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ASSESSMENT OF GENETIC DIVERSITY AMONG CHICKPEA (*CICER ARIETINUM* L.) GENOTYPES

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ABSTRACT

The present investigation was conducted during the 2023–24 rabi season at BAC Farm Gate, BAU, Sabour (Bhagalpur) to evaluate 36 chickpea genotypes, including four checks (BG 3043, GNG 2207, PG 186 and BG 372), for genetic divergence using 11 quantitative traits. The aim was to identify high-yielding and suitable parents for future breeding programmes through genetic diversity analysis using Mahalanobis D^2 statistics. Maximum intra-cluster distance was observed in Cluster III, followed by Cluster I, indicating wide genetic variability within these groups. The highest inter-cluster distance was recorded between Cluster IV and Cluster V, followed by Cluster V and Cluster VI, suggesting greater genetic diversity among these groups. Cluster means revealed: Cluster I with early maturity, Cluster III with early flowering and more secondary branches, Cluster IV with high biological yield, harvest index, and seed yield per plant, Cluster V with more pods and branches and Cluster VI with shorter plant height but higher biological yield. These findings highlight promising parents for hybridization aimed at yield improvement in chickpea.

Key words : Chickpea, Mahalanobis D^2 statistics, Cluster analysis, Genetic diversity.

Introduction

Chickpea (*Cicer arietinum* L.) belongs to the family Fabaceae, subfamily Faboideae. It is a self-pollinating, cool-season legume with a chromosome number of $2n = 16$. Chickpea is cultivated widely across Asia, East Africa, America, and Europe, and is moderately drought-tolerant. Archaeological evidence from Hacilar, Turkey, indicates its cultivation as early as 5450 BC (Helbaek, 1970). Globally, chickpea ranks third among pulse crops after field peas and dry beans (Jagadish and Jayalakshmi, 2014).

India is the largest producer of chickpea, contributing nearly 50% of the global pulse production. During 2022–23, India produced 26.06 million tonnes of pulses from 28.90 million hectares with a productivity of 902 kg/ha. Chickpea alone accounted for 12.27 million tonnes from 10.47 million hectares with a productivity of 1172 kg/ha. In Bihar, total chickpea production was 57 thousand tonnes from 53 thousand hectares with a productivity of 1076 kg/ha (Agricultural Statistics Division, 2023–24).

Genetic diversity is fundamental for crop improvement. It facilitates conservation, genotype selection and identification of superior germplasm. Effective utilization of diversity ensures the selection of favorable traits, either individually or in combination, to enhance yield and stability. Germplasm acts as a reservoir of useful genes, which are vital for hybridization, selection, and breeding programmes. Pre-breeding helps broaden the genetic base and overcome bottlenecks, thus enabling the development of superior gene pools. D^2 analysis groups genotypes into relatively homogeneous clusters, making it an effective tool for identifying diverse parents. The present study was therefore undertaken to assess the genetic diversity and heterotic potential of chickpea genotypes for use in breeding programmes (Panwar *et al*., 2024).

Materials and Methods

The experimental material consisted of 36 chickpea genotypes sown on 30 November 2023 at BAC Farm

Gate, Bihar Agricultural University, Sabour (Bhagalpur). The experiment was laid out in a randomized complete block design (RCBD) with three replications during the rabi season of 2023–24. Each plot measured 4.8 m^2, with a single 4-m row. Row spacing was maintained at 30 cm, and plant spacing at 30 × 10 cm. Standard recommended agronomic practices were followed to raise a healthy crop.

Data were recorded on 11 quantitative traits: days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, total number of pods per plant, number of effective pods per plant, 100-seed weight (g), biological yield (g), seed yield per plant (g) and harvest index (%).

Genetic divergence was analyzed using Mahalanobis D^2 statistics as described by Rao (1952), which is widely used to estimate genetic distance between genotypes based on multiple traits. Data analysis was performed using Windostat version 9.2 software.

Results and Discussion

Genetic Diversity

Cluster analysis based on 11 traits grouped the 36 genotypes into six clusters (Table 1, Fig. 1). Cluster I had the maximum number of genotypes (15; 41.66%), followed by Cluster II (13; 36.11%), Cluster III (4; 11.11%), Cluster IV (2; 5.56%), while Clusters IV and VI were monogenotypic (2.78%). Similar clustering patterns were reported earlier by Nimbalkar *et al*. (2017), Balasaheb *et al*. (2018), Kumari *et al*. (2023), Kumar *et al*. (2023) and Srikanth *et al*. (2024).

Maximum intra-cluster distance was observed in Cluster III (46.28), followed by Cluster I (43.45), Cluster II (34.84) and Cluster V (33.16), suggesting wide genetic variability within these groups. The lowest intra-cluster distance (0.00) was found in Clusters IV and VI, as expected from their monogenotypic nature.

The highest inter-cluster distance was observed between Cluster IV and Cluster VI (591.32), followed by Cluster V and Cluster VI (476.93), Cluster II and Cluster V (354.37), Cluster III and Cluster IV (305.79), and Cluster II and Cluster IV (301.65). These large distances indicate substantial diversity and parents chosen from such clusters may yield superior recombinants. Similar findings were also reported by Nimbalkar *et al*. (2017), Kumari *et al*. (2023) and Srikanth *et al*. (2024).

Cluster means showed wide variation across traits

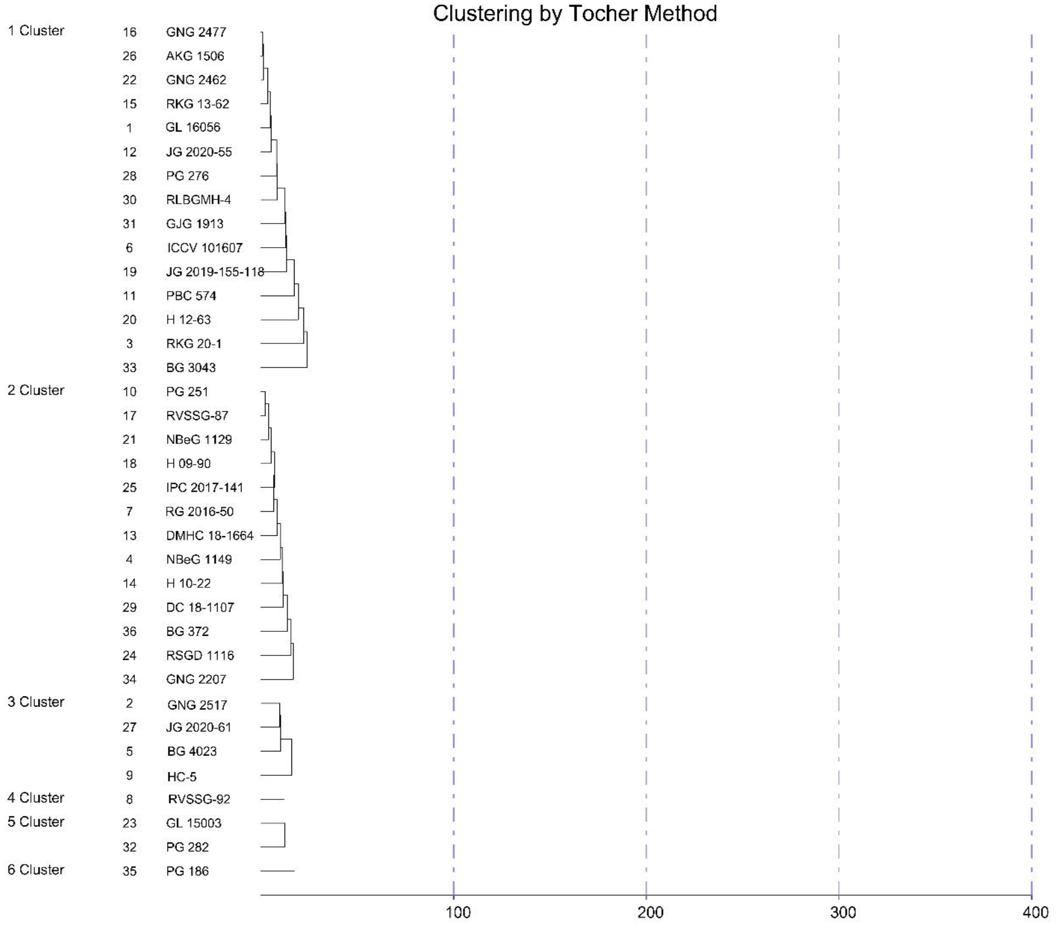

Fig. 1 : Cluster analysis dendrogram.

Table 1 : Distribution of 36 chickpea genotypes in various clusters.

Cluster I	15	GL 16056, RKG 20-1, ICCV 101607, PBC 574, JG 2020-55, RKG 13-62, GNG 2477, JG 2019-155-118, H 12-63, GNG 2462, AKG 1506, PG 276, RLBGMH-4, GJG 1913, BG 3043
Cluster II	13	NBeG 1149, RG 2016-50, PG 251, DMHC 18-1664, H 10-22, RVSSG-87, H 09-90, NBeG 1129, RSGD 1116, IPC 2017-141, DC 18-1107, GNG 2207, BG 372
Cluster III	4	GNG 2517, BG 4023, HC-5, JG 2020-61
Cluster IV	1	RVSSG-92
Cluster V	2	GL 15003, PG 282
Cluster VI	1	PG 186

Table 2 : Average intra and inter cluster distance values among six clusters for 36 genotypes of chickpea.

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster ‘!	43.45	107.66	164.29	102.27	187.38	299.36
Cluster a!		34.84	176.30	301.65	354.37	119.28
Cluster b!			46.28	305.79	141.55	207.96
Cluster c!				0.00	174.83	591.32
Cluster d!					33.16	476.93
Cluster e!						0.00

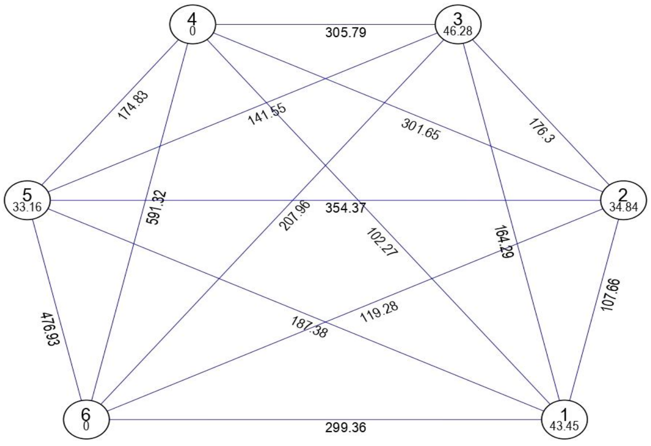

Fig. 2 : Euclidean^2 distance.

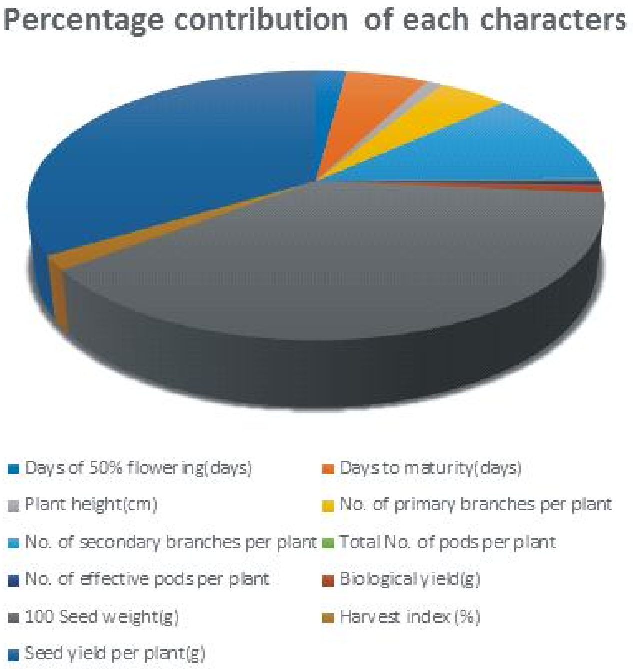

Fig. 3 : Contribution of eleven characters towards genetic divergence of 36 genotypes of Chickpea.

(Table 3). Cluster I had the lowest mean days to maturity (108.80), indicating early maturity. Cluster II recorded the lowest mean for pods per plant, effective pods, branches, harvest index and seed yield, indicating scope for improvement. Cluster III showed higher mean values for flowering, plant height, and secondary branches. Cluster IV recorded maximum seed weight (29.67 g), harvest index (48.50) and seed yield per plant (16.45 g), while having the lowest biological yield (80.33 g). Cluster V recorded maximum pods per plant (60.70), effective pods (53.37), and primary branches (3.54). Cluster VI showed maximum biological yield (121.67 g) but the lowest plant height (53.00 cm) and 100-seed weight (15.00 g).

Contribution of Traits

The relative contribution of traits towards genetic divergence revealed that 100-seed weight (38.57%) and seed yield per plant (33.97%) were the most important contributors, followed by number of secondary branches (11.56%) and days to maturity (5.56%). Traits such as total pods per plant (0.16%), effective pods (0.63%), and biological yield (0.95%) contributed the least (Table 4, Fig. 3). Similar results were reported by Agrawal *et al.* (2018), Yadav *et al.* (2023), Kumari *et al.* (2023) and Srikanth *et al.* (2024).

Table 3 : Mean values of clusters of different characters towards genetic divergence in 36 chickpea genotypes.

Characters	Days to 50 % flowering (days)	Days to maturity (days)	Plant height (cm)	No. of primary branches per plant	No. of secondary branches per plant	Total No. of pods per plant	No. of effective pods per plant	Biological yield (g)	100 Seed weight (g)	Harvest index (%)	Seed yield per plant (g)
Cluster I	77.44	108.80	60.92	2.51	5.58	47.98	41.93	101.36	23.57	45.38	12.92
Cluster II	79.10	111.59	60.79	2.18	4.93	45.03	38.98	107.44	17.22	40.28	9.86
Cluster III	76.00	112.50	65.55	3.13	6.49	55.17	47.80	103.50	18.25	41.73	11.70
Cluster IV	78.33	122.00	59.40	2.67	5.87	50.60	45.33	80.33	29.67	48.50	16.45
Cluster V	82.67	109.33	54.93	3.54	5.57	60.70	53.37	119.00	24.18	45.83	15.84
Cluster VI	82.67	117.00	53.00	2.33	5.07	47.20	40.07	121.67	15.00	47.63	10.46

Table 4 : Contribution of different characters towards genetic divergence of 36 chickpea genotypes.

Source	Times ranked 1st	Contribution %
Days to 50% flowering (days)	13	2.06%
Days to maturity(days)	35	5.56%
Plant height(cm)	7	1.11%
No. of primary branches per plant	29	4.6%
No. of secondary branches per plant	73	11.56%
Total No. of pods per plant	1	0.16%
No. of effective pods per plant	4	0.63%
Biological yield(g)	6	0.95%
100 Seed weight(g)	243	38.57%
Harvest index (%)	11	1.75%
Seed yield per plant(g)	214	33.97%

Conclusion

The study revealed considerable genetic variability among chickpea genotypes. Cluster I showed early maturity, Cluster IV recorded superior seed weight, harvest index and seed yield, while Cluster V exhibited superiority in pods and branching traits. Genotypes such as RVSSG-92 (Cluster IV), GL 15003 and PG 282 (Cluster V) were identified as potential parents for hybridization programmes. These genotypes may be effectively utilized in chickpea improvement programmes targeting yield and yield-attributing traits.

Authors' contribution

Hemchand Kumar and Manoj Kumar were primarily responsible for conducting the field experimentation, data recording, and initial analysis. Ashutosh Kumar, Priyanka Kumari, and Brajesh Kumar contributed to the preparation, critical review, and refinement of the manuscript. All authors read and approved the final version of the manuscript.

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