines of conduct of test for DUS approved by the Protection of Plant Varieties and Farmers' Rights Authority (PPV&FRA).

3. RESULTS AND DISCUSSION

Thirty genotypes in the present study were grouped into five clusters on the basis of Tocher's method, described by Rao (1952). Among the five, Cluster I was the largest with 23 genotypes followed by Cluster II with 4 genotypes (Table 1 and Fig. 1). Cluster III, IV and V were mono-genotypic, thus indicating the existence of wide diversity from the rest.

Data was revealed from Table 2 and Fig. 2, that inter-cluster distances were greater than intra-cluster distances, thus revealing the existence of a considerable amount of genetic diversity among the genotypes. The smaller values of intra-cluster distances indicated that the genotypes could be closely related in their evolutionary process and may have similar evolutionary factors. The highest intra-cluster distance was recorded in cluster I whereas the lowest intra-cluster distance was recorded in cluster III, IV and V (Table 2 and Fig. 2). The highest inter-cluster distance was recorded between cluster IV and V with a value of 473.91followed by cluster IIIandV (258.44), cluster I and V (183.96), cluster II and IV (158.34), cluster I and IV (134.77), cluster II and V (129.77), clusterII and III (83.76), cluster IandII (80.39), cluster and (67.72) and cluster and IV (46.93) having lowest inter-cluster distance. Therefore, it is suggested that if diverse genotypes from these groups may be used in the breeding programme as genotypes belonging to the clusters with maximum inter-cluster distance are genetically more divergent and there is a scope for hybridization between genotypes of divergent clusters are likely to produce a wide range of variability with desirable segregants. The minimum inter-cluster distance between cluster III and IV, Cluster I and III and cluster II and III shows genetically less diverse genotypes in these clusters.

Cluster means are also having importance in the selection of a genotype as a donor parent for the improvement of a particular trait. It was found that cluster V had the highest mean for days to 50% flowering, days to maturity and wilt incidence per cent. Cluster III had the highest mean for germination percentage (Table 3). Cluster II had the highest mean for 100-seed weight and plant height. Cluster I had the highest mean for number of primary branches per plant, number of pods per plant and yield per plant whereas cluster IV had the highest mean for the number of seeds per pod and number of seeds per plant. To improve any particular trait, donors for hybridization could be selected from respective clusters.

The utility of D^2 analysis is enhanced by its application to estimate the relative contribution of various characters to genetic divergence. It was found that 100-seed weight with 49.89% showed maximum contribution towards divergence followed by days to maturity (29.20%) and days to 50% flowering (12.41%). Least contribution was shown by germination percentage and number of seeds per plant (0.23%) whereas no contribution towards divergence was shown by plant height and yield per plant (Table 4). Therefore, selection for such traits may give more emphasis for the hybridization programme to create variability and will provide immense scope for the improvement of yield components through the efeective selection.There are discrepancies in the results which might be due to the diverse sets of material and also due to the role of environmental variability that was in contrast with the results of Dwevedi and Lal (2009); Ahmad et al. (2010); Nimbalkar et al. (2017), Agrawal et al. (2018), Balasaheb et al. (2018), Thakur et al. (2018) and Tamvar et al. (2019).

Table 1. Grouping of 30 genotypes into different clusters

Cluster	Number of Entries	Entries
I	23	GNG 1581, KWR 108, PG 186, BG 372, GCP 105, Birsa Chana 3, BAUG 124, KPG 59, BAUG 15, BAUG 115, JG 14, BAUG 123, BAUG 125, BAUG 131, JG (2017-49), RKG 13-515, BAUG 132, BAUG 127, BAUG 106, BAUG 126, BAUG 128, BG 3043, BAUG 130
II	4	BAUG 116, BAUG 129, BAUG 121, BAUG 107
III	1	BAUG 109
IV	1	BAUG 108
V	1	GNG 1958

Table 2. Average inter and intra cluster distance values among five clusters for 30 genotypes of chickpea

	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5
Cluster1	34.4	80.39	67.72	134.77	183.96
Cluster2		25.29	83.76	158.34	129.77
Cluster3			0	46.93	258.44
Cluster4				0	473.91
Cluster5					0

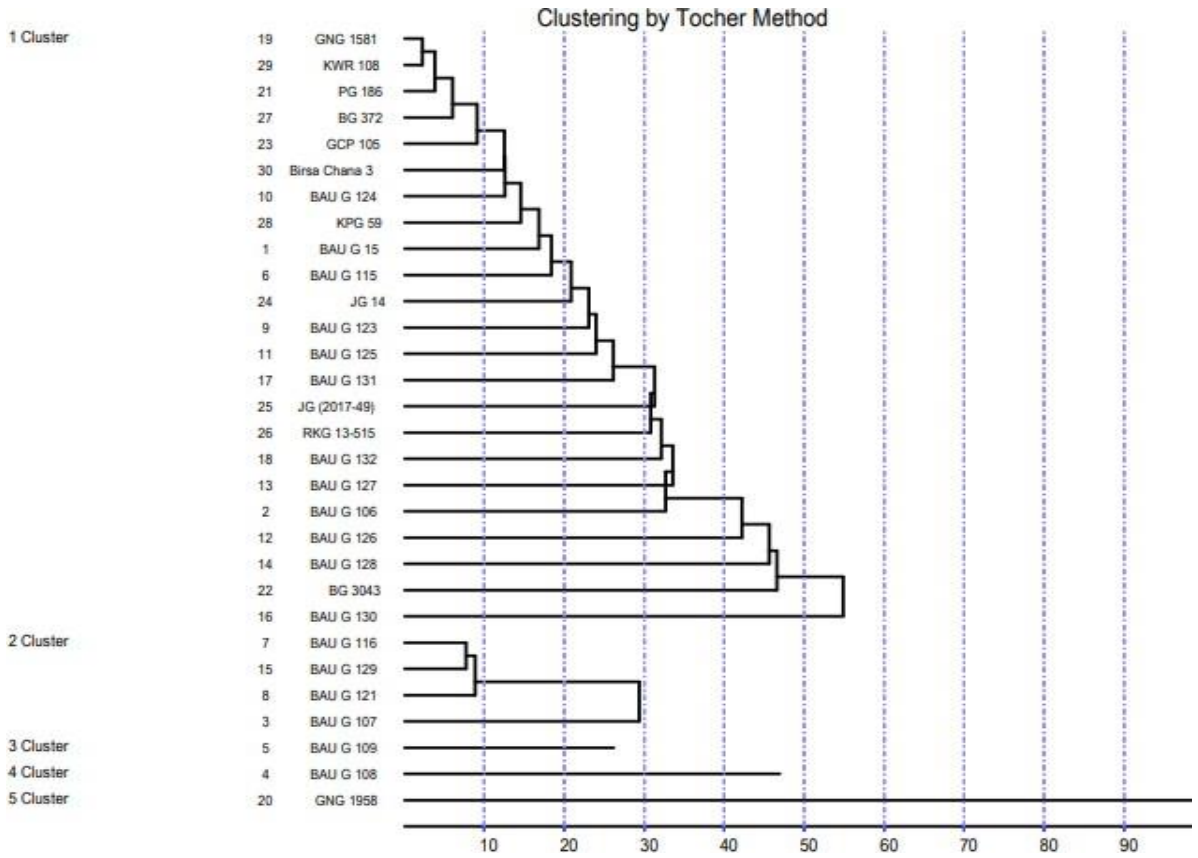

Fig. 1. Figure representing clustering by Tocher's method

3.1 Qualitative Traits Characterization

The observations for qualitative characterization of thirty chickpea genotypes were recorded as per the guidelines of conduct of test for DUS approved by the Protection of Plant Varieties and Farmers' Rights Authority (PPV&FRA) in 2007. Based on flower colour, the chickpea genotypes were divided into two groups *viz.,* pink and blue (Fig. 3). All genotypes had pink colour flowers except for BAUG 106, BAUG 115, BAUG 126, BAUG 130 and KPG 59 which had blue coloured flower (Table 5). Further,the genotypes were characterized into three groups based on seed colour namely, brown, deep brown and reddish brown (Fig. 4). Only BAUG 123 genotype showed reddish-brown colour (Table 5). Based on seed testa texture, the chickpea genotypes were classified into three groups namely, rough, smooth and tuberculated (Fig. 5). Only two genotypes *viz.,* BAUG 128 and RKG 13-515 were recorded for tuberculated seed testa texture. The majority of genotypes (20) had rough seed testa texture (Table 5). Similar results corroborate with the findings of Joshi and Aggarwal (2016), Gediyaet al., (2018), Singh et al (2018), Adem and Tesso (2019), Kumawat et al (2020), Janghelet al., (2020) and Nandedkar et al (2021).

Table 3. Cluster means of different traits

	Germination percentage	Days to 50% flowering	Days to maturity	Plant Height	Number of primary branches Per plant	Number of pods per Plant	Number of seeds per pod	Number of seeds per plant	100 seed weight (g)	Wilt incidence percentage	Yield/plant (g)
ClusterI	67.46	78.61	118.06	51.84	4.22	63.91	1.45	93.52	18.08	5.11	14.70
ClusterII	71.67	74.17	118.00	53.63	4.13	62.08	1.22	75.72	25.76	4.64	12.12
ClusterIII	81.67	64.00	116.00	47.87	3.67	56.67	1.20	67.73	17.33	5.73	11.33
ClusterIV	76.67	62.00	102.00	52.40	4.20	61.67	1.67	102.07	17.60	6.70	16.37
ClusterV	50.00	81.00	138.00	51.47	3.80	60.67	1.20	73.00	25.53	5.83	11.47

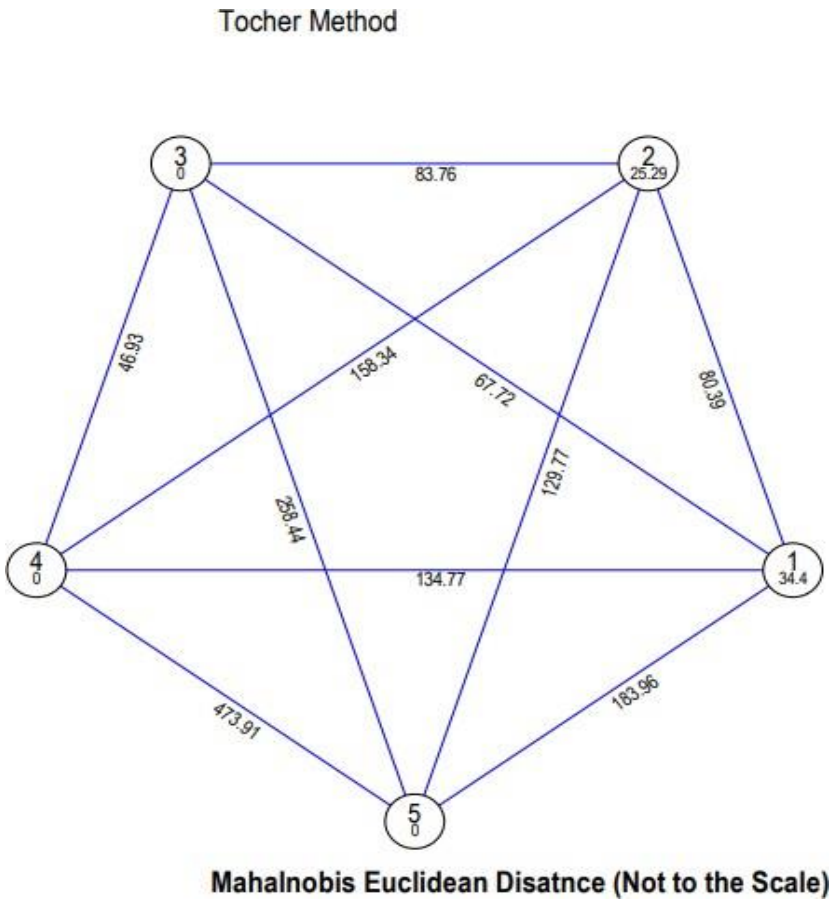

Fig. 2. Figure representing inter and intra–cluster distance

Fig. 3. Flower colour

Table 4. Percent contribution of each trait towards genetic divergence

Source	Contribution%
Germination%	0.23%
Days to 50%Flowering	12.41%
Days to Maturity	29.20%
Plant Height	0.00%

Source	Contribution%
No. of Primary Branches	2.07%
No. of Pods Per Plant	0.23%
No. of Seeds Per Pod	0.69%
No. of Seeds Per Plant	0.23%
100 Seed Weight	49.89%
Wilt Incidence Percentage	5.06%
YIELD/PLANT(G)	0.00%

Fig. 4. Seed colour

Table 5. List of qualitative characters for thirty genotypes

SL. NO.	Entry	Flower colour	Seed colour	Seed testa texture
1	BAUG 15	PINK	DEEP BROWN	ROUGH
2	BAUG 106	BLUE	BROWN	ROUGH
3	BAUG 107	PINK	BROWN	ROUGH
4	BAUG 108	PINK	BROWN	ROUGH
5	BAUG 109	PINK	DEEP BROWN	ROUGH
6	BAUG 115	BLUE	BROWN	SMOOTH
7	BAUG 116	PINK	DEEP BROWN	SMOOTH
8	BAUG 121	PINK	DEEP BROWN	ROUGH
9	BAUG 123	PINK	REDDISH BROWN	SMOOTH
10	BAUG 124	PINK	DEEP BROWN	SMOOTH
11	BAUG 125	PINK	BROWN	ROUGH
12	BAUG 126	BLUE	BROWN	ROUGH
13	BAUG 127	PINK	DEEP BROWN	SMOOTH
14	BAUG 128	PINK	DEEP BROWN	TUBERCULATED
15	BAUG 129	PINK	DEEP BROWN	ROUGH
16	BAUG 130	BLUE	BROWN	ROUGH
17	BAUG 131	PINK	BROWN	SMOOTH
18	BAUG 132	PINK	BROWN	ROUGH
19	GNG 1581	PINK	BROWN	ROUGH
20	GNG 1958	PINK	DEEP BROWN	ROUGH
21	PG 186	PINK	BROWN	ROUGH
22	BG 3043	PINK	DEEP BROWN	ROUGH
23	GCP 105	PINK	DEEP BROWN	SMOOTH
24	JG 14	PINK	DEEP BROWN	ROUGH
25	JG (2017-49)	PINK	DEEP BROWN	ROUGH
26	RKG 13-515	PINK	DEEP BROWN	TUBERCULATED
27	BG 372	PINK	BROWN	ROUGH
28	KPG 59	BLUE	BROWN	ROUGH
29	KWR 108	PINK	BROWN	SMOOTH
30	Birsa Chana 3	PINK	BROWN	ROUGH

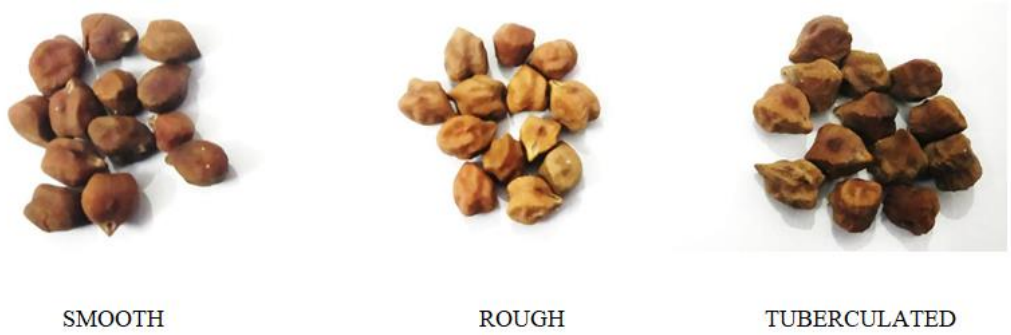

Fig. 5. Seed Testa texture

4. CONCLUSION

Based on D^2statistics the thirty genotypes were grouped into five clusters with cluster I having the maximum number of genotypes (23). The inter-cluster distances were greater than intra-cluster distances, thus revealing the existence of a considerable amount of genetic diversity among the genotypes. The highest inter-cluster distance was recorded between clusters IV and V followed by cluster III and V and cluster I and V. The parents for hybridization could be selected based on their large inter-cluster distance for isolating useful recombinants in the segregating generations.

In the present study, the highest contribution towards genetic divergence was found for 100-seed weight followed by days to maturity and days to 50% flowering. Therefore, more emphasis should be given to these traits for selection to create genetic variability.

Based on inter-cluster distances, cluster means and *per se* performance observed in the present study the genotypes GNG 1958, GCP 105, JG 14, BAUG 15, BAUG 107, BAUG 108, BAUG 109, BAUG 115, BAUG 121, BAUG 123, BAUG 124 and BAUG 129 were found superior to be suitable for crop improvement.

The morphological DUS descriptors *viz.,* flower colour, seed colour and seed texture were able to distinguish chickpea genotypes distinctively and uniformly and least affected by environmental factors and thus can be used for germplasm characterization in chickpea.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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