



Genetic Variability, Character Association and Genetic Divergence Analysis in Chickpea (*Cicer arietinum* L.) Genotypes

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ABSTRACT

Background: Chickpea (*Cicer arietinum* L.) classified as one of the greatest prominent pulse crops in India and contributes substantially to nutritional security through its high protein content. Genetic improvement of chickpea requires comprehensive knowledge on degree of the variability available within breeding materials and connection among different genotypes facilitates identification of promising parents and effective selection process. Keeping in view, the present study was done to examine the heritability, genetic variability, genetic divergence and trait associations among forty one chickpea genotypes in the agroclimatic circumstances of western Uttar Pradesh.

Methods: The experiment was conducted on 41 genotypes of chickpea in Research Farm of Department of Genetic and Plant Breeding, CCS University Meerut (UP) India. Each genotype was sown during *rabi* season 2021-22 utilizing randomized block design involving three replications. Five plant were randomly selected were utilized to record data for every genotype in each replication, covering the eleven characteristic traits that were being studied.

Result: ANOVA demonstrated sufficient variability among the all evaluated genotypes for each trait. The highest GCV and PCV estimates were found for no. of seeds/plant, number of pods plant, hundred seeds weight, seed yield per plant, biological yield/plant, branches/plant, total seeds/ pods, plant height. Heritability (bs) with GA as % of mean was highest for number of seeds/plant, followed by pods/plant, biological yield/plant, 100 seed weight, seed yield/plant, no. of seeds/pod. Correlation result demonstrate the number of seeds per plant significant positive associated with seed/ plant, pods/plant, harvest index, primary branches/plant, no. of seeds/pod, biological yield/plant. Path analysis demonstrated the harvest index, biological yield, no. of seed/pod and plant height exerted greatest positive direct effects on seed yield. In contrast, hundred seed weight, branches/plant, total seeds/plant, pods/plant revealed negative direct effect on seed yield. The intra cluster distance ranged from 2.261 to 2.918 in cluster I and III, respectively. Between cluster III and II showed high inter cluster distance in compression to between cluster I and III, cluster I and II. The genotypes RHD-52, BG-372, JG-2001-115 and K-1065 were identified as suitable for early flowering and maturity, whereas JG-226, DC-18-1107, ICC-8948, JG-2001-115, ICC-7549 and P-1106 were found superior for seed yield performance.

Key words: Chickpea, Correlation and path coefficient, Genetic divergence, Genetic variability, Heritability, Seed yield.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is commonly known as gram or bengal gram, is an important food legume crop belong to the Fabaceae family. It is widely grown across South Asia, Mediterranean basin, Australia, North America and East Africa. Chickpea seeds are rich in protein (18-24%), carbohydrates, vitamins and essential minerals, making them an important component of human nutrition. Based on seed characteristics, cultivated chickpea is classified into two major market types, namely *desi* and *kabuli*. *Desi* chickpea possesses coloured and angular seeds, whereas *kabuli* chickpea is characterized by larger cream-coloured seeds with a smooth seed coat.

Despite its economic importance, the productivity of chickpea remains below its genetic potential due to limited utilization of the complicated inheritance of yield along with related characteristics, as well as the restricted use of available genetic variability. Yield is a multigenic characteristic greatly influenced by environmental conditions and interactions among component characters.

The low genetic composition of the available cultivars is the main cause of this. In order for a plant breeder to select optimum yielding genotypes and genetic diversity is essential for crop development and a requirement for any

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breeding program. Estimates of a population's heritability and genetic advancement provide insight into the anticipated gain in subsequent generations. Plant breeders can choose a particular genotype from various genetic populations with the use of heritability estimation.

Information regarding the interconnection between seed yield and its related character is required for any successful selection. By using the correlation along with path coefficient analysis, one can statistically estimate the association of one or more characteristics. Correlation analysis is employed in plant breeding to quantify the degree (strength) and the direction of an association among several variables, as well as to identify the component traits that may be utilized in selection for chickpea improvement.

The correlation coefficients were partitioned into direct and indirect effects for different independent traits through path coefficient analysis. Genetic divergence analysis provides valuable information regarding the extent of diversity among genotypes and facilitates identification of genetically distinct parents for hybridization programme. Crosses involving parents with diverse genetic backgrounds have a greater likelihood of generating transgressive segregants and therefore increase the diversity among populations. Therefore, the current research was conducted to assess heritability, correlation, genetic variability, path coefficient analysis, genetic divergence among forty-one chickpea genotypes for identifying important traits and superior genotypes useful in chickpea breeding programmes.

MATERIALS AND METHODS

The experimental material utilized in the current investigation consists of forty-one chickpea genotypes. These genotypes were procured from IIPR Kanpur, CSA Kanpur and SVPUAT Meerut (Table 1).

Experimental site and experimental design

The experimental material was examined in randomized block design with three replications at research farm of the

Department of Genetics and Plant Breeding, CCS University Meerut, Uttar Pradesh, during the *rabi* season of 2021-2022. The genotypes were planted by dibbling seeds in single rows of 4 m long, maintaining 30 cm spacing between rows and between plants 10 cm. To ensure optimal crop growth and development, all necessary agronomic practices were implemented.

Statistical analysis

The statistical analysis was performed using the mean values of each genotype for all characters across replications. Analysis of variance was conducted according to the procedure described by Panse and Sukhatme (1967). Phenotypic and genotypic coefficients of variation (PCV and GCV) were estimated following Burton and Devane (1953). Broad-sense heritability and genetic advance were calculated as suggested by Johnson *et al.* (1955). Correlation coefficients were determined using the method of Al-Jibouri *et al.* (1958), while path coefficient analysis was performed following Dewey and Lu (1959). Cluster analysis was carried out using squared Euclidean distance and genetic divergence was estimated through the Mahalanobis D^2 statistic (1936). As the experiment was conducted at a single site during one crop season, calculation of variability, genetic advance and heritability should be interpreted under the prevailing environmental conditions. Further validation through multi-location and multi-season testing is necessary for broader applicability of the observed genetic parameters. Statistical computations were performed using SPAR software developed by the IASRI, New Delhi.

RESULTS AND DISCUSSION

Analysis of variance

The mean of square (Table 2) attributable to treatment for all traits under study were highly significant at 1% level of probability ($P \leq 0.01$), reveal the existence of substantial genetic variation among the evaluated genotypes for all

Table 1: The present experimental material consists of forty-one genotypes of chickpea.

S. no.	Genotypes	S. no.	Genotypes	S. no.	Genotypes
1	JG-14-16	15	JG-63	29	ICC-15926
2	GNG-469	16	JG-412	30	JG-2001-115
3	JG-14	17	ICC 8948	31	DAHODYLIAL
4	JG-11	18	KMS-384	32	JG-130
5	DC-18-1107	19	GR-3	33	IPC-9-21
6	RVG-203	20	PANT-G-1114	34	JG-2002-82
7	PBG-5	21	JG-1435	35	BKG-26212
8	JG-12	22	6954-2	36	80137
9	ICC-15921	23	BG-372	37	RSG-888
10	JG-9-14	24	RHG-44	38	P-1167
11	JG-226	25	SC-3	39	K-1065
12	RHD-52	26	C-911	40	P-1106
13	JG-114	27	1-3-1	41	ICC-7549
14	JG-141	28	K-1089		-

characters examined. The observed variability provides ample scope for the selection of promising genotypes that may either be released as varieties or utilized as donor parents in future chickpea breeding and hybridization programmes. The variation detected among these genotypes may be attributed to differences in their genetic constitution along with the influence of environmental factors. Comparable finding has also been documented by Thapa *et al.* (2023); Yadav *et al.* (2024); Kumar *et al.* (2025).

Phenotypic and genotypic coefficient of variation

A high magnitude of genetic variability among genotypes offers greater scope for efficient selection and genetic enhancement in crop improvement programmes. Hence, PCV and GCV are widely applied to study the significance of the variability existing among genotypes. The reason behind using GCV is that it indicates the heritable part of the total variance. In the present investigation, PCV estimates were greater than the corresponding GCV values for all studied characters (Table 3 and Fig 1), suggesting that the observed variability was governed by both genetic factors and environmental influences affecting the expression of the traits.

GCV and PCV were noticed highest for seeds/plant, then by total pods/plant, 100 seed weight, seed yield/plant, biological yield, primary branches, seeds/ pod, plant height. This specify the existence of substantial variability for these traits and suggests considerable scope for their improvement through suitable breeding strategies. The value of GCV and PCV ranged from 0.42% and 0.68% for days to maturity 43.2% and 44.50% for no. of seeds plant, respectively. Similar observations were reported by Thapa *et al.* (2022); Jain *et al.* (2023); Prathyusha *et al.* (2024); Patel *et al.* (2025).

Heritability and genetic advance

The proportion of overall phenotypic variation that can be attributed to genetic variables is known as heritability and it is an essential measure for determining how characteristics are passed from parents to progeny. Genetic advance is the expected enhancement brought about by selection and it expressed as the deviation between mean genotypic value of chosen individuals and that of the original population prior to selection and magnitude of genetic advance depends on heritability, selection intensity and genetic variability. Thus, genetic advance as well as heritability are considered major criteria for selecting and improving desirable traits. The prevalence of additive gene expression in the inheritance of a characteristic is typically indicated by high heritability combined with significant genetic advance, which creates favourable conditions for efficient selection. Conversely, moderate or high heritability associated with low genetic advance demonstrated that the predominant of non-additive gene effect, thereby reducing the efficiency of selection.

The highest heritability estimated were recorded for no. of seeds/plant (93.44%), then by total pods/plant

Table 2: Analysis of variance (ANOVA) for eleven characters in forty-one genotypes of chickpea.

Source of variation	d.f.	Days to flowering	Days to maturity	Plant height	No of pod/plant	No of seed/pod	No of seed/plant	Primary branch	100 seed weight (gm)	Biological yield (gm)	Harvest index	Seed yield/plant (gm)
Replication	2	5.34	2.01	35.77	4.88	0.02	14.51	3.99	0.03	38.50	33.26	5.19
Treatment	40	22.63**	2.16**	31.34**	85.99**	0.19**	302.91**	2.27**	61.53**	268.58**	81.56**	67.29**
Error	80	4.24	0.77	6.27	2.59	0.02	6.93	0.62	2.00	11.14	17.13	4.42

d.f.= Degree of freedom.

*, **Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively.

(91.47%), hundred seed weight (90.85%), biomass/plant (88.51%), seed yield (82.58%), no. of seeds/pod (77.97%), reflecting a strong genetic control over these traits. The seeds/plant, biomass/plant and total pods/plant revealed the greatest genetic advance. The characters with greatest GA as % of mean were seeds/plant (85.66%), next to it by pods/plant (61.43%), hundred seed weight (54.71%), biomass/plant (43.34%), seed yield (42.39%), seeds/pod (33.08%). The combination of high heritability and GA as % of mean was reported for seeds/plant, pods/plant, hundred seed weight, biomass/plant, seed yield, seeds/pod, reveal that these characters are primarily determined by additive gene action and can be successfully enhanced by direct selection. The results are presented in Table 3 and Fig 2. Similar finding has also been reported by Verma *et al.* (2023); Jain *et al.* (2023); Itana *et al.* (2024); Patel *et al.* (2025).

Correlation coefficient analysis

Successful selection programmes largely depend on understanding the relationship among different traits and these association are statistically evaluated through correlation and path analysis. Correlation examine the interdependence among traits and provides information regarding both the direction and degree (magnitude) of association between two or more variables. Additionally, it helps discover significant characteristics that can be considered as selection parameters for genetic enhancement of seed yield. In this investigation, seed yield/plant revealed significant positive relationship with pods/plant, seeds/pod, seeds/plant, harvest index, biological yield/plant (Table 4).

Among the inter trait association, no. of seeds/plant reported significant positive relationship with pods/plant, seeds/pod, primary branches/plant, biomass/plant, whereas exhibiting negative relationship with hundred seed weight. Primary branches displayed positive significant relationship with pods/plant, seeds/plant, biomass/plant. Hundred seed weight was positively significantly associated with days to maturity and flowering, plant height, whereas it demonstrates negative correlation with seeds/plant, seeds/pod, pods/plant. Biological yield with maturity days, plant height, seeds/pods, pods/plant, seeds/plant, branches/plant. These imply that the characteristics mentioned above should be considered as essential selection criteria in order to increase chickpea seed yield. Similar finding has been reported by Ningwal *et al.* (2023); Jain *et al.* (2023); Kumar *et al.* (2025).

Path coefficient analysis

Path coefficient, commonly known as standardized partial regression coefficients, are valuable statistical measures that partition correlation in both direct as well as indirect effect of various independent traits on dependent trait. This tool offers valuable information for determining crucial traits to consider into account in selection programs meant to increase yield and is therefore widely used in indirect selection. The interrelationship among

Table 3: Estimates of heritability (bs), genetic advance as percent of mean, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for eleven characters.

Characters	Mean	Min.	Max.	Heritability (%)	GA	GA as % of mean	GCV (%)	PCV (%)
Days to flowering	132.61	127.33	138.67	59.11	3.92	2.96	1.87	2.43
Days to maturity	162.41	161.00	164.67	37.71	0.86	0.53	0.42	0.68
Plant height	30.03	25.53	41.67	57.14	4.50	14.99	9.63	12.73
No of pod/plant	16.91	8.47	28.13	91.47	10.39	61.43	31.18	32.60
No of seed/pod	1.33	1.00	1.90	77.97	0.44	33.08	18.18	20.59
No of seed/plant	23.09	7.73	47.67	93.44	19.78	85.66	43.02	44.50
Primary branch	4.61	2.60	6.53	46.86	1.05	22.67	16.08	23.49
100 seed weight (gm)	15.99	10.89	28.00	90.85	8.75	54.71	27.86	29.23
Biological yield (gm)	41.43	19.80	66.33	88.51	17.95	43.34	22.36	23.77
Harvest index	49.08	34.40	56.65	55.64	7.12	14.51	9.44	12.66
Seed yield/plant (gm)	20.22	10.21	30.91	82.58	8.57	42.39	22.64	24.92

component traits may differ in both magnitude and direction, which can mask the actual association between related characters and seed yield. Hence, to evaluate each trait's unique contribution, it is essential to divided correlation into direct and indirect effect.

All of the investigated characters' direct and indirect influences on seed yield were calculated (Table 5 and 6). Path analysis revealed, seeds/pod, biomass/plant, plant height, harvest index exerted strong positive direct effect towards seed yield. In contrast hundred seed weight, seeds/plant, branches/plant, pods/plant revealed negative direct impact on seed yield, suggesting that their relationship with yield was mainly result of indirect influences through other contributing traits rather than their own direct effect. Maturity and flowering days, plant height, hundred seed weight, seeds/pod, pods/plant, seed/plant, branches/plant, exhibited indirect positive effect towards seed yield by biological yield. Similarly, pods/plant, flowering days, seeds/pod, seeds/plant contributed indirect positive

effect towards seed yield through harvest index. Comparable findings have also been reported by Ningwal *et al.* (2023); Jain *et al.* (2023); Kakaei *et al.* (2025).

Genetic divergence

The degree of genetic variability present in a crop population plays an essential role in determining the efficacy of any breeding and improvement programs. Genetic diversity is a crucial factor in choosing distinct parents for hybridization programs. It can be efficiently quantified using biometrical approaches such as Mahalanobis D^2 statistics (Mahalanobis, 1936) which is widely employed for identifying genetically diverse parents suitable for planned hybridization. Genetic divergence analysis based on Mahalanobis D^2 statistics and grouping by Tocher's method (Rao, 1952) classified the 41 chickpea genotypes into three distinct clusters (Table 7 and Fig 3). The majority of genotypes were found in Clusters I as well as II, with sixteen genotypes each, whereas Cluster III comprised only nine genotypes.

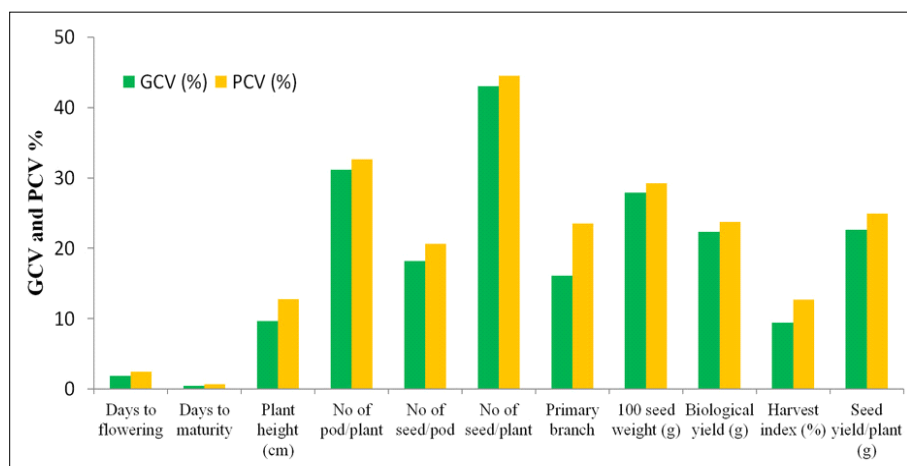


Fig 1: Genotypic and phenotypic coefficient of variance for eleven characters of chickpea.

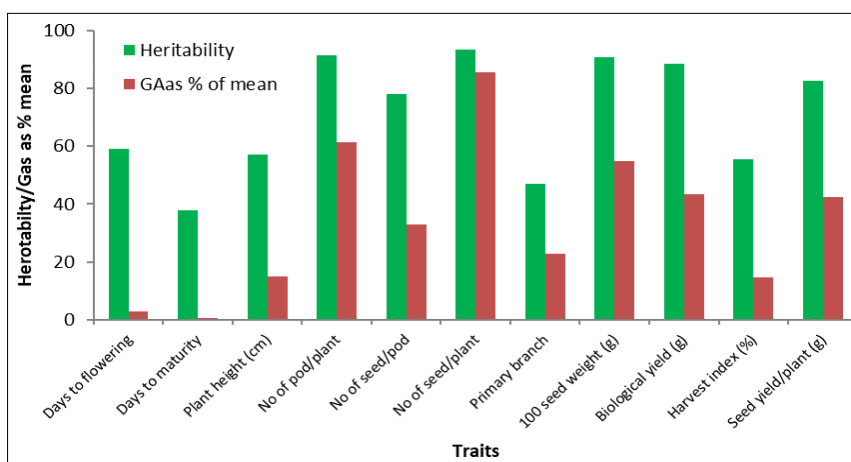


Fig 2: Heritability, genetic advance % of mean of eleven characters of chickpea.

Table 4: Estimates of genotypic correlation coefficient (above diagonal) and phenotypic correlation coefficient (below diagonal) among the eleven characters in chickpea.

Characters	Days to flowering	Days to maturity	Plant height	No. of pod/plant	No. of seed/pod	No. of seed/plant	Primary branch	100 seed weight (gm)	Biological yield (gm)	Harvest index	Grain yield/plant (gm)
Days to flowering	-	0.985**	0.439**	-0.066	-0.219*	-0.093	-0.075	0.329**	0.139	-0.338**	0.004
Days to maturity	0.403**	-	0.769**	-0.098	-0.322**	-0.177*	-0.001	0.449**	0.225*	-0.508**	0.025
Plant height	0.291**	0.428**	-	-0.115	-0.396**	-0.241**	0.059	0.511**	0.204*	-0.444**	0.035
No. of pod/plant	-0.043	-0.037	-0.066	-	0.535**	0.937**	0.457**	-0.553**	0.701**	-0.065	0.654**
No. of seed/pod	-0.125	-0.215*	-0.247**	0.446**	-	0.636**	0.105	-0.561**	0.411**	-0.082	0.372**
No. of seed/plant	-0.043	-0.079	-0.143	0.895**	0.545**	-	0.312**	-0.660**	0.680**	-0.027	0.646**
Primary branch	0.014	0.074	0.114	0.311**	-0.004	0.230**	-	0.097	0.553**	-0.104	0.505**
100 seed weight (gm)	0.230**	0.263**	0.374**	-0.509**	-0.503**	-0.617**	0.058	-	0.012	0.094	0.057
Biological yield (gm)	0.123	0.204*	0.191*	0.650**	0.332**	0.654**	0.462**	0.019	-	-0.173	0.916**
Harvest index	-0.213*	-0.266**	-0.233**	-0.023	0.011	-0.016	-0.155	0.064	-0.184*	-	0.228*
Grain yield/plant (gm)	0.018	0.071	0.090	0.602**	0.328**	0.611**	0.348**	0.053	0.862**	0.326**	-

*, ** = Significant at P = 0.05 and P = 0.01 levels, respectively.

Table 5: Direct effect (bold values) and indirect effects of different characters towards grain yield at genotypic level.

Characters	Days to flowering	Days to maturity	Plant height	No. of pod/plant	No. of seed/pod	No. of seed/plant	Primary branch	100 seed weight (gm)	Biological yield (gm)	Harvest index	R with seed yield /plant (gm)
Days to flowering	-0.0101	0.0312	0.0083	0.0008	-0.0032	0.0108	-0.0011	-0.0312	0.1471	-0.1486	0.004
Days to maturity	-0.0099	0.0316	0.0145	0.0012	-0.0048	0.0206	0.0000	-0.0426	0.2378	-0.2233	0.025
Plant height	-0.0044	0.0243	0.0188	0.0015	-0.0059	0.0281	0.0008	-0.0484	0.2154	-0.1949	0.035
No. of pod/plant	0.0007	-0.0031	-0.0022	-0.0126	0.0079	-0.1090	0.0064	0.0524	0.7415	-0.0286	0.654**
No. of seed/pod	0.0022	-0.0102	-0.0075	-0.0067	0.0148	-0.0741	0.0015	0.0532	0.4348	-0.0361	0.372**
No. of seed/plant	0.0009	-0.0056	-0.0045	-0.0118	0.0094	-0.1164	0.0044	0.0626	0.7190	-0.0117	0.646**
Primary branch	0.0008	0.0000	0.0011	-0.0057	0.0016	-0.0363	0.0141	-0.0092	0.5847	-0.0456	0.505**
100 seed weight (gm)	-0.0033	0.0142	0.0096	0.0070	-0.0083	0.0769	0.0014	-0.0948	0.0130	0.0411	0.057
Biological yield (gm)	-0.0014	0.0071	0.0038	-0.0088	0.0061	-0.0791	0.0078	-0.0012	1.0579	-0.0759	0.916**
Harvest index	0.0034	-0.0161	-0.0084	0.0008	-0.0012	0.0031	-0.0015	-0.0089	-0.1828	0.4394	0.228*

Residual effect = 0.0053.

Table 6: Direct effect (bold values) and indirect effects of different characters towards grain yield at phenotypic level.

Characters	Days to flowering	Days to maturity	Plant height	No. of pod/plant	No. of seed/pod	No. of seed/plant	Primary branch	100 seed weight (gm)	Biological yield (gm)	Harvest index	R with seed yield /plant (gm)
Days to flowering	0.0023	0.0004	0.0092	0.0005	-0.0015	0.0008	-0.0002	-0.0050	0.1202	-0.1089	0.018
Days to maturity	0.0009	0.0010	0.0136	0.0004	-0.0026	0.0015	-0.0013	-0.0058	0.1990	-0.1361	0.071
Plant height	0.0007	0.0004	0.0317	0.0008	-0.0030	0.0027	-0.0020	-0.0082	0.1861	-0.1194	0.090
No. of pod/plant	-0.0001	0.0000	-0.0021	-0.0117	0.0054	-0.0170	-0.0055	0.0112	0.6332	-0.0115	0.602**
No. of seed/pod	-0.0003	-0.0002	-0.0079	-0.0052	0.0121	-0.0104	0.0001	0.0111	0.3233	0.0056	0.328**
No. of seed/plant	-0.0001	-0.0001	-0.0045	-0.0105	0.0066	-0.0190	-0.0041	0.0135	0.6370	-0.0080	0.611**
Primary branch	0.0000	0.0001	0.0036	-0.0036	-0.0001	-0.0044	-0.0177	-0.0013	0.4506	-0.0793	0.348**
100 seed weight (gm)	0.0005	0.0003	0.0119	0.0059	-0.0061	0.0117	-0.0010	-0.0219	0.0184	0.0329	0.053
Biological yield (gm)	0.0003	0.0002	0.0061	-0.0076	0.0040	-0.0124	-0.0082	-0.0004	0.9744	-0.0943	0.862**
Harvest index	-0.0005	-0.0003	-0.0074	0.0003	0.0001	0.0003	0.0027	-0.0014	-0.1794	0.5120	0.326**

Residual effect = 0.0062.

Table 7: Distribution of forty-one genotypes of chickpea in different clusters.

Clusters	Number of genotypes	Name of genotypes
I	16	JG-14-16, JG-14, RVG-203, PBG-5, JG-12, ICC- 15921, JG-412, KMS-384, GR-3, PANT-G-1114, JG-1435, RHG-44, C-911, JG-130, JG-114, BKG-26212
II	16	JG-9-14, JG-226, RHD-52, 1107, JG-63, 8948, 6954-2, BG-372, ICC-15926, JG-2001-115, IPC-9-21, JG-2002-82, ICC-7549, RSG-888, K-1065, P-1106
III	9	GNG-469, JG-11, 1-3-1, JG-141, SC-3, K-1089, 80137, DAHODYLIAL, P-1167

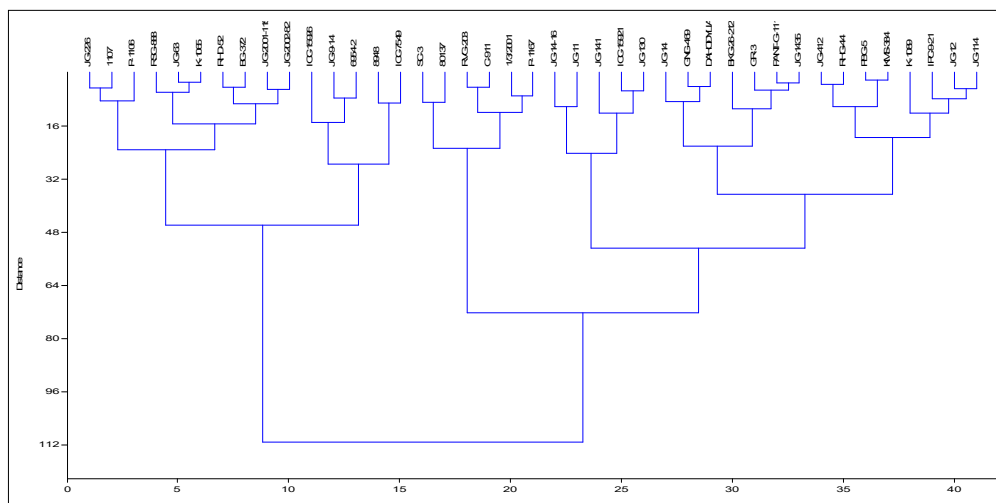


Fig 3: Dendrogram depicting the clustering of chickpea genotypes based on seed yield and its attributing traits.

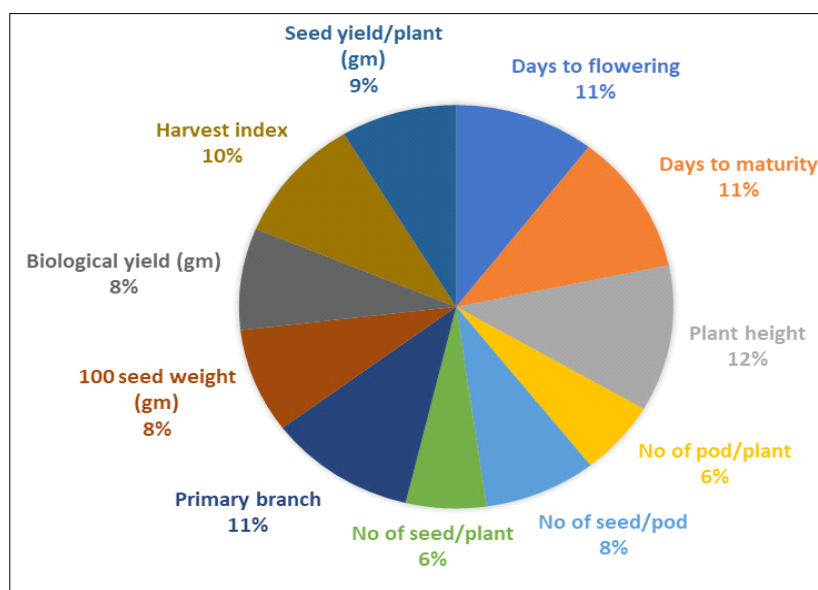


Fig 4: Per cent contribution of yield and its attributing traits towards total genetic divergence among genotypes.

Table 8: Average inter and intra-cluster (bold values) distances between different clusters involving forty-one genotypes of chickpea.

Clusters	I	II	III
I	2.261		
II	3.262	2.529	
III	3.510	4.432	2.918

An examination of Table 8 revealed that Cluster III (D=2.918) had the largest intra-cluster distance, in comparison to Cluster II and I (D=2.529 and D=2.261), respectively. These values confirm that the genotypes categorized inside each cluster exhibit adequate genetic variation.

The inter cluster distance revealed that cluster II and III were the most divergent, exhibiting the highest distance (D=4.432) then between Cluster I and III (D=3.510) and Cluster I and II (D=3.262). These clusters' genotypes were genetically distinct and might be considered potential progenitors in hybridization programs for improving yield and other desirable traits.

Cluster III recorded maximum values of cluster mean for primary branches, plant height, 100 seed weight. Cluster II exhibited superior for total pods/plant, seed yield, biomass/plant, seeds/pods, seeds/plant. Cluster I found best for harvest index and minimum mean value for maturity and flowering days (Table 9). Minimum cluster means for flowering and maturity indicate the suitability of this cluster for developing early flowering and early maturing chickpea genotypes.

Table 9: Cluster mean values for eleven characters in chickpea.

Clusters	Days to flowering	Days to maturity	Plant height	No. of pod/plant	No. of seed/pod	No. of seed/plant	Primary branch	100 seed weight (gm)	Biological yield/plant (gm)	Harvest index	Grain yield/plant (gm)
I	Mean	131.17	161.90	28.59	13.93	1.24	17.64	4.40	35.05	51.28	17.93
	SE±	2.49	0.56	1.68	2.23	0.16	4.67	0.57	7.09	4.86	4.26
II	Mean	132.56	162.33	29.12	21.99	1.55	33.45	4.72	47.17	48.37	22.71
	SE±	2.35	0.69	1.99	4.21	0.23	6.80	0.98	6.92	4.70	3.32
III	Mean	135.26	163.44	34.22	13.18	1.11	14.37	4.80	42.56	46.44	19.86
	SE±	1.91	0.58	3.74	3.96	0.11	4.19	1.11	10.72	5.64	5.87

Genotypes exhibiting superior mean performance within a cluster may either be directly utilized as pureline varieties after evaluation or employed as promising parents in hybridization programmes for chickpea improvement. In cluster II, the genotypes RDH-52, BG-372, JG-2001-115 and K-1065 were identified as suitable for early flowering and maturity. Genotypes JG-226, DC-18-1107, ICC-8948, JG-2001-115, ICC-7549 and P-1106 were found superior for seed yield. Likewise, DC-18-1107, ICC-8948, 6954-2, ICC-15926, ICC-7549 and P-1106 were suitable for total seeds/plant and no. of pods/plant. In cluster III, the genotypes JG-141, DAHODYLIAL and SC-3 were identified as desirable for 100 seed weight, whereas RVG-203 and C-911 from cluster I were found promising for biological yield.

Character contribution towards genetic divergence

The relative contribution of eleven attributes in relation to genetic divergence is illustrated in Fig 4. Among all the evaluated characters, the greatest contribution to genetic diversity was recorded for plant height (11.75%) then by days to maturity (11.25%), primary branches/ plant (11.00%), days to flowering (10.45%) and harvest index (10.06%). Similar discovery has been earlier discovered by Patel *et al.* (2025); Swetha *et al.* (2024); Yadav *et al.* (2023).

CONCLUSION

Based on the current investigation, it can be stated that chickpea genotypes evaluated revealed sufficient genetic variability for all characters, indicating considerable scope for selection, development off transgressive segregants and genetic enhancement in chickpea. The consistently higher PCV values for 11 characters than correspond GCV, suggest the observed variation was governed by environment and genetic variation among genotypes influenced trait expression. Genetic improvement may not always be achieved through selection based only on heredity. Therefore, Heritability and genetic advancement performed together give a more trustworthy basis for identifying superior genotypes in crop improvement programmes. For all trait combinations, correlation at genotypic level were greater than corresponding phenotypic correlation, demonstrated the associations between these characters were predominantly genetically in nature and could be effectively exploited through indirect selection.

The calculations of intra and inter-cluster distances demonstrated the presence of adequate genetic diversity both within and between clusters. Between clusters II and III, found greater inter cluster distance, this reveal the greater amount of diversity between the genotypes grouped into both clusters. Hybridization involving genotypes from these divergent clusters may generate optimum variability and widespread heterosis in segregating generations, thereby facilitating chickpea improvement. The current study's findings showed that there was a significant amount of genetic heterogeneity among the assessed chickpea

genotypes, offering ample opportunities for effective selection and breeding advancement. The superior performance of genotypes such as JG-226, DC-18-1107, ICC-8948, ICC-7549, P-1106 and JG-2001-115 for seed yield and associated traits suggests their potential utility as promising parents in future chickpea breeding programmes. However, their performance should be validated across multiple locations and seasons before their broader utilization in breeding programmes.

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Disclaimers

The views expressed in this article are solely of the authors and do not necessarily represent the views of their affiliated institutions. The authors are responsible for the accuracy and completeness of the information provided.

Conflict of interest

The authors declare that there are no conflicts of interest regarding the publication of this article. No funds were available for supporting the manuscript.

REFERENCES

- Al-Jibouri, H.A., Miller, P.A. and Robinson, H.F. (1958). Genotype and environment variances and co-variances in an upland cotton cross of inter-specific origin. *Agronomy Journal*. **50**: 633-637.
- Burton, G.W. and De Vane, E.H. (1953). Estimating heritability in tall fescue (*Festuca arundinacea* L.) from replicated clonal material. *Agronomy Journal*. **45**: 478-481.
- Dewey, D.R. and Lu, K.H. (1959). A correlation and path- coefficient analysis of components of crested wheatgrass seed production. *Agronomy Journal*. **51**(8): 515-518.
- Itana, T., Mohammed, W. and Abady, S. (2024). Genetic variability, heritability and expected genetic advance of yield and yield related traits in desi type chickpea (*Cicer arietinum* L.) at bule hora, Southern Ethiopia. *Advances in Bioscience and Bioengineering*. **12**(2): 37-44.
- Jain, S.K., Sharma, L.D., Gupta, K.C., Kumar, V. and Yadav, M.R. (2023). Variability and character association for yield and quantitative traits under late sown conditions in chickpea (*Cicer arietinum* L.). *Legume Research-An International Journal*. **46**(4): 408-412. doi: 10.18805/LR-4432.
- Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*. **47**: 314-318.
- Kakaei, M. and Farshadfar, M. (2025). Studies on genetic parameters, heritability and path analysis under irrigated and rainfed conditions in chickpea. *Plant Molecular Biology Reporter*. pp.1-12.
- Kumar, S., Gupta, K., Kumar, A. and Singh, P.K. (2025). Genetic variability and correlation studies for grain yield and its component traits in desi chickpea (*Cicer arietinum* L.). *Environment and Ecology*. **43**(3A): 795-801.
- Mahalanobis, P.C. (1936). On the Generalized Distance in Statistics. *Proc. Nat. Ins. Sci. India*. **12**: 49-55.
- Ningwal, R., Tripathi, M.K., Tiwari, S., Yadav, R.K., Tripathi, N., Solanki, R.S., Asati, R. and Yasin, M. (2023). Assessment of genetic variability, correlation and path coefficient analysis for yield and its attributing traits in chickpea (*Cicer arietinum* L.). *The Pharma Innovation Journal*. **12**: 4851-4859.
- Pansee, V.G. and Sukhatme, P.V. (1967). Statistical Methods for Agricultural Workers. Indian Council of Agricultural Research. New Delhi, p 337.
- Patel, T., Babbar, A., Behera, K., Anand, K.J., Patel, M., Kujur, M.J. and Katara, V.K. (2025). Integrating diversity analysis and morphological characterization for strategic trait selection in advanced breeding lines of chickpea (*Cicer arietinum* L.). *Legume Research-An International Journal*. **48**(12): 1969-1978. doi: 10.18805/LR-5468.
- Prathyusha, A., Kumar, D.U.K. and Parveen, S. (2024). Genetic variability, heritability, genetic advance for yield and yield related attributes in chickpea (*Cicer arietinum* L.). *Environment and Ecology*. **42**(1A): 332-334.
- Rao, C.R. (1952). Advanced Statistical Methods in Biometrical Research. John Wiley and Sons, New York, p 390.
- Swetha, D.B., Kumam, S. and Kumar, A. (2024). Evaluation of genetic divergence in chickpea (*Cicer arietinum* L.) germplasm. *Environment and Ecology*. **42**(2): 399-404.
- Thapa, R.S., Singh, T., Kumar, A., Khan, A.A., Kumar, S. and Pratap, D. (2023). Genotype $\times$ environment (G $\times$ E) interaction and stability analysis for seed yield and its component traits in chickpea (*Cicer arietinum* L.). *Agricultural Research Journal*. **60**(5): 646-653.
- Thapa, R.S., Singh, T., Kumar, A., Kumar, H. and Pratap, D. (2022). Genetic divergence, variability and character association analysis in chickpea (*Cicer arietinum* L.) genotypes under normal and late sown conditions. *Electronic Journal of Plant Breeding*. **13**(2): 616-623.
- Verma, V., Gathiye, G.S., Biswal, M. and Kumar, A. (2023). Evaluation of genetic variability, heritability and genetic advance of chickpea (*Cicer arietinum* L.) genotypes under organic condition. *International Journal of Plant and Soil Science*. **35**(19): 800-806.
- Yadav, A., Nath, S., Bharti, B., Singh, S., Yadav, S., Bhardwaj, R. and Yadav, S.K. (2024). Genetic variability studies in chickpea (*Cicer arietinum* L.) for yield and contributing traits through half-diallel mating strategy under late-sown conditions. *Legume Research-An International Journal*. **47**(12): 2042-2048. doi: 10.18805/LR-5391.
- Yadav, R.K., Tripathi, M.K., Tiwari, S., Asati, R., Chauhan, S., Sikarwar, R.S. and Yasin, M. (2023). Evaluation of genetic diversity through D2 statistic in chickpea (*Cicer arietinum* L.). *International Journal of Environment and Climate Change*. **13**(10): 1598-1611.