DECIPHERING GENETIC DIVERSITY IN ADVANCED CHICKPEA (CICER ARIETINUM L.) BREEDING LINES

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ABSTRACT
Chickpea has played a major role in the realization of the "Pulse Revolution" in India, making the country nearly self-sufficient in pulse production. However, modern plant breeding and intensive agricultural practices have narrowed the genetic base of cultivated chickpea, necessitating the exploration of new sources of genetic variability for use in breeding programmes. A genetic diversity study was conducted on 20 promising advanced breeding lines of chickpea (*Cicer arietinum* L.) using Mahalanobis D² statistics. Based on D² values and Tocher's method of clustering, the 20 genotypes were grouped into 10 clusters under different sowing environments. Under timely sown conditions, cluster I contained the maximum number of genotypes (11). Similarly, under late sown conditions, cluster I comprised the highest number of genotypes (13). For the pooled analysis across environments, cluster I again included the maximum number of genotypes (10). The maximum intra-cluster distance under the pooled environment was observed in cluster IV, indicating substantial genetic divergence among the genotypes within this cluster.

KEYWORDS: Chickpea, D², Tocher's method, Pooled analysis.

1. INTRODUCTION
India is a global leader in pulse production, with the country growing a wide variety of pulses year-round across its diverse climates. Among the many pulses cultivated, chickpea, also known as gram or Bengal gram, stands out as the most widely farmed rabi pulse crop in India. Chickpea (*Cicer arietinum* L., 2n=2x=16) is an annual legume that is believed to have originated in the south eastern region of Turkey known for its adaptability to cool-season conditions. Chickpea is a self-pollinating crop with a genome size of 738 mbp. It is an important legume, contributing significantly to both global food security and the Indian agricultural economy. Chickpea boasts a stronger nutritional profile Chickpea, play a vital role in ensuring nutritional security, as they are both produced and consumed in large quantities globally. Chickpeas are particularly rich in protein (21.5–28.9%), carbohydrates (52–70%), fat (4–10%), crude fiber (3–6%), soluble sugars (3–8%), and ash (3%). They also provide essential minerals such as calcium, phosphorus, iron, and zinc, along with valuable vitamins (El-A dawy, 2002).

Globally pulses are being cultivated in 170 countries and covering about 96 m ha area which produces about 96 m tones pulses with 1000 kg/ha productivity (FAOSTAT 2023). In India during 2024-25, pulses were grown in 27.6 m ha area with an estimated production of 25.2 m tonnes (Third advance estimates 2024-25). Rabi pulses occupy 50% of the total area under pulses (13.9 m ha) and contribute about 61% in production (15.5 m tonnes). Chickpea is the major rabi pulse with a share of about 45 % to the total pulse basket of the country.

Modern plant breeding and agricultural systems have narrowed the base for the genetic diversity of cultivated chickpea and to explore new sources of variation that might be used in plant breeding programmes. Chickpea is currently grown world over in an area of 14.1 m ha with annual production of 16.5 m tones (FAOSTAT 2024). India is the largest producer of chickpea with more than 2/3rd share in area and production of chickpea in the world. Chickpea has played a major role in realization of 'Pulse Revolution' in India making the country nearly self-sufficient in pulses. During 2024-25 the crop was grown in an area of 9.6 m ha with a production of 11.34 m tonnes (Third advance estimates 2024-25)

During 2021-22 (fourth estimate), chickpea production of India was 13.75 million tonnes from an acreage of 10.91 million ha. with a productivity of 12.6 q./ha (DES 2023, MOAF&W, GoI). Chickpea solely contributes nearly 50% of the Indian pulse production. States contribution to national production in terms of lakh tonnes viz., Maharashtra (30.60), Madhya Pradesh (24.58), Rajasthan (19.75), Gujarat (14.79) Uttar Pradesh (6.68), Karnataka (4.05), Jharkhand (3.57) Andhra Pradesh (3.07) Chhattisgarh (3.03) and Telangana (1.11), are major chickpea producing states of India (Project Coordinator's Report 2024-25, ICAR, AICRP, Rabi Pulses). Chickpea has a diverse consumption pattern in the Indian market. The food products include immature green grain (desi type), mature grain (desi/kabuli type), flour of mature grain (besan, desi type), roasted grain (desi type), flour of roasted grain (shattu, desi type), split grain or pulse (dahl, desi type), snacks (namkeens, desi and kabuli type), flakes (desi type), baked products (from flour, desi type), sweets/savories (from flour, desi type) and various tertiary processed products (cuisines).. The global chickpeas market grew from $13.93 billion in

2022 to $14.9 billion in 2023 at a compound annual growth rate (CAGR) of 7.0%. The chickpeas market is expected to grow to $19.19 billion in 2027 at a CAGR of 6.5%. During 2021, INDIA's share in global Export of chickpea was 5.87% and share in Import was 12.51% (ICAR, AICRP on chickpea report 2021-22). Share of India in global chickpea Production was 73.46% during 2020.

2. METHODOLOGY

The present investigation entitled "Genetic Diversity Analysis in Chickpea Advance Breeding Lines" was carried out during the rabi 2023-24 and 2024-25.

2.1 Experimental Material and Methods:- Location of work- Field experiment was conducted under two locations COA, J.N.K.V.V, Jabalpur (MP) during rabi season 2023-24 and 2024-25. KVK, MP

2.2 Details of experiment- The experimental material consists of 20 advance breeding lines of chickpea received from AICRP on Rabi Pulses, Department of Genetics and Plant Breeding, COA, J.N.K.V.V, Jabalpur (MP).

Table 1. Details of experiment

Year/Season	**2- Rabi 2023-24 and 2024-25**
Environment	E I- Timely Planting Condition, E II- Late sown (Jabalpur) E III- Timely sown, E IV- Late sown (Chhindwara) E V- Timely Planting Condition, E VI- Late sown (Jabalpur) E VII- Timely sown, E VIII- Late sown (Chhindwara)
Experimental design	Randomized Complete Block Design (RCBD)
No. of rows per genotype	4 rows
Row length	4.0 m
Plant to Plant distance	6.0-8.0 cm
Row to row distance	30.0 cm

3. RESULT AND DISCUSSION

Grouping of 20 chickpea genotypes (table. 2) into 10 clusters by Tocher's method for timely sown condition revealed that cluster no I consists of maximum number of genotypes namely JG 2021-71, ICC 191618, ICCV 181606, JG 2022-7, JG 2022-73, JG 2022-6, JG 2022-1, JG 2022-2, JG 2020-634958, JG 2021-70, JG 18 followed by only 1 for other remaining genotypes.

Table.2rouping of 20 chickpea genotypes into 10 clusters by Tocher's method for timely sown condition

Cluster No.	Number of Genotypes	Genotypes
I	11	JG 2021-71, ICC 191618, ICCV 181606, JG 2022-7, JG 2022-73, JG 2022-6, JG 2022-1, JG 2022-2, JG 2020-634958, JG 2021-70, JG 18
II	1	JG 2022-9
III	1	JG 2022-5
IV	1	JG 24
V	1	JG 2016-9651
VI	1	JG 36
VII	1	JG 2022-3
VIII	1	JG 2023-84
IX	1	JG 2022-4
X	1	JG 2022-8

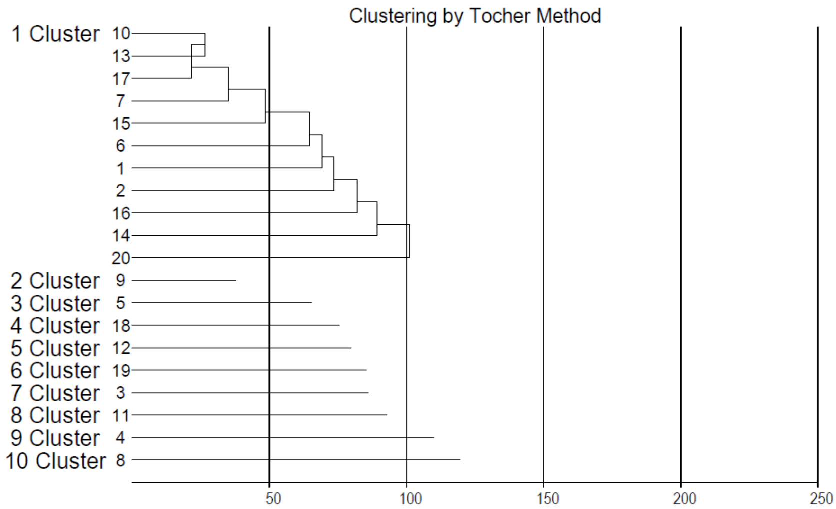

Diagram 1. Clustering by Tocher's method for timely sown condition

Table.3 Percent contribution of 14 characters for diversity in chickpea advance breeding lines

Source	Times ranked 1 st	% Contribution
1	9	4.74
2	3	1.58
3	21	11.05
4	0	0.00
5	10	5.26
6	4	2.11
7	27	14.21
8	26	13.68
9	1	0.53
10	22	11.58
11	39	20.53
12	28	14.74
13	0	0.00
14	0	0.00

Table.4Cluster distances of 20 chickpea ABL's into 10 clusters for timely sown condition

	Cluster 1	Cluster 2	Cluster3	Cluster4	Cluster5	Cluster6	Cluster7	Cluster8	Cluster 9	Cluster10
Cluster 1	9.22	12.43	12.18	11.06	13.07	12.83	12.61	12.86	12.41	13.02
Cluster 2	12.43	0.00	13.06	17.43	10.13	16.15	12.60	14.06	13.63	17.46
Cluster 3	12.18	13.06	0.00	11.65	15.32	9.24	11.68	14.29	14.95	17.55
Cluster 4	11.06	17.43	11.65	0.00	16.76	13.62	14.36	16.21	12.94	15.60
Cluster 5	13.07	10.13	15.32	16.76	0.00	16.46	15.14	10.03	14.16	18.37
Cluster 6	12.83	16.15	9.24	13.62	16.46	0.00	13.28	14.94	17.39	15.85
Cluster 7	12.61	12.60	11.68	14.36	15.14	13.28	0.00	14.31	12.76	11.23
Cluster 8	12.86	14.06	14.29	16.21	10.03	14.94	14.31	0.00	15.75	17.36
Cluster 9	12.41	13.63	14.95	12.94	14.16	17.39	12.76	15.75	0.00	15.10
Cluster 10	13.02	17.46	17.55	15.60	18.37	15.85	11.23	17.36	15.10	0.00

Table.5Cluster mean performance for 14 characters of 20 chickpea ABL's

	DFF	DM	PH	PHFFN	ST	PB	SB

Group 1	54.24	114.15	57 38	26.49	3.65	3.38	11.78
Group 2	52.00	111.00	51.28	24.88	3.25	2.85	13.00
Group 3	54.00	117.00	56.61	27.49	4.27	3.33	10.89
Group 4	57.00	116.00	68.97	34.48	4.53	3.78	14.45
Group 5	53.00	112.00	57.56	28.59	3.76	4.20	14.34
Group 6	44.00	112.00	50.56	22.56	3.58	3.11	7.78
Group 7	55.00	116.00	57.13	29.45	3.64	3.55	9.72
Group 8	63.00	121.33	57.20	29.55	3.45	3.34	11.67
Group 9	51.00	107.00	66.63	30.97	4.15	3.00	13.45
Group 10	53.00	113.00	54.90	23.08	3.43	2.67	8.45

	NPPP	**NEPPP**	**NSPP**	**HSW**	**BYPP**	**HI**	**SYPP**
Group 1	60.40	55.72	1.33	27.89	45.28	45.63	20.73
Group 2	63.45	56.82	1.07	25.60	38.59	40.56	15.70
Group 3	61.00	55.85	1.13	27.97	36.64	48.05	17.66
Group 4	66.89	59.78	1.35	32.00	49.33	52.19	25.81
Group 5	59.67	54.67	1.31	18.42	40.52	32.49	13.18
Group 6	53.39	51.12	1.52	19.58	29.01	52.37	15.21
Group 7	73.01	68.28	1.31	24.72	46.24	47.70	22.09
Group 8	57.56	54.34	1.33	20.14	45.96	31.31	14.43
Group 9	67.67	59.08	1.08	28.64	46.54	39.40	18.38
Group 10	69.00	64.78	1.60	23.63	50.74	48.44	24.66

Where, 1. DFF: Days to 50% flowering, 2. DM: Days to maturity, 3. PH: Plant height (cm), 4. PHFFN: Plant height at first fruiting node (cm), 5. ST: Stem thickness (mm), 6. PB: Number of primary branches per plant, 7. SB: Number of secondary branches per plant, 8. NPPP: Number of pods per plant, 9. NEPPP: Number of effective pods per plant,10. NSPP: Number of seeds per pod, 11. HSW: Hundred seed weight (g), 12. BYPP: Biological yield per plant (g), 13. HI: Harvest index (%), 14.SYPP: Seed yield per plant (g).

Maximum expression of genotypes (Table.4) towards diversity was observed for 100 seed weight (20.53%) followed by biological yield per plant (14.21), number of secondary branches per plant (14.21) and number of pods per plant (13.68). Pahre et al., (2014) and Kuldeep et al., (2015) reported that 100 seed weight and number of pods per plant contributed maximum towards genetic diversity.

The average cluster mean of ten clusters for 14 characters revealed that none of the clusters contained genotype with all the desirable characters and so recombinant breeding between genotypes of different clusters is needed (Table 5). The genotype in group 3 recorded highest cluster mean for days to maturity (117.00) followed by number of pods per plant (73.01) in group 7, plant height (66.63) in group 9, number of effective pods per plant (68.28) in group 7, days to 50% flowering in group 8 (63.00), harvest index (52.37) in group 4 and lowest with number of seeds per pod (1.07).

Genetic diversity analysis within and between cluster revealed that the genotypes of the same cluster had little divergence from each other with respect to the character studied. The hybridization between the genotypes of the same cluster thus, may not provide good sergeants.

Table.6 Grouping of 20 chickpea ABL's into 10 clusters by Tocher's method for late sown condition

Cluster No.	**Number of Genotypes**	**Genotypes**
I	13	JG 2021-70, JG 2020-634958, JG 2022-73, JG 2022-7, ICC 191618, JG 2021-71, JG 2022-6, ICCV 181606, JG 2022-5, JG 2022-1, JG 2022-2, JG 24, JG 18
II	1	JG 2023-84
III	3	JG 2022-4, JG 2022-9, JG 2022-3
IV	1	JG 2016-9651
V	1	JG 2022-8
VI	1	JG 36

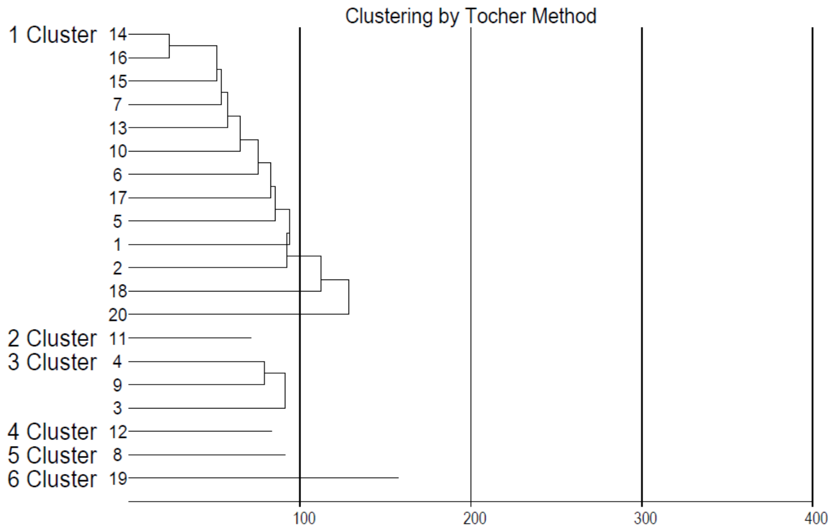

Diagram 2. Clustering by Tocher's method for late sown condition

Table.7 Percent contribution of 14 characters for diversity in chickpea advance breeding lines

Source	Times ranked 1 st	% Contribution
1	6	3.16
2	3	1.58
3	11	5.79
4	5	2.63
5	7	3.68
6	12	6.32
7	6	3.16
8	27	14.21
9	4	2.11
10	32	16.84
11	48	25.26
12	7	3.68
13	19	10.00
14	3	1.58

Table.8Cluster distances of 20 chickpea ABL's into 6 clusters for late sown condition

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	10.12	12.71	12.82	14.33	13.22	14.62
Cluster 2	12.71	0.00	14.18	12.07	15.55	15.53
Cluster 3	12.82	14.18	10.85	14.17	14.07	17.13
Cluster 4	14.33	12.07	14.17	0.00	17.81	18.11
Cluster 5	13.22	15.55	14.07	17.81	0.00	17.05
Cluster 6	14.62	15.53	17.13	18.11	17.05	0.00

Table.9Cluster mean performance for 14 characters of 20 chickpea ABL's

	DFF	DM	PH	PHFFN	ST	PB	SB
Group 1	54.38	113.62	55.90	26.68	3.84	3.47	12.46
Group 2	62.33	120.33	58.70	28.45	3.51	3.55	11.97
Group 3	52.89	111.11	57.67	28.00	3.63	3.25	12.52
Group 4	52.00	111.00	58.00	27.26	3.67	4.22	15.78
Group 5	54.33	112.00	52.89	21.52	3.45	2.56	9.89
Group 6	43.33	110.67	48.45	20.37	3.50	2.23	7.64

	NPPP	NEPPP	NSPP	HSW	BYPP	HI	SYPP
Group 1	61.71	57.16	1.31	28.32	45.29	46.77	21.25
Group 2	62.7	56.97	1.33	20.21	44.91	34.14	15.33
Group 3	72.47	68.62	1.14	26.44	44.38	46.84	20.85
Group 4	65.78	61.72	1.31	18.45	43.18	34.58	14.86
Group 5	68.79	63.89	1.66	23.21	49.83	49.48	24.65
Group 6	53.63	51.89	1.56	19.78	27.92	57.28	15.96

Grouping of 20 chickpea genotypes (Table 6) into six clusters using Tocher's method under late-sown conditions revealed that cluster I contained the maximum number of genotypes (13), namely JG 2021-70, JG 2020-634958, JG 2022-73, JG 2022-7, ICC 191618, JG 2021-71, JG 2022-6, ICCV 181606, JG 2022-5, JG 2022-1, JG 2022-2, JG 24, and JG 18, followed by cluster III, which comprised three genotypes.

The maximum contribution of individual traits to genetic diversity among the genotypes (Table 8) was observed for number of seeds per pod (25.26%), followed by 100-seed weight (16.84%) and number of pods per plant (14.21%). This indicates that 100-seed weight and number of pods per plant were the major contributors to genetic divergence under late-sown conditions.

The average cluster means of six clusters for fourteen characters revealed that none of the clusters possessed genotypes with all desirable traits, indicating the need for recombinant breeding involving genotypes from different clusters (Table 9). Cluster II recorded the highest mean values for days to maturity (120.33), days to 50% flowering (62.33), and plant height (58.70). Cluster III exhibited the highest mean for number of pods per plant (72.47) and number of effective pods per plant (68.62). The highest harvest index (49.48) was observed in cluster V, while the lowest mean value was recorded for number of seeds per pod (1.14).

Table.10Grouping of 20 chickpea genotypes into 7 clusters by Tocher's method for pooled environmental condition

Cluster No.	Number of Genotypes	Genotypes
I	10	JG 2021-71, ICC 191618, JG 2022-7, JG 2022-73, ICCV 181606, JG 2022-6, JG 2022-2, JG 2022-1, JG 2021-70, JG 2020-634958
II	1	JG 2022-9
III	1	JG 2022-5
IV	5	JG 24, JG 18, JG 2022-4, JG 2022-3, JG 2022-8
V	1	JG 2016-9651
VI	1	JG 36
VII	1	JG 2023-84

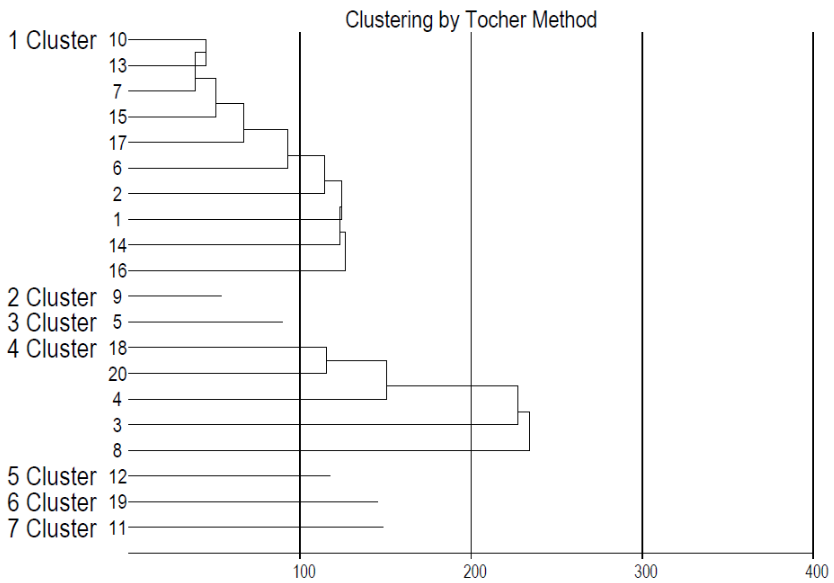

Diagram 3. Clustering by Tocher's method for timely sown condition

Table.11Cluster distances of 20 chickpea ABL's into 7 clusters for pooled environment

	Group. 1	Group. 2	Group.3	Group.4	Group.5	Group.6	Group.7
Group 1	10.98	13.72	13.96	14.71	14.43	14.86	15.23
Group 2	13.72	0.00	13.87	18.15	13.47	17.26	18.33
Group 3	13.96	13.87	0.00	16.56	17.33	12.05	17.59
Group 4	14.71	18.15	16.56	16.27	19.45	19.04	19.96
Group 5	14.43	13.47	17.33	19.45	0.00	16.77	14.03
Group 6	14.86	17.26	12.05	19.04	16.77	0.00	17.28
Group 7	15.23	18.33	17.59	19.96	14.03	17.28	0.00

Table.12Percent contribution of 14 characters for diversity in chickpea advance breeding lines for pooled environment

Source	Times ranked 1 st	% Contribution
1	20	10.53
2	3	1.58
3	26	13.68
4	1	0.53
5	11	5.79
6	5	2.63
7	21	11.05
8	30	15.79
9	1	0.53
10	23	12.11
11	32	16.84
12	14	7.37
13	1	0.53
14	2	1.05

Table.13Cluster mean performance for 14 characters of 20 chickpea ABL's

	DFF	DM	PH	PHFFN	ST	PB	SB
Group 1	53.90	113.93	56.92	26.11	3.58	3.37	11.58
Group 2	52.00	111.00	51.28	24.88	3.25	2.85	13.00
Group 3	54.00	117.00	56.61	27. 49	4.27	3.33	10.89
Group 4	54.73	113.67	61.92	29.64	4.03	3.29	11.97
Group 5	53.00	112.00	57.56	28.59	3.76	4.20	14.34
Group 6	44.00	112.00	50.56	22.56	3.58	3.11	7.78
Group 7	63.00	121.33	57.20	29.55	3.45	3.34	11.67

	NPPP	NEPPP	NSPP	HSW	BYPP	HI	SYPP
Group 1	59.93	55.28	1.34	27.07	44.31	45.05	19.98
Group 2	63.45	56.82	1.07	25.60	38.59	40.56	15.70
Group 3	61.00	55.85	1.13	27.97	36.64	48.05	17.66
Group 4	68.34	62.41	1.33	29.02	49.58	47.83	23.84
Group 5	59.67	54.67	1.31	18.42	40.52	32.49	13.18
Group 6	53.39	51.12	1.52	19.58	29.01	52.37	15.21
Group 7	57.56	54.34	1.33	20.14	45.96	31.31	14.43

Table 14. Intra-cluster distances for pooled environment

Cluster I	10.98
Cluster II	0.00
Cluster III	0.00
Cluster IV	16.27
Cluster V	0.00
Cluster VI	0.00
Cluster VII	0.00

Grouping of 20 chickpea genotypes (Table 10) into seven clusters using Tocher's method under timely sown conditions revealed that cluster I contained the maximum number of genotypes (10), namely JG 2021-71, ICC 191618, JG 2022-7, JG 2022-73, ICCV 181606, JG 2022-6, JG 2022-2, JG 2022-1, JG 2021-70, and JG 2020-634958. This was followed by cluster IV, which comprised five genotypes (JG 24, JG 18, JG 2022-4, JG 2022-3, and JG 2022-8). The remaining clusters were monogenotypic, each containing a single genotype.

The genotype in cluster VII (Table 11) recorded the highest cluster mean for days to maturity (121.33), days to 50% flowering (63.00), and biological yield per plant (45.96). Cluster IV exhibited the highest mean values for number of pods per plant (68.34), number of effective pods per plant (62.41), plant height (61.92), and seed yield per plant (23.84). The highest harvest index (52.37) was observed in cluster VI, while the maximum hundred-seed weight (27.97) was recorded in cluster I. Cluster V showed the highest means for number of secondary branches (14.34) and number of primary branches (4.20), whereas cluster III recorded the maximum stem thickness (4.27). The lowest mean value for number of seeds per pod (1.02) was observed in cluster II. Similar findings have been reported by Lal et al. (2001) and Dwevedi and Lal (2001).

The maximum contribution of individual traits to genetic diversity among the genotypes (Table 12) was recorded for 100-seed weight (16.84%), followed by number of seeds per pod (15.79%), plant height (13.68%), number of secondary branches per plant (12.11%), and days to 50% flowering (10.53%). This indicates that 100-seed weight and number of pods per plant were the major contributors to genetic divergence under pooled environmental conditions.
The average cluster means of seven clusters for fourteen characters revealed that none of the clusters contained genotypes possessing all desirable traits, indicating the necessity of recombinant breeding involving genotypes from different clusters (Table 13).
The maximum intra-cluster distance under pooled environmental conditions was observed in cluster IV (16.27), indicating a wide genetic divergence among the advanced breeding lines within this cluster. A high intra-cluster distance reflects greater internal heterogeneity, suggesting substantial variability among its constituent genotypes and highlighting the effectiveness of the clustering method in grouping genetically related lines while accommodating natural variation.

4. CONCLUSION

The present study demonstrated substantial genetic diversity among the 20 advanced chickpea breeding lines under timely-sown, late-sown, and pooled environmental conditions. Mahalanobis D^2 analysis followed by Tocher's clustering effectively differentiated the genotypes into distinct groups, confirming the presence of considerable genetic divergence. Under pooled conditions, seven clusters were identified, with Cluster I containing the maximum number of genotypes, while Cluster IV exhibited the highest intra-cluster distance (16.27), indicating considerable variability within this group. The contribution of individual traits to genetic divergence varied with the sowing environment. Under pooled conditions, 100-seed weight (16.84%), number of seeds per pod (15.79%), plant height (13.68%), number of secondary branches (12.11%), and days to 50% flowering (10.53%) were important contributors to diversity. Under late-sown conditions, number of seeds per pod, 100-seed weight, and number of pods per plant contributed substantially to genetic divergence. Importantly, no single cluster possessed genotypes with all desirable traits, indicating that selection of parents from genetically diverse clusters would be advantageous for recombination and development of superior chickpea genotypes. Therefore, the diverse advanced breeding lines identified in this study can serve as valuable parental material for future chickpea improvement programmes, particularly for combining desirable yield-related and adaptive traits and broadening the genetic base of cultivated chickpea. The study establishes that exploitation of inter-cluster genetic divergence, particularly involving genotypes possessing complementary desirable traits, offers good potential for developing high-yielding and better-adapted chickpea varieties.

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