

## Characterization of chickpea (*Cicer arietinum* L.) genotypes based on agro-morphological traits

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### ABSTRACT

The current study evaluated 44 chickpea genotypes during Rabi 2023-24 for seed yield and its component traits at Research cum Instructional Field, Department of Genetics and Plant Breeding, IGKV, Raipur College of Agriculture, Raipur Chhattisgarh. The experiment was conducted in Randomized Block Design with 44 genotypes in three replications to assess the genetic variability parameters, correlation, path and genetic divergence analysis. The mean sum of squares for genotypes were highly significant for all the traits except number of primary branches, number of secondary branches, pods per plant and seed yield per plant. PCV were greater in magnitude than the GCV. High magnitude of PCV coupled with GCV was exhibited only by plot yield in grams and number of primary branches. High heritability coupled with high genetic advance as per cent of mean was recorded by plot yield in grams, number of primary branches and biological yield. Overall, plot yield in grams and number of primary branches were the only traits to have high values of PCV, GCV,  $h^2_{(bs)}$  and GA as percent of mean. Plot yield in grams had significant and positive correlation with hundred seed weight, harvest index and seed yield per plant whereas, significant negative correlation was recorded by days to 50 % flowering. Based on direct and indirect effect, high positive direct effect on seed yield was exhibited by pods per plant, followed by hundred seed weight and harvest index at phenotypic level. The 44 genotypes were grouped into 6 clusters. The highest number of genotypes appeared in Cluster I, which contain 39 genotypes followed by Cluster II, III, IV, V, and VI had one accession, respectively.

**Keywords:** Chickpea, genetic variability, correlation, path and genetic divergence analysis

### INTRODUCTION

Chickpea (*Cicer arietinum* L.), a winter annual crop belongs to the family Leguminaceae / Fabaceae. The Greek term Kirois is the source of the English name *Cicer*, which alludes to the famous Roman family Cicero. *Arietinum*, which alludes to the chickpea's ram-like head shape, is derived from the Latin word *arise*, which means ram (Singh and Choudhary, 1985). The usual chromosomal number for *Cicero* species is  $2n=2x=16$  (Bentham and Hooker, 1970). However, different numbers for chickpea ( $2n=2x=14, 16, 24, 32$ ) and other wild *Cicer* species ( $2n=14, 16, 24$ ) have been reported but could not be verified by other researchers. It is mostly raised as a rain-fed crop in India. Chickpeas not only contribute significantly to human nutrition but also maintain soil productivity by fixing up to 141 kg of nitrogen per hectare. The degree of genetic variability and the heritability of desired traits are key factors in crop genetic improvement. A statistical tool for determining the degree (strength) and direction of a relationship between two or more variables is the correlation

coefficient. During the selection process, it is possible to remove characters that are not very important by estimating the correlation coefficient. To ascertain an attribute's true contribution as well as its influence through other features, the path analysis assists in dividing the correlation coefficient of yield components with seed yield into its direct and indirect effects.

### MATERIALS AND METHODS

The experiment material comprised of a set of 44 chickpea genotypes including 5 checks (Table 1). The experiment was carried out at Genetics and Plant Breeding Farm, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G) during Rabi season of 2023-24. The chickpea seeds were sown in the field, in RBD with 3 replications on 7<sup>th</sup> November, 2023. Each plot comprised of 4 rows of 4m length in each replication. The row x row and plant x plant distance of 30 cm and 10 cm and net plot area was 4.8 m<sup>2</sup>. Random five plants are selected from each of the plot in each replication and were taken for collecting data on

yield and yield attributing traits. The observations for thirteen yield traits days to 50% flowering (DTF), days to maturity (DM), plant height (cm) (PH), height of first pod (cm) (HOFP), primary branches per plant (PB), secondary branches per plant (SB), number of pods per plant (PPP),

number of seeds per pod (SPP), 100 seed weight(g) (HSW), biological yield (BY) (g), harvest index (HI) (%), seed yield per plant (SYP) (g), and plot yield (g) (PYG) were recorded.

Table 1: List of chickpea genotypes

S. No.	Coded entries	Decoded entries	S. No.	Coded entries	Decoded entries	S. No.	Coded entries	Decoded entries
1	RG 2021-75	ICCV08102 X JG 36	16	RG 2022-47	IPC 18-129	31	RG 2023-10	ICCX 191055-B-B
2	RG 2022-09	TCh22-9	17	RG 2022-48	IPC 14-88	32	RG 2023-11	ICCX 191056-B-B
3	RG 2022-10	TCh22-10	18	RG 2022-49	IPC 16-127	33	RG 2023-12	ICCX 191057-B-B
4	RG 2022-28	RVG 205 x PKV Harita	19	RG 2022-51	IPC 17-361	34	RG 2023-13	ICCX 191058-B-B
5	RG 2022-29	RVG 203 x RVG 204	20	RG 2022-53	IPC 19-222	35	RG 2023-14	ICCX 191059-B-B
6	RG 2022-30	RVG 204 x ICCV 4958	21	RG 2022-54	IPC 17-253	36	RG 2023-15	ICCX 191060-B-B
7	RG2022-31	JG 2020-10 (JG 16 x JG 17)	22	RG 2023-1	ICCX 191042-B-B	37	RG 2023-16	ICCX 191075-B-B
8	RG 2022-35	IPC 15-147	23	RG 2023-2	ICCX 191043-B-B	38	RG 2023-17	ICCX 191100-B-B
9	RG 2022-36	IPC 16-06	24	RG 2023-3	ICCX 191046-B-B	39	RG 2023-18	ICCX 191104-B-B
10	RG 2022-38	IPC 16-53	25	RG 2023-4	ICCX 191047-B-B	40	Indira Chana 1	C#1
11	RG 2022-39	IPC 16-136	26	RG 2023-5	ICCX 191049-B-B	41	CG Chana 2	C#2
12	RG 2022-42	IPC 17-78	27	RG 2023-6	ICCX 191050-B-B	42	CG Lochan Chana	C#3
13	RG 2022-43	IPC 17-93	28	RG 2023-7	ICCX 191051-B-B	43	CG Akshay Chana	C#4
14	RG 2022-44	IPC 17-110	29	RG 2023-8	ICCX 191052-B-B	44	JG24	C#5
15	RG 2022-45	IPC 17-308	30	RG 2023-9	ICCX 191053-B-B			

## RESULTS AND DISCUSSION

The results of the analysis of variance indicated that the mean sum of squares for genotypes was highly significant for all the traits except number of primary branches, number of secondary branches, pods per plant and seed yield per plant. In chickpea, Ningwal *et al.*, 2023, Naz *et al.*, 2021, Mihoriya *et al.*, 2023, Johnson *et al.*, (2016), Takkuri *et al.*, (2017), Kashyap *et*

*al.* (2003), Puri *et al.* (2013), Singh and Kumar (2008), Patel and Babbar (2005) and Parikh *et al.*, 2024 discovered high variability in all yield-related variables. This clearly illustrates that all genotypes have variability in all aspects. The fact that genotype x environment interaction accounts for such a large and reasonably significant portion of total variation indicates that genotypes react to the environment differently.

Table 2: Genetic variability parameters for thirteen yield attributing traits

Traits	P level	GM	Min	Max	PCV (%)	GCV (%)	h <sup>2</sup> <sub>(bs)</sub> (%)	GA as % of mean
DTF	**	53.34	37.67	66.67	15.60	14.33	84.47	27.14
DM	**	103.08	100.00	106.67	2.24	1.71	58.40	2.69
PH	**	59.78	36.40	73.07	11.45	10.72	87.71	20.69
HOFP	**	38.53	21.73	45.53	15.01	13.00	75.00	23.20
NPB	NS	3.18	2.20	4.70	23.33	20.04	73.78	35.46
NSB	NS	2.56	1.87	4.87	35.89	16.20	20.39	15.07
PPP	**	18.68	10.47	26.40	25.64	6.35	6.13	3.24
SPP	NS	1.07	1.00	1.53	13.32	7.14	28.73	7.88
HSW	**	20.38	12.30	26.36	20.21	12.48	38.12	15.87
BY	**	61.93	35.67	84.67	20.85	19.59	88.25	37.91
HI	**	38.97	25.63	51.21	18.33	10.75	34.43	13.00
SYP	NS	20.41	9.50	31.97	36.58	10.40	8.09	6.09
PYG	**	400.13	152.00	588.67	24.49	22.12	81.62	41.17

DTF = Days to flowering; DM = Days to maturity; PH = Plant height (cm); HOFP = Height of first pod (cm); PB = Primary branches; SB = Secondary branches; PPP = Pods per plant; SPP = Seeds per pod; HSW = Hundred seed weight (g); BY = Biological yield (g); SYP = Seed yield per plant (g); HI = Harvest index (%); PYG = Plot yield (g); \*\* = highly significant at 0.01 probability level; NS = non-significant

High PCV was observed in plot yield in grams, seed yield per plant, number of secondary branches, pods per plant, number of primary branches, hundred seed weight and biological yield whereas the rest of the traits exhibited moderate to low values for PCV. These results are in conformity with the findings of Ningwal *et al.*, 2023; Sriraj and Gurjar, 2022; Mihoriya *et al.*, 2023; Neethu *et al.*, 2020; Manasa *et al.*, 2020 and Arora *et al.*, 2018. High magnitude of PCV coupled with GCV was exhibited only by plot yield in grams and number of primary branches.

High heritability was observed by biological yield followed by plant height, days to 50% flowering, plot yield in grams, height of first pod, number of primary branches whereas rest of the traits had moderate to low values of heritability. Gautam *et al.*, 2021; Kebede *et al.*, 2023 and Kumar *et al.*, 2019 have also reported similar results. High values for heritability indicate that it may be due to higher contribution of genotypic components. The traits namely, plot yield in grams, biological yield, number of primary branches, height of first pod, days to 50% flowering, plant height showed high magnitudes for genetic advance as per cent of mean. High heritability coupled with high genetic advance as per cent of mean was recorded by plot yield in grams, number of primary branches and biological yield.

It clearly indicates that most likely the heritability is due to additive gene effects and selection may be effective. Apart from these two traits, rest the entire traits exhibited moderate to low magnitude of  $h^2$  and GA. High heritability with low genetic advance as percentage of mean indicates non-additive (dominance and epistasis) gene action. Overall, plot yield in grams and number of primary branches are the only traits to show high values of PCV, GCV,  $h^2$  (broad sense) and GA as percent of mean.

**Correlation coefficient analysis:** At phenotypic level, plot yield in grams showed significant and positive relation with hundred seed weight, harvest index and seed yield per plant whereas, significant negative correlation was recorded by days to 50 % flowering. The significant and positive association was recorded between seed yield per plant and hundred seed weight, pods per plant, and harvest index, plant height, number of secondary branches and

biological yield and negative association with days to 50 % flowering. Harvest index had significant and positive association with hundred seed weight and pods per plant whereas, negative association was recorded between days to 50 % flowering, days to maturity, plant height, height of first pod and biological yield. Biological yield exhibited significant and positive association with days to maturity, plant height, height of first pod, number of primary branches, and pods per plant. Hundred seed weight had negative association with days to 50 % flowering and days to maturity.

Pods per plant had significant positive association with plant height, number of primary branches and number of secondary branches. Number of secondary branches had positive association with primary branches and negative association with plant height. Number of primary branches had positive relation with days to 50 % flowering. Height of first pod had positive association with plant height; days to 50 % flowering had positive association with days to maturity. In our study the magnitude of genotypic correlation ( $r_g$ ) was high as compared to phenotypic correlation ( $r_p$ ), it means there is strong association between the traits genetically, but the phenotypic value is lessened by the significant interaction of environment. These results are in conformity with the findings of Shafique *et al.* (2016), Jadhav *et al.* (2014), Padmavathi *et al.*, (2013), Sreelakshmi *et al.*, (2010), Thakur and Sirohi (2009) and Babbar *et al.* (2012).

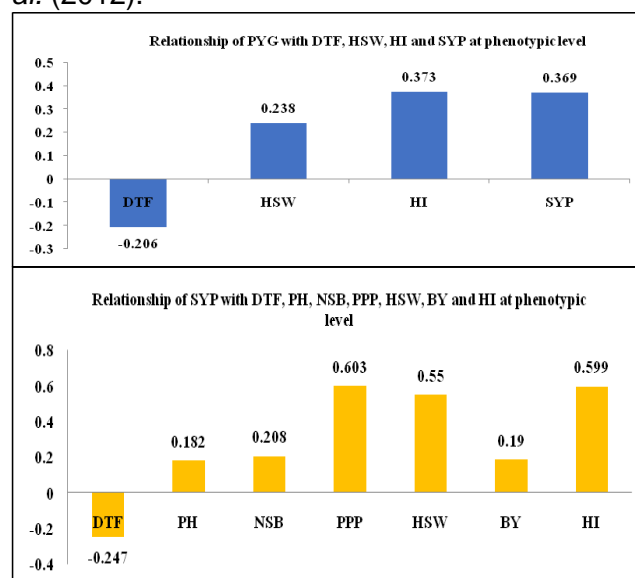


Fig 1: Upstream and downstream association of PYG and SYP with other yield traits

Table 3: Association analysis (phenotypic = P and genotypic = G) of thirteen yield attributing traits

Traits		DTF	DM	PH	HOFP	NPB	NSB	PPP	SPP	HSW	BY	HI	SYP	PYG
DTF	P	1.000												
	G	1.000												
DM	P	0.178*	1.000											
	G	0.241**	1.000											
PH	P	0.020 <sup>NS</sup>	-0.135 <sup>NS</sup>	1.000										
	G	0.055 <sup>NS</sup>	-0.166 <sup>NS</sup>	1.000										
HOFP	P	0.122 <sup>NS</sup>	0.107 <sup>NS</sup>	0.638**	1.000									
	G	0.147 <sup>NS</sup>	0.114 <sup>NS</sup>	0.739**	1.000									
NPB	P	0.274**	0.168 <sup>NS</sup>	-0.154 <sup>NS</sup>	-0.083 <sup>NS</sup>	1.000								
	G	0.306**	0.342**	-0.223*	-0.050 <sup>NS</sup>	1.000								
NSB	P	-0.101 <sup>NS</sup>	0.165 <sup>NS</sup>	-0.235**	-0.141 <sup>NS</sup>	0.307**	1.000							
	G	-0.343**	0.556**	-0.591**	-0.404**	0.559**	1.000							
PPP	P	0.016 <sup>NS</sup>	0.096 <sup>NS</sup>	0.173*	-0.010 <sup>NS</sup>	0.356**	0.398**	1.000						
	G	-0.010 <sup>NS</sup>	0.199*	0.548**	0.047 <sup>NS</sup>	0.887**	-0.628**	1.000						
SPP	P	-0.123 <sup>NS</sup>	-0.167 <sup>NS</sup>	0.095 <sup>NS</sup>	0.119 <sup>NS</sup>	-0.022 <sup>NS</sup>	-0.039 <sup>NS</sup>	-0.014 <sup>NS</sup>	1.000					
	G	-0.223*	-0.555**	0.267**	0.223*	-0.016 <sup>NS</sup>	-0.065 <sup>NS</sup>	-0.143 <sup>NS</sup>	1.000					
HSW	P	-0.330**	-0.268**	0.155 <sup>NS</sup>	0.113 <sup>NS</sup>	-0.161 <sup>NS</sup>	-0.008 <sup>NS</sup>	-0.089 <sup>NS</sup>	0.081 <sup>NS</sup>	1.000				
	G	-0.651**	-0.499**	0.215*	0.233**	-0.372**	-0.408**	-0.810**	0.302**	1.000				
BY	P	0.156 <sup>NS</sup>	0.222*	0.245**	0.265**	0.323**	0.010 <sup>NS</sup>	0.267**	-0.046 <sup>NS</sup>	0.046 <sup>NS</sup>	1.000			
	G	0.182*	0.261**	0.249**	0.336**	0.380**	0.005 <sup>NS</sup>	0.885**	-0.106 <sup>NS</sup>	-0.004 <sup>NS</sup>	1.000			
HI	P	-0.390**	-0.319**	-0.187*	-0.403**	-0.107 <sup>NS</sup>	0.148 <sup>NS</sup>	0.204*	0.068 <sup>NS</sup>	0.370**	-0.311**	1.000		
	G	-0.618**	-0.536**	-0.335**	-0.653**	-0.199*	0.373**	-0.012 <sup>NS</sup>	0.235**	0.290**	-0.576**	1.000		
SYP	P	-0.247**	-0.108 <sup>NS</sup>	0.182*	-0.023 <sup>NS</sup>	0.053 <sup>NS</sup>	0.208*	0.603**	0.149 <sup>NS</sup>	0.550**	0.190*	0.599**	1.000	
	G	-1.019**	-0.724**	0.418**	-0.156 <sup>NS</sup>	-0.203*	-0.421**	-0.126 <sup>NS</sup>	0.343**	0.697**	0.342**	0.808**	1.000	
PYG	P	-0.206*	-0.034 <sup>NS</sup>	0.130 <sup>NS</sup>	-0.158 <sup>NS</sup>	0.024 <sup>NS</sup>	0.077 <sup>NS</sup>	0.171 <sup>NS</sup>	0.027 <sup>NS</sup>	0.238**	0.025 <sup>NS</sup>	0.373**	0.369**	1.000
	G	-0.226**	0.036 <sup>NS</sup>	0.154 <sup>NS</sup>	-0.122 <sup>NS</sup>	-0.006 <sup>NS</sup>	0.201*	0.520**	0.051 <sup>NS</sup>	0.471**	0.040 <sup>NS</sup>	0.527**	1.342**	1.000

\* and \*\* significant at 0.05 and 0.01 probability level, DTF = Days to flowering; DM = Days to maturity; PH = Plant height (cm); HOFP = Height of first pod (cm); PB = Primary branches; SB = Secondary branches; PPP = Pods per plant; SPP = Seeds per pod; HSW = Hundred seed weight (g); BY = Biological yield (g); SYP = Seed yield per plant (g); HI = Harvest index (%); PLYG = Plot yield (g)

**Path coefficient analysis:** The correlation coefficients between grain yield and other yield attributing characters were partitioned into direct and indirect effects and are presented in Table 4. Path coefficient study was carried out by considering the grain yield as the dependent variable and rest of the characters as the independent variables. Based on direct and indirect effect recorded for the traits under present investigation, it was observed that the high positive direct effect on seed yield was exhibited by pods per plant, followed by hundred seed weight and harvest index at phenotypic level.

Plot yield in grams followed by hundred seed weight showed positive indirect effect on seed yield per plant via harvest index whereas, days to flowering, days to maturity and height of first pod exhibited negative indirect effect on seed yield per plant via harvest index. Primary branches had moderate indirect effect on seed yield per plant through biological yield. Days to maturity, height of first pod, plot yield in grams had low indirect effect on seed yield per plant via biological yield. Harvest index and plot yield in grams showed positive indirect effect on seed yield per plant via hundred seed weight. High positive indirect effect of seed yield per plant was achieved by plot yield in grams, number of secondary branches and seeds per pod via harvest index whereas very high negative indirect was recorded by height of first pod and high negative indirect effect was exhibited by days to flowering, days to maturity, plant height,

number of primary branches and seeds per pod via harvest index on seed yield per plant. High positive indirect effect was recorded by pods per plant and number of primary branches per plant via biological yield on seed yield per plant and negative high indirect effect was recorded by harvest index on seed yield per plant via biological yield per plant. The moderate positive indirect effect was recorded by days to maturity, plant height and height of first pod on seed yield via biological yield.

The high positive indirect effect on seed yield per plant was showed by plot yield in grams, harvest index and seeds per pod whereas, high negative indirect effect was observed by pods per plant, days to flowering, days to maturity, number of primary branches and number of secondary branches via hundred seed weight. High to moderate positive indirect effect was shown by number of primary branches, biological yield, plot yield in grams and plant height via pods per plant on seed yield per plant. Hundred seed weight exhibited high negative indirect effect on seed yield per plant via pods per plant. Pods per plant, hundred seed weight and harvest index recorded high positive direct effect on seed yield per plant both at phenotypic as well as genotypic level. Gulwane *et al.*, 2022; Neethu and Lavanya, 2020; Tsehaye *et al.*, 2020; Hailu *et al.*, 2021 and Dawane *et al.*, 2020 also reported similar results, which implies that direct selection for these traits would improve the plant yield.

Table 4: Phenotypic direct and indirect effects of thirteen yield traits with seed yield per plant (SYP) as dependent variable

Traits	DTF	DM	PH	HOFP	NPB	NSB	PPP	SPP	HSW	BY	HI	PYG	r <sub>p</sub>
DTF	0.047	0.016	0.001	-0.001	-0.023	0.005	0.009	-0.014	-0.150	0.022	-0.153	-0.005	-0.247**
DM	0.008	0.092	-0.004	-0.001	-0.014	-0.007	0.054	-0.019	-0.122	0.031	-0.125	-0.001	-0.108 <sup>NS</sup>
PH	0.001	-0.012	0.032	-0.004	0.013	0.011	0.096	0.011	0.070	0.035	-0.073	0.003	0.182*
HOFP	0.006	0.010	0.020	-0.006	0.007	0.006	-0.006	0.014	0.051	0.037	-0.158	-0.004	-0.023 <sup>NS</sup>
NPB	0.013	0.015	-0.005	0.000	-0.083	-0.014	0.198	-0.003	-0.073	0.046	-0.042	0.001	0.053 <sup>NS</sup>
NSB	-0.005	0.015	-0.007	0.001	-0.026	-0.045	0.221	-0.004	-0.004	0.001	0.058	0.002	0.208*
PPP	0.001	0.009	0.006	0.000	-0.030	-0.018	0.555	-0.002	-0.040	0.038	0.080	0.005	0.603**
SPP	-0.006	-0.015	0.003	-0.001	0.002	0.002	-0.008	0.114	0.037	-0.006	0.027	0.001	0.149 <sup>NS</sup>
HSW	-0.016	-0.025	0.005	-0.001	0.013	0.000	-0.050	0.009	0.454	0.007	0.146	0.006	0.550**
BY	0.007	0.020	0.008	-0.002	-0.027	0.000	0.148	-0.005	0.021	0.141	-0.122	0.001	0.190*
HI	-0.018	-0.029	-0.006	0.002	0.009	-0.007	0.113	0.008	0.168	-0.044	0.393	0.010	0.599**
PYG	-0.010	-0.003	0.004	0.001	-0.002	-0.003	0.095	0.003	0.108	0.004	0.147	0.026	1.000

RESIDUAL EFFECT = 0.155; Bold values shows direct and normal values shows indirect effects

DTF = Days to flowering; DM = Days to maturity; PH = Plant height (cm); HOFP = Height of first pod (cm); PB = Primary branches; SB = Secondary branches; PPP = Pods per plant; SPP = Seeds per pod; HSW = Hundred seed weight (g); BY = Biological yield (g); SYP = Seed yield per plant (g); HI = Harvest index (%); PYG = Plot yield (g)

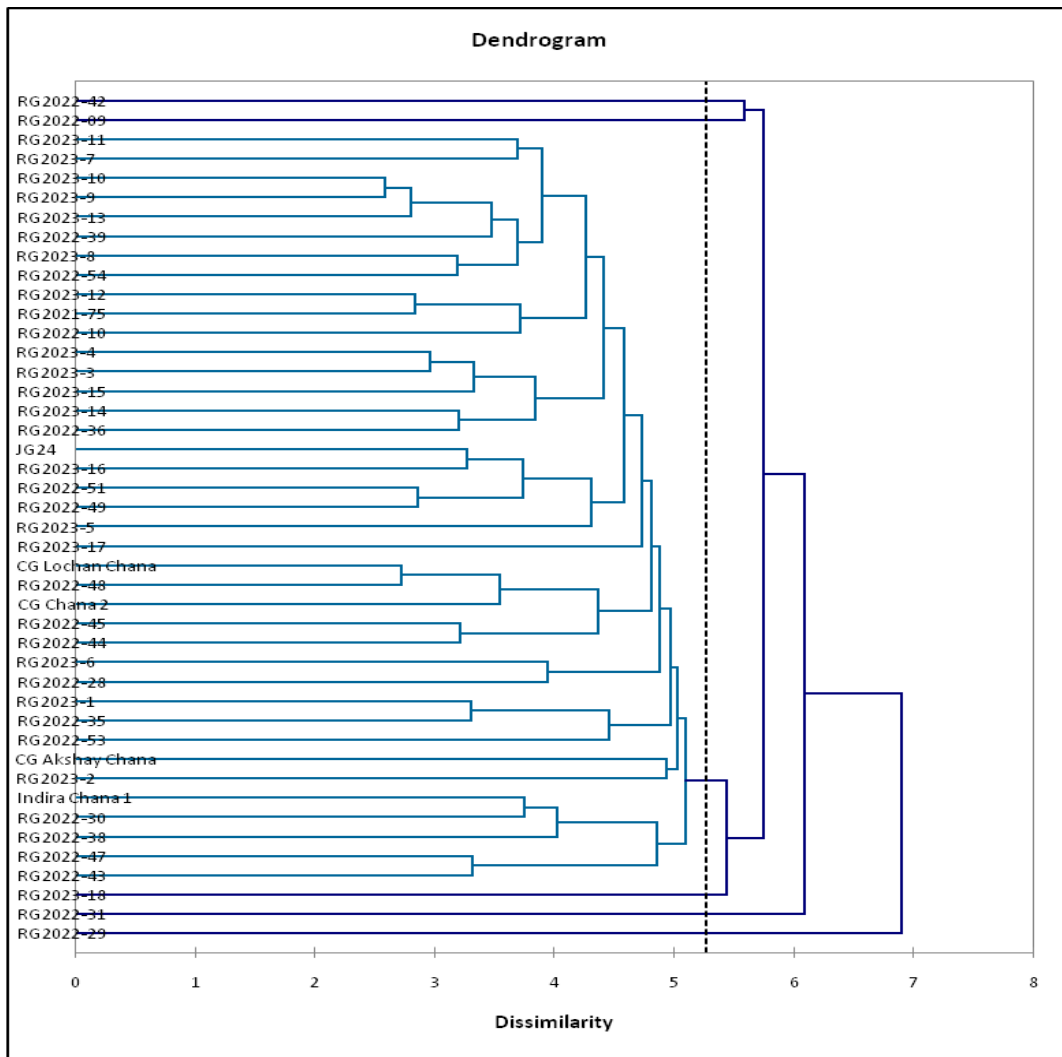


Fig 2: Dendrogram of 44 chickpea genotypes derived by UPGMA from 13 yield traits

Table 5: Clustering patterns of 44 chickpea genotypes

Cluster	No. of genotypes	Genotypes
I	39	RG2021-75, RG2022-10, RG2022-28, RG2022-30, RG2022-35, RG2022-36, RG2022-38, RG2022-39, RG2022-43, RG2022-44, RG2022-45, RG2022-47, RG2022-48, RG2022-49, RG2022-51, RG2022-53, RG2022-54, RG2023-1, RG2023-2, RG2023-3, RG2023-4, RG2023-5, RG2023-6, RG2023-7, RG2023-8, RG2023-9, RG2023-10, RG2023-11, RG2023-12, RG2023-13, RG2023-14, RG2023-15, RG2023-16, RG2023-17, Indira Chana 1, CG Chana 2, CG Lochan Chana, CG Akshay Chana, JG24
II	1	RG2022-09
III	1	RG2022-29
IV	1	RG2022-31
V	1	RG2022-42
VI	1	RG2023-18

**Genetic divergence analysis:** Cluster analysis among 44 chickpea genotypes was studied. The clustering pattern of all the genotypes has been presented in Table 6. The 44 entries were grouped into 6 clusters. The highest number of

genotypes appeared in Cluster I, which contain 39 genotypes followed by Cluster II, III, IV, V, and VI had one accession, respectively. The pattern of group constellation proved the existence of significant amount of variability.

The inter and intra cluster distances among ten clusters were computed and are given in Table 4.13. The intra cluster distance ranged from 0.00 (cluster II, III, IV, V and VI) to 75.71 (Cluster I). The maximum intra cluster distance 75.71 was shown by Cluster I having thirty-nine genotypes. The minimum intra cluster distance was recorded 0.00 in clusters II, III, IV, V and VI having single genotype in each of these clusters, respectively. The highest inter cluster distance was found between cluster II and V (283.47) followed by Cluster II and VI (183.76), cluster III and V (174.40), Cluster II and IV (157.48). The lowest inter cluster distance was recorded between cluster I and IV (26.83). The inter-cluster distances in present study were higher than the Intra cluster distance in all cases reflecting wider diversity among the breeding lines of the distant group.

Table 6: Estimates of intra (diagonal and bold) and inter cluster distances among ten clusters

Clusters	I	II	III	IV	V	VI
I	75.71	132.63	47.89	26.83	152.01	53.09
II		0.00	129.19	157.48	283.47	183.76
III			0.00	54.86	174.40	73.89
IV				0.00	128.85	29.27
V					0.00	106.75
VI						0.00

The cluster mean values showed a wide range of variations for all the characters undertaken in the study. Cluster I had high means for plant height; cluster II for days to 50% flowering, number of primary branches and plot yield in grams; Cluster III for number of secondary branches, and harvest index; cluster IV for seeds per pod, hundred seed weight and seed yield per plant; Cluster V for days to maturity, height of first pod, pods per plant and biological yield; cluster VI for days to flowering (early).

Table 7: Cluster mean for quantitative characters in 44 genotypes of chickpea

Cluster	DTF	DM	PH	HOPF	NPB	NSB	PPP	SPP	HSW	BY	HI	SYP	PYG
1	53.99	103.07	60.70	38.86	3.14	2.40	18.62	1.07	20.41	62.28	38.60	20.32	401.91
2	64.33	106.00	60.40	38.40	4.70	4.53	22.13	1.00	18.23	63.33	37.53	20.58	534.00
3	37.67	103.33	36.40	21.73	2.53	4.87	10.47	1.00	21.04	35.67	51.21	16.70	415.67
4	46.67	100.00	54.33	35.47	3.47	2.80	18.13	1.53	22.21	64.00	42.63	23.52	378.00
5	54.67	106.67	52.33	46.53	4.60	4.07	22.53	1.07	18.05	78.00	34.37	19.05	251.33
6	38.00	100.00	59.80	37.80	2.27	2.87	22.47	1.00	21.28	55.33	44.05	26.03	352.67

DTF = Days to flowering; DM = Days to maturity; PH = Plant height (cm); HOPF = Height of first pod (cm); PB = Primary branches; SB = Secondary branches; PPP = Pods per plant; SPP = Seeds per pod; HSW = Hundred seed weight (g); BY = Biological yield (g); SYP = Seed yield per plant (g); HI = Harvest index (%); PYG = Plot yield (g)

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