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Genetic divergence and character association studies in chickpea (*Cicer arietinum* L.) genotypes for seed yield and its component traits

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Abstract

The present investigation was conducted during Rabi 2025-26 at the Agricultural Research farm of FASAI, Rama University, Kanpur-209217 on 34 genotypes, including 4 checks, evaluated in a Randomized Block Design with three replications. The analysis of variance revealed that the mean sum of squares due to genotypes was highly significant for all the characters studied, indicating the presence of substantial variability among the genotypes for the traits under investigation. The estimates of phenotypic coefficient of variation (PCV) were marginally higher than the corresponding genotypic coefficient of variation (GCV), suggesting a relatively minor influence of environmental factors on trait expression. High heritability coupled with high genetic advance was observed for seed yield per plant, 100-seed weight, plant height, number of secondary branches per plant, number of primary branches per plant and harvest index, indicating the predominance of additive gene action and the effectiveness of selection for these traits. Correlation analysis indicated that seed yield per plant exhibited a positive and significant association with plant height, biological yield per plant and harvest index at both genotypic and phenotypic levels. Divergence analysis grouped the 34 chickpea genotypes into twelve clusters. Cluster I contained the maximum number of genotypes (19), followed by Cluster III (3 genotypes), while Clusters II and IV each comprised 2 genotypes; the remaining clusters were monogenotypic. The highest intra-cluster distance was observed in Cluster IV, followed by Cluster III. The maximum inter-cluster distance was recorded between Cluster X and Cluster V, followed by Cluster XII and Cluster X, indicating the existence of wide genetic diversity among these clusters. Among the traits, plant height contributed the highest percentage to total genetic divergence, followed by harvest index.

Based on overall performance, the genotypes PBC-536, PBC-540, PBC-542 and PBC-562 were identified as superior for seed yield and its contributing traits, including number of primary branches per plant, number of secondary branches per plant and number of pods per plant. These genotypes may therefore be considered promising candidates for utilization in future chickpea breeding program.

Keywords: Chickpea (*Cicer arietinum* L.), correlation, D² analysis, GCV, PCV, clustering

Introduction

Pulses, the edible dry seeds of Leguminosae plants, are valued for their high protein, dietary fiber, mineral content, and low fat and cholesterol levels, making them important for nutritional security and management of metabolic disorders (Rawal and Navarro, 2019). Among pulses, chickpea (*Cicer arietinum* L.) is one of the most widely cultivated cool-season grain legumes and is commonly known as the “King of Pulses.” It is a self-pollinated diploid species (2n=14) belonging to the family Fabaceae and is believed to have originated in southeastern Turkey from its wild progenitor *Cicer reticulatum* (Helbaek, 1970; Georgina Pearman, 2005). Two major cultivated types, desi and kabuli, differ mainly in seed size, colour, and geographical distribution (Moreno and Cubero, 1978).

Chickpea seeds contain about 21-24% protein, 62% carbohydrates, and essential minerals such as calcium, phosphorus, and iron, making them an economical source of plant-based nutrition (Ali *et al.*, 2011). The crop also improves soil fertility through symbiotic nitrogen fixation by *Rhizobium* spp. India contributes nearly 77% of the world's chickpea area and production. During 2023-24, chickpea occupied 10.91 million hectares with a production of 13.75 million tonnes and productivity of 1260 kg ha⁻¹ (Anonymous, 2022) [15, 4, 14, 11, 1, 2].

Genetic variability and heritability studies are crucial for chickpea improvement, particularly for yield-related traits such as pods per plant, branches, and harvest index (Kumar *et al.*, 2012; Malik *et al.*, 2014). Therefore, evaluation of diverse germplasm is essential for identifying superior genotypes for future breeding programmes [23].

Materials and Methods

The experimental material, comprising thirty-four diverse chickpea genotypes along with four standard checks, was evaluated using a Randomized Block Design (RBD) with three replications. Each genotype was sown in a plot measuring 4.0 m × 1.50 m, consisting of five rows of 4 m length. A spacing of 40 cm between rows and 10 cm between plants was maintained. All recommended agronomic practices were uniformly followed to ensure the establishment of a healthy and optimal crop stand. Observations on various quantitative traits under study were recorded from five randomly selected competitive plants per genotype in each replication. However, days to 50%

flowering and days to maturity were recorded on a whole-plot basis.

Result and Discussion

Analysis of variance

The analysis of variance revealed that mean squares due to genotypes were highly significant for all the traits studied, including yield and its component characters in chickpea (Table 1). Significant differences among genotypes were observed for days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, 100-seed weight (g), biological yield per plant (g), seed yield per plant (g), harvest index (%), and protein content (%). These findings are in agreement with earlier reports by Jakhar *et al.* (2016) and Bhanu *et al.* (2017), who also observed significant variation among chickpea genotypes for the traits under study. The presence of substantial variability among genotypes indicates ample scope for improvement through selection and hybridization [5, 3].

Table 1: Analysis of Variance (ANOVA) for yield and its related traits in chickpea

SN	Characters	Replication	Genotype	Error
		[2]	[33]	[66]
1	Days to 50% flowering	11.21	26.22**	5.93
2	Days to maturity	11.94	29.46**	3.99
3	Plant height(cm)	1.42	114.87**	6.23
4	Number of primary branches per plant	0.70	3.09**	0.24
5	Number of secondary branches per plant	1.08	5.01**	0.38
6	Pods per plant	5.88	37.62**	6.95
7	100-Seed weight(g)	0.12	30.72**	0.77
8	Biological yield per plant(g)	6.71	17.37**	2.78
9	Seed yield per plant(g)	0.16	21.56**	0.26
10	Harvest index (%)	20.42	139.45**	21.98
11	Protein content (%)	0.08	6.55**	0.06

Genetic Variability parameters estimate

The analysis of genetic variability among 34 chickpea genotypes (Table 2) revealed considerable variation for most of the studied traits, indicating good scope for selection and crop improvement. Among all characters, seed yield per plant (SYPP) recorded the highest genotypic coefficient of variation (GCV = 22.68%) and phenotypic coefficient of variation (PCV = 23.09%), followed by hundred seed weight (HSW) with GCV and PCV values of 20.77% and 21.56%, respectively. This suggests the presence of substantial variability for these economically important traits. Primary branches per plant also exhibited relatively high variability with GCV of 18.63% and PCV of 20.87%.

High heritability estimates were observed for protein content (97.39%), seed yield per plant (96.48%), and hundred seed weight (92.82%), indicating that these traits are largely governed by genetic factors and less influenced by the environment. Plant height also showed high

heritability (85.31%) coupled with high genetic advance as percent of mean (GAM = 24.98%), suggesting additive gene action and effectiveness of selection.

The highest GAM was recorded for seed yield per plant (45.89%), followed by hundred seed weight (41.21%) and primary branches per plant (34.27%). These traits may respond effectively to direct selection in breeding programmes. In contrast, days to maturity showed comparatively low GCV (2.95%) and GAM (5.01%), indicating limited variability. Overall, the results suggest that traits like seed yield, hundred seed weight, plant height, and number of branches are promising selection criteria for improving chickpea productivity.

Similar findings were also reported by Mohammed *et al.* (2019), Mohibullah *et al.* (2020), Singh *et al.* (2021), Nikita and Lal (2022), Thapa *et al.* (2022), Nikita and Lal (2022), Thapa *et al.* (2022) and Nikhitha, P. and Walia, P. (2022) [8, 10, 17, 13, 22, 12].

Table 2: Genetic variability parameters for yield and its contributing traits in chickpea

Characters	Range	Mean	GCV (%)	PCV (%)	h ² (%)	GA	GAM (%)
DFF	42.04-53.21	47.93	5.43	7.43	53.29	3.91	8.16
DTM	91.18-104.36	98.77	2.95	3.58	68.01	4.95	5.01
PHT (cm)	33.80-58.14	45.84	13.13	14.21	85.31	11.45	24.98
PBP	3.07-6.92	5.23	18.63	20.87	79.70	1.79	34.27
SBP	7.59-13.66	10.67	11.65	12.99	80.43	2.30	21.53
PP	68.47-91.78	61.74	5.18	6.71	59.53	5.08	8.23
HSW (g)	10.70-21.92	15.22	20.77	21.56	92.82	6.27	41.21
BYPP(g)	15.82-24.40	20.73	10.64	13.33	63.64	3.62	17.48
SYPP(g)	8.02-18.67	11.75	22.68	23.09	96.48	5.39	45.89
HI (%)	41.40-65.55	51.24	12.21	15.26	64.04	10.32	20.13
PC (%)	18.82-24.18	21.01	7.00	7.10	97.39	2.99	14.24

Correlation coefficient estimates for seed yield and its component traits

The genotypic (rg) and phenotypic (rp) correlation analysis revealed important associations among yield and yield contributing traits in chickpea. In most cases, genotypic correlations were higher than phenotypic correlations, indicating strong genetic control over these characters (Table 3). Seed yield per plant (SYPP) showed strong positive association with important traits such as plant height (PHT) (rg = 0.73**, rp = 0.66**), biological yield per plant (BYPP) (rg = 0.43**, rp = 0.34**) and harvest index (HI) (rg = 0.51**, rp = 0.43**). This indicates that these traits contributed directly towards higher seed yield and may be useful selection criteria in breeding programmes. Days to 50% flowering (DFF) also exhibited positive correlation with BYPP (rg = 0.67**, rp = 0.44**) and HI (rg = 0.40*, rp = 0.22), suggesting that moderately late flowering genotypes accumulated better biomass and yield. Plant height had highly significant positive association with BYPP (rg =

0.75**, rp = 0.54**) and HI (rg = 0.71**, rp = 0.52**), indicating that taller plants performed better in terms of biomass production and yield efficiency. Pods per plant (PP) showed positive correlation with HI (rg = 0.57**, rp = 0.24*), while hundred seed weight (HSW) was positively associated with HI (rg = 0.40*, rp = 0.34**). These traits also contributed positively towards yield improvement. On the other hand, days to maturity (DTM) showed significant negative correlation with seed yield per plant (rg = -0.42**, rp = -0.33*), indicating that delayed maturity may reduce yield under the studied conditions. Similar findings have been reported by Joshi and Yasin (2015), Srivastava *et al.* (2017), Kumar *et al.* (2018), Singh *et al.* (2021), and Thapa *et al.* (2022) [6, 19, 7].

Overall, the study suggested that plant height, biological yield per plant, harvest index and pods per plant were the major yield contributing traits and should be given importance during selection for yield improvement in chickpea.

Table 3: Estimation of genotypic (rg) and phenotypic (rp) correlation coefficient for different characters in chickpea

S. No.	Character		DTM	PHT (CM)	PBP	SBP	PP	HSW	BYPP	HI (%)	PC	SYPP (g)
1.	DFF	rg	-0.00	0.42*	-0.07	-0.00	0.39	0.09	0.67**	0.40*	-0.16	0.19
		rp	0.02	0.31*	-0.10	0.03	0.14	0.09	0.44**	0.22	-0.12	0.16
2.	DTM	rg		-0.13	-0.35*	-0.10	0.17	0.14	-0.16	-0.11	0.03	-0.42**
		rp		-0.10	-0.20	-0.07	0.12	0.16	-0.08	-0.08	0.02	-0.33*
3.	PHT	rg			0.02	0.10	0.33	0.17	0.75**	0.71**	-0.08	0.73**
		rp			-0.01	0.11	0.27*	0.15	0.54**	0.52**	-0.07	0.66**
4.	PBP	rg				0.18	-0.26	-0.34*	0.04	-0.26	0.18	-0.04
		rp				0.19	-0.17	-0.26	0.01	-0.04	-0.16	0.16
5.	SBP	rg					-0.13	-0.15	0.08	-0.02	0.33*	0.06
		rp					-0.07	-0.13	0.06	-0.02	0.29*	0.05
6.	PP	rg						0.22	0.16	0.57**	-0.33	-0.16
		rp						0.14	0.19	0.24*	-0.27*	-0.13
7.	HWS	rg							0.29	0.40*	-0.19	0.19
		rp							0.19	0.34**	-0.19	0.18
8.	BYPP	rg								0.46*	-0.07	0.43**
		rp								-0.03	-0.07	0.34**
9.	HI	rg									-0.12	0.51**
		rp									-0.08	0.43**
10.	PC	rg										-0.08
		rp										-0.08
11.	SYPP	rg										00.00
		rp										00.00

DFF - Days to 50% Flower	DTM - Days to maturity	SBP - Secondary Branch/ Palnt	PP - Number of Pods/ Pods Plant	HI (%) - Harvest Index	SYPP - Seed Yield / Plant
PHT - Plant Height (cm)	PBP - Primary Branch / Plant	HSW - 100 Seed weight (g)	BYPP - Biological Yield/ Plant (g)	PC - Protein Content	

Genetic divergence and clustering of similar genotypes

The genetic divergence analysis using Mahalanobis D² statistics revealed considerable diversity among the chickpea genotypes, indicating good scope for selection of diverse parents in breeding programmes. Based on Tocher's clustering method, the 34 genotypes were grouped into twelve clusters. Cluster I contained the maximum number of genotypes (19), showing the presence of considerable similarity among most of the entries, whereas clusters V to XII were monogenotypic, indicating high uniqueness of those genotypes.

The cluster mean analysis showed wide variation for different yield and yield contributing traits (Table 4.). Seed yield per plant ranged from 8.51 g in Cluster V to 14.79 g in Cluster XII. Higher seed yield was associated with superior values of important traits such as pods per plant, biological

yield and harvest index. Cluster XI recorded the highest number of pods per plant (67.64), while Cluster X showed maximum harvest index (65.55%). Cluster IX possessed the highest 100-seed weight (21.92 g), whereas Cluster VII recorded maximum protein content (24.18%). Plant height varied from 36.77 cm in Cluster VII to 53.19 cm in Cluster X.

The intra- and inter-cluster distance analysis indicated substantial genetic divergence among clusters. The maximum inter-cluster distance was observed between Cluster X and Cluster V (15.99), followed by Cluster XII and Cluster X (15.59), suggesting that genotypes belonging to these clusters are highly diverse and may be utilized for hybridization to obtain better recombinants and heterotic combinations (Table 6). On the other hand, the minimum inter-cluster distance was observed between Cluster VI and

Cluster V (6.34), indicating close genetic similarity among genotypes of these clusters.

Among the different traits, plant height contributed the maximum towards total genetic divergence (34.69%), followed by harvest index (16.67%) and number of pods per plant (10.86%). In contrast, primary branches per plant contributed the least (1.00%). The results indicated that traits like plant height, harvest index and pods per plant

played a major role in creating genetic variability among the chickpea genotypes and may be considered important during parent selection in chickpea improvement programmes (Table 5).

These findings are in agreement with earlier reports by Thakur *et al.* (2018), Singh *et al.* (2020), Reddy *et al.* (2021), and Tenge *et al.* (2022) [21, 18, 16, 20].

Table 4: Clustering pattern of different genotypes in different clusters.

Clusters	Number of genotypes	Name of genotype
I	19	PBC-535, PBC-536, PBC-537, PBC-538, PBC-539,
		PBC-540, PBC-541, PBC-542, PBC-544, PBC-545,
		PBC-546, PBC-549, PBC-552, PBC-553, PBC-556,
		PBC-560, PBC-561, PBC-562, PBC-563
II	2	PBC-547, JG-16
III	3	PBC-558, PC-1, VIJAY
IV	2	PBC-548, PBC-554
V	1	GCP-101
VI	1	PBC-543
VII	1	PBC-557
VIII	1	PBC-550
IX	1	PBC-559
X	1	PBC-555
XI	1	PBC-551
XII	1	PBC-534

Table 5: Per cent contribution of each character towards total divergence.

S. No.	Characters	Contribution%
1.	Days to 50% flowering	9.33
2.	Days to maturity	10.47
3.	Plant height(cm)	34.69
4.	Number of primary branches	1.00
5.	Number of secondary branches	1.70
6.	Pods per plant	10.86
7.	100-Seed weight	9.35
8.	Biological yield per plant(g)	2.47
9.	Seed yield per plant(g)	1.71
10.	Harvest index (%)	16.67
11.	Protein content (%)	1.75

Table 6: Average intra and inter-cluster distance based on corresponding D2 values

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	4.75	6.51	7.12	7.66	7.28	8.3	8.57	7.57	7.72	9.43	9.27	8.62
II		2.15	8.78	9.68	10.07	6.77	8.09	10.69	10.14	11.92	13.12	11.34
III			4.86	9.74	8.58	9.58	9.19	10.81	9.81	10.46	11.63	8.84
IV				5.87	8.8	10.01	8.94	9.77	9.59	11.43	13.2	8.11
V					0	6.34	13.34	9.78	11.33	15.99	10.21	11.31
VI						0	11.2	10.61	14.17	8.13	10.49	12.38
VII							0	8.3	13.68	15.02	8.98	13.09
VIII								0	11.73	11.28	12.31	13.29
IX									0	10.12	10.55	13.01
X										0	14.21	15.59
XI											0	11.44
XII												0

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