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## CHARACTERIZATION OF DESI CHICKPEA (*CICER ARIETINUM L.*) FOR YIELD AND YIELD RELATED TRAITS

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### ABSTRACT

This study was conducted to determine heritability, variability, path analysis, cluster analysis and correlations between yield and yield related traits in 39 chickpea (*Cicer arietinum L.*). Direct and indirect effects of traits with seed yield per plant were investigated. Genotypic variance was the highest for plot yield in grams, followed by biological yield, and secondary branches. High heritability was recorded by days to maturity, plant height, height of first pod, secondary branches and biological yield were greater than those for the other traits. Plant height, height of first pod, pods per plant, hundred seed weight, biological yield per plant and seed yield per plant showed very strong association with plot yield in grams at phenotypic level. The maximum inter cluster distance was recorded between III and VIII followed by cluster IV and VIII, Cluster III and VI, cluster VII and VIII and cluster III and V. The minimum inter cluster was showed by cluster I and V. The path coefficient analysis based on seed yield per plant, as a dependent variable, exhibited high positive direct effects pods per plant and hundred seed weight showed the highest direct influence. Therefore, this research suggests that pod per plant and hundred seed weight can be good selection criteria for improving seed yield per plant in chickpea.

**Keywords** : Chickpea, *Cicer arietinum*, genetic variability, correlation, path coefficient analysis and cluster analysis

### Introduction

In the world, chickpeas rank second in importance among pulse crops, after dry beans. It is a vital source of food for humans and animals, and it also contributes to the fertility of the soil, especially in arid regions. Because of their high protein content, pulses constitute a distinctive group of food crops in global agriculture. The most frequent Rabi crop in Indian diets, pulses are highly sensitive and used extensively to provide about 30% of daily protein needs. Path coefficient analysis, on the other hand, aids in evaluating the direct and indirect effects of traits on their characteristics, while genetic variation among trait types is required for choice criteria. Further, determining the seed yield and

yield components requires the investigation of path coefficients. In addition, the correlation coefficients can be separated into direct and indirect components, and the path coefficient analysis measures the direct impacts of one variable on the other. The association between the variables is not adequately represented by the correlation. In this research, a capacity to separate the correlation factor into its various components is significant (Dewey & Lu 1959).

### Materials and Methods

The study was conducted during the 2023-24 Rabi season at the Research and Instructional Farm, Genetics and Plant Breeding Department, College of Agriculture, Indira Gandhi Agricultural University,

Raipur, Chhattisgarh. Chhattisgarh is situated between 17°14'N and 24°45'N latitudes and 79°16' E and 84°15' E longitudes. Raipur (C.G.) is lies at 21°16'N latitude and 81°36' E longitude with an altitude of (289.60 m) above mean sea level. The total rainfall during crop growing period was (68.60 mm). The study involved evaluating 39 chickpea genotypes (Table 1) using a randomized complete block design (RBD) with three replications. Row and plant spacing were set at 30 cm and 10 cm, respectively, following standard agronomic practices. Thirteen traits were measured, including days to 50% flowering (DTF), days to maturity (DTM), height of the first pod (HOFP), plant height (PH), number of primary branches (NPB), number of secondary branches (NSB), number of seeds per pod (NSP), number of pods per plant (NPP), 100 seed weight (HSW), biological yield per plant (BY), harvest-index (%) (HI), and plot yield (PLYG) in grams. Mean values were used to calculate variability parameters like range, standard deviation, and coefficient of variation. ANOVA was conducted using O.P.STAT software (Sheoran *et al.*, 1998). Coefficient of variation for traits was calculated per Burton and De Vane's formula (1953) and categorized as higher (> 20%), moderate (10% - 20%), or low (<10%). Broad sense heritability was assessed as low, moderate, or high following Hanson *et al.*'s formula (1956) and Johnson *et al.*'s criteria (1955). Expected genetic advance (GA) was determined as per Johnson *et al.* approach (1955). Correlation analysis was performed using Miller *et al.*'s methodology (1958). Path Analysis, introduced by Wright (1921) and applied by Dewey and Lu (1959), assessed direct and indirect effects of independent variables on a dependent variable. Interpretation followed Lenka and Mishra's scale (1973). Using XLSTAT 2014 software, the Agglomerative Hierarchical approach was used to cluster the data, and the Un-weighted Pair Group approach with Arithmetic Averages (UPGMA) method was used to generate the cluster analysis from the standardized data matrix.

## Results and Discussion

The results of the analysis of variance indicated that the mean sum of squares for replication were non-significant for most of the characters except secondary branches and pods per plant. The mean sum of squares for genotypes was significant for all the traits except pods per plant, seeds per pod, harvest index and seed yield per plant exhibiting non-significant results. Commonly utilized techniques to evaluate the amount of heritable and non-heritable variation in the material under study include PCV and GCV. The magnitudes of PCV were found to be greater than those of GCV,

suggesting that the environment plays a major role in altering the genotypic impacts and, in turn, phenotypic consequences. The comprehensive outcomes are listed in (Table 2). Secondary branches, biological yield, and plot yield in grams all contributed to the achievement of high PCV and high GCV values. It is implied by this that character expression is influenced by the environment in addition to genetics. For their respective features in chickpea, Aswathi *et al.* (2019), Babbar *et al.* (2015), Basha *et al.* (2018), Parhe *et al.* (2014), Ramanappa *et al.* (2013), and Vishnu *et al.* (2018) reported similar findings.

Genetic advance under selection is determined by genetic diversity, heritability, and selection intensity. Heritability is based on total genetic variance, which includes fixable (additive) and non-fixable (dominance and epistatic) so variance, even though the characteristics are less impacted by environmental factors, selection for improvement of such traits may not be effective. High heritability was recorded by days to maturity, plant height, height of first pod, secondary branches and biological yield. GA as per cent of mean, high values were recorded by secondary branches, plant height, and height of first pod, primary branches, hundred seed weight, biological yield and plot yield in grams. Overall, high  $h^2$  coupled with high GA was exhibited by plant height, height of first pod, secondary branches, biological yield and plot yield in grams. High heritability and genetic advance values show that additive genes control the traits, and the high heritability is most likely the result of the additive gene effects (Table 2.) Choosing these characters for further attempts at improvement may work well. Low genetic advance values together with high heritability suggest the presence of non-additive gene activity on the traits. The high heritability was caused by environmental factors rather than genetics. Similar findings in chickpea are corroborated by research conducted by Ramanappa *et al.* (2013), Vishnu *et al.* (2018), Puri *et al.* (2013), Malik *et al.* (2014), Hagos *et al.* (2018), and Biru *et al.* (2017).

Correlation analysis is used to determine the degree of association between two variables. Selection process efficacy is also impacted by degree of association. Pearson (1904) developed the notion of the degree of association between independent and dependent variables, while Searle (1961) outlined the mathematical application of these relationships at the phenotypic, genotypic, and environmental levels. Galton (1888) first proposed the idea of such relationships. At the phenotypic level, there was a substantial correlation between the characteristics, plant height, height of the first pod, number of pods per

plant, 100 seed weight, biological yield per plant, and seed yield per plant, and the plot yield in grams (Table 3). Seed yield per plant showed significant and positive relation with primary branches per plant, secondary branches per plant, pods per plant, hundred seed weight, and biological yield per plant. Harvest index recorded significant positive association with plant height, height of first pod, primary branches per plant, pod per plant and biological yield per plant. Primary branches, secondary branches and pods per plant showed positive significant whereas days to 50% flowering showed negative association with biological yield per plant. Seeds per pod showed positive relation with days to maturity. Pods per plant reported to have positive significant association with primary branches and secondary branches per plant whereas it also exhibited significant negative association with days to 50% flowering. Days to 50% flowering, plant height and height of first pod showed negative association with secondary branches per plant. Primary branches reported to have positive relation with plant height. Likewise, height of first pod had positive correlation with days to 50% flowering and plant height. Days to maturity also reported positive correlation with days to 50% flowering. In our study, the genotypic correlation was higher than the phenotypic correlation. This indicates that there is a substantial genetic relationship between the features, but the environment has a large impact on the phenotypic value. These outcomes are consistent with the research conducted by Jadhav *et al.* (2014), Padmavathi *et al.* (2013), Sreelakshmi *et al.* (2010), Thakur and Sirohi (2009), Dasgupta *et al.* (1992), Babbar *et al.* (2012), and Shafique *et al.* (2016). To separate the correlation into measures of direct and indirect effects, path coefficient analysis is useful. It calculates the independent factors' direct and indirect effects on the dependent variable (Table 4).

The path coefficient analysis was carried out by using the correlation coefficient between different quantitative characters to obtain direct and indirect effects of different characters on grain yield per plant. Both direct and indirect effects were noted for the features being studied. It was found that pods per plant, followed by the weight of 100 seeds, had the most positive direct effect on seed yield. In addition, there was a low positive direct influence on seed production indicated by biological yield. Traits namely, number of secondary branches and harvest exhibited moderate negative direct effect on seed yield per plant. Plant height and height of first pod showed low positive indirect effect on seed yield per plant via number of secondary branches. Likewise, pods per plant and biological yield per plant showed low negative indirect effect on seed yield per plant through number of

secondary branches. Number of primary branches, number of secondary branches and biological yield showed positive high indirect effect through pods per plant on seed yield. Harvest index and plot yield in grams also exhibited positive moderate indirect effect on seed yield per plant via pods per plant. Days to 50% flowering were the only trait to possess negative moderate indirect effect on seed yield via pods per plant. 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. Apart from this, biological yield also reported low positive direct effect on seed yield. Traits namely, number of secondary branches and harvest exhibited moderate negative direct effect on seed yield per plant. Plant height and height of first pod showed low positive indirect effect on seed yield per plant via number of secondary branches. Likewise, pods per plant and biological yield per plant showed low negative indirect effect on seed yield per plant through number of secondary branches. Number of primary branches, number of secondary branches and biological yield showed positive high indirect effect through pods per plant on seed yield. Harvest index and plot yield in grams also exhibited positive moderate indirect effect on seed yield per plant via pods per plant. Days to 50% flowering were the only trait to possess negative moderate indirect effect on seed yield via pods per plant. Path analysis permits the examination of direct effects of various characters on yield as well as their indirect effects via other component traits. It provides the basis for selection of superior genotypes from the diverse breeding population. The study examined the clustering patterns of 39 chickpea genotypes, which are shown in (Table 5) and (Fig. 1).

The 39 entries were grouped into 8 clusters, with Cluster II having the most genotypes (28), followed by Cluster V (3 accessions), Cluster IV, and VII (2 accessions), and Cluster I, III, VI, and VIII each having one accession. The group constellation pattern demonstrated the presence of a considerable amount of variability. In clusters I, III, VI, and VIII, the intra-cluster distance was 0.00; in cluster VII, it was 181.28. Cluster VII, with two genotypes (ICCV231146 and ICCV231136), exhibited the largest intra-cluster distance (181.28), followed by cluster V (175.99) and cluster II (123.21), with three and twenty-eight genotypes, respectively, and cluster IV, with 39.83. The largest inter-cluster distance was measured between III and VIII (347.79), followed by III and V

(215.76), IV and VIII (303.20), III and VI (288.64), and VII and VIII (234.66). Cluster I and cluster V displayed the lowest inter-cluster scores (32.19). 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 1:** List of chickpea genotypes used in the study

S. No.	Accession No.	S. No.	Accession No.	S. No.	Accession No.
1	ICCV231102	14	ICCV231124	27	ICCV231132
2	ICCV231104	15	ICCV231130	28	ICCV231133
3	ICCV231107	16	ICCV231140	29	ICCV231136
4	ICCV231110	17	ICCV231142	30	ICCV231137
5	ICCV231111	18	ICCV231146	31	ICCV231138
6	ICCV231112	19	ICCV231106	32	ICCV231139
7	ICCV231113	20	ICCV231108	33	ICCV231141
8	ICCV231116	21	ICCV231109	34	ICCV231143
9	ICCV231118	22	ICCV231125	35	ICCV231144
10	ICCV231119	23	ICCV231127	36	ICCV231145
11	ICCV231120	24	ICCV231128	37	NBeG 47 (C)
12	ICCV231122	25	ICCV231129	38	JG 14 (C)
13	ICCV231123	26	ICCV231131	39	CG Chana 2 (C)
	ICCV231123				

**Table 2:** Genetic variability parameters for thirteen yield attributing traits

Parameters	GM	Min.	Max.	PCV (%)	GCV (%)	$h^2_{(bs)}$ (%)	GA as % of mean
DTF	56.71	51.00	62.50	6.38	5.05	62.85	8.25
DM	108.72	105.50	115.50	2.18	1.84	71.41	3.20
PH	50.96	36.40	70.90	14.05	13.10	86.92	25.16
HOFP	27.71	18.60	35.10	15.78	14.21	81.06	26.35
PB	2.65	1.20	4.50	32.89	19.37	34.69	23.50
SB	6.84	2.30	12.70	41.08	39.20	91.07	77.06
PPP	26.07	12.00	45.80	41.83	16.06	14.74	12.70
SPP	1.08	1.00	1.40	13.35	5.73	18.42	5.07
HSW	23.08	14.64	31.05	16.24	13.30	67.07	22.44
BY	14.91	5.60	21.60	28.89	26.30	82.84	49.31
HI	39.21	24.83	69.68	35.73	17.64	24.37	17.93
SYP	35.10	21.39	52.39	29.55	12.40	17.62	10.73
PYG	382.50	54.89	685.01	45.99	32.21	49.05	46.48

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)

## Conclusions

The present investigation concludes that among 39 genotypes of chick pea. Seed yield and its components appeared to contain a lot of genetic variability which can be used in selection. High mean values indicate that there is enough variability in the population, implying that there is more chance for genotype selection and improvement on these

characteristics. Plant height, height of first pod, pods per plant, hundred seed weight, biological yield per plant and seed yield per plant showed very strong association with plot yield in grams at phenotypic level. High positive direct effect on seed yield was exhibited by pods per plant followed by hundred seed weight. Two genotypes ICCV 231140 and ICCV 231138 possessed high plot yield in grams.

Traits		DTF	DM	PH	HOFP	NPB	NSB	PPP	SPP	HSW	BY	HI	SYP	PYG
DTF	P	<b>1.000</b>												
	G	<b>1.000</b>												
DM	P	0.225 <sup>*</sup>	<b>1.000</b>											
	G	0.373 <sup>**</sup>	<b>1.000</b>											
PH	P	0.178 <sup>NS</sup>	-0.041 <sup>NS</sup>	<b>1.000</b>										
	G	0.215 <sup>NS</sup>	0.031 <sup>NS</sup>	<b>1.000</b>										
HOFP	P	0.318 <sup>**</sup>	0.013 <sup>NS</sup>	0.838 <sup>**</sup>	<b>1.000</b>									
	G	0.415 <sup>**</sup>	0.070 <sup>NS</sup>	0.922 <sup>**</sup>	<b>1.000</b>									
NPB	P	-0.026 <sup>NS</sup>	0.079 <sup>NS</sup>	0.260 <sup>*</sup>	0.178 <sup>NS</sup>	<b>1.000</b>								
	G	-0.049 <sup>NS</sup>	0.135 <sup>NS</sup>	0.349 <sup>**</sup>	0.375 <sup>**</sup>	<b>1.000</b>								
NSB	P	-0.381 <sup>**</sup>	-0.064 <sup>NS</sup>	-0.465 <sup>**</sup>	-0.618 <sup>**</sup>	0.062 <sup>NS</sup>	<b>1.000</b>							
	G	-0.509 <sup>**</sup>	-0.021 <sup>NS</sup>	-0.571 <sup>**</sup>	-0.746 <sup>**</sup>	0.044 <sup>NS</sup>	<b>1.000</b>							
PPP	P	-0.288 <sup>*</sup>	-0.117 <sup>NS</sup>	0.139 <sup>NS</sup>	-0.134 <sup>NS</sup>	0.444 <sup>*</sup>	0.487 <sup>**</sup>	<b>1.000</b>						
	G	-0.784 <sup>**</sup>	0.180 <sup>NS</sup>	-0.161 <sup>NS</sup>	-0.497 <sup>**</sup>	0.575 <sup>**</sup>	0.980 <sup>**</sup>	<b>1.000</b>						
SPP	P	-0.067 <sup>NS</sup>	0.349 <sup>**</sup>	0.087 <sup>NS</sup>	0.067 <sup>NS</sup>	0.116 <sup>NS</sup>	-0.068 <sup>NS</sup>	-0.071 <sup>NS</sup>	<b>1.000</b>					
	G	0.042 <sup>NS</sup>	0.723 <sup>**</sup>	0.216 <sup>NS</sup>	0.314 <sup>**</sup>	0.266 <sup>*</sup>	-0.133 <sup>NS</sup>	-0.355 <sup>**</sup>	<b>1.000</b>					
HSW	P	0.076 <sup>NS</sup>	0.022 <sup>NS</sup>	-0.216 <sup>NS</sup>	-0.162 <sup>NS</sup>	-0.145 <sup>NS</sup>	0.216 <sup>NS</sup>	-0.023 <sup>NS</sup>	-0.012 <sup>NS</sup>	<b>1.000</b>				
	G	0.233 <sup>*</sup>	-0.034 <sup>NS</sup>	-0.227 <sup>*</sup>	-0.197 <sup>NS</sup>	-0.051 <sup>NS</sup>	0.279 <sup>*</sup>	0.015 <sup>NS</sup>	-0.200 <sup>NS</sup>	<b>1.000</b>				
BY	P	-0.279 <sup>*</sup>	-0.146 <sup>NS</sup>	0.058 <sup>NS</sup>	-0.136 <sup>NS</sup>	0.281 <sup>*</sup>	0.516 <sup>**</sup>	0.504 <sup>**</sup>	-0.028 <sup>NS</sup>	0.115 <sup>NS</sup>	<b>1.000</b>			
	G	-0.301 <sup>**</sup>	-0.190 <sup>NS</sup>	0.079 <sup>NS</sup>	-0.164 <sup>NS</sup>	0.566 <sup>**</sup>	0.553 <sup>*</sup>	1.162 <sup>**</sup>	-0.118 <sup>NS</sup>	0.113 <sup>NS</sup>	<b>1.000</b>			
HI	P	0.027 <sup>NS</sup>	0.041 <sup>NS</sup>	0.297 <sup>**</sup>	0.262 <sup>*</sup>	0.225 <sup>*</sup>	0.180 <sup>NS</sup>	0.321 <sup>**</sup>	0.199 <sup>NS</sup>	-0.190 <sup>NS</sup>	0.421 <sup>**</sup>	<b>1.000</b>		
	G	0.074 <sup>NS</sup>	0.433 <sup>**</sup>	0.328 <sup>*</sup>	0.115 <sup>NS</sup>	0.719 <sup>**</sup>	0.234 <sup>*</sup>	0.121 <sup>NS</sup>	1.192 <sup>**</sup>	-0.141 <sup>NS</sup>	0.781 <sup>**</sup>	<b>1.000</b>		
SYP	P	-0.189 <sup>NS</sup>	-0.111 <sup>NS</sup>	-0.015 <sup>NS</sup>	-0.204 <sup>NS</sup>	0.224 <sup>*</sup>	0.311 <sup>**</sup>	0.663 <sup>**</sup>	-0.134 <sup>NS</sup>	0.427 <sup>**</sup>	0.372 <sup>**</sup>	-0.107 <sup>NS</sup>	<b>1.000</b>	
	G	-0.468 <sup>**</sup>	-0.032 <sup>NS</sup>	-0.176 <sup>NS</sup>	-0.437 <sup>**</sup>	0.365 <sup>**</sup>	0.652 <sup>*</sup>	0.356 <sup>**</sup>	-0.332 <sup>**</sup>	0.930 <sup>**</sup>	0.624 <sup>**</sup>	-0.743 <sup>**</sup>	<b>1.000</b>	
PYG	P	0.016 <sup>NS</sup>	0.112 <sup>NS</sup>	0.336 <sup>**</sup>	0.228 <sup>*</sup>	0.176 <sup>NS</sup>	-0.137 <sup>NS</sup>	0.258 <sup>*</sup>	0.166 <sup>NS</sup>	0.247 <sup>*</sup>	0.261 <sup>*</sup>	0.087 <sup>NS</sup>	0.311 <sup>**</sup>	<b>1.000</b>
	G	0.129 <sup>NS</sup>	0.183 <sup>NS</sup>	0.471 <sup>**</sup>	0.412 <sup>**</sup>	0.332 <sup>**</sup>	-0.255 <sup>*</sup>	0.477 <sup>**</sup>	-0.210 <sup>NS</sup>	0.335 <sup>**</sup>	0.352 <sup>**</sup>	0.344 <sup>**</sup>	0.667 <sup>**</sup>	<b>1.000</b>

\* and \*\* significant at 0.05 and 0.01 probability level, DTF = Days to flowering; DM = Days to maturity; PH = Plant height; 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).

Traits	DTF	DM	PH	HOFP	NPB	NSB	PPP	SPP	HSW	BY	HI	PYG
DTF	<b>-0.016</b>	0.003	-0.001	-0.025	0.001	0.107	-0.235	0.001	0.033	-0.049	-0.007	-0.001
DM	-0.004	<b>0.012</b>	0.000	-0.001	-0.002	0.018	-0.095	-0.007	0.009	-0.026	-0.011	-0.004
PH	-0.003	0.000	<b>-0.005</b>	-0.066	-0.006	0.130	0.113	-0.002	-0.092	0.010	-0.082	-0.013
HOFP	-0.005	0.000	-0.004	<b>-0.079</b>	-0.004	0.173	-0.110	-0.001	-0.069	-0.024	-0.072	-0.009
NPB	0.000	0.001	-0.001	-0.014	<b>-0.022</b>	-0.018	0.362	-0.002	-0.062	0.049	-0.062	-0.007
NSB	0.006	-0.001	0.002	0.049	-0.001	<b>-0.280</b>	0.396	0.001	0.092	0.091	-0.050	0.005
PPP	0.004	-0.001	-0.001	0.011	-0.010	-0.136	<b>0.815</b>	0.001	-0.010	0.089	-0.088	-0.010
SPP	0.001	0.004	0.000	-0.005	-0.003	0.019	-0.057	<b>-0.021</b>	-0.005	-0.005	-0.055	-0.007
HSW	-0.001	0.000	0.001	0.013	0.003	-0.061	-0.019	0.000	<b>0.427</b>	0.020	0.052	-0.010
BY	0.004	-0.002	0.000	0.011	-0.006	-0.145	0.411	0.001	0.049	<b>0.176</b>	-0.116	-0.010
HI	0.000	0.000	-0.001	-0.021	-0.005	-0.051	0.261	-0.004	-0.081	0.074	<b>-0.276</b>	-0.003
PYG	0.000	0.001	-0.002	-0.018	-0.004	0.038	0.210	-0.003	0.105	0.046	-0.024	<b>-0.040</b>

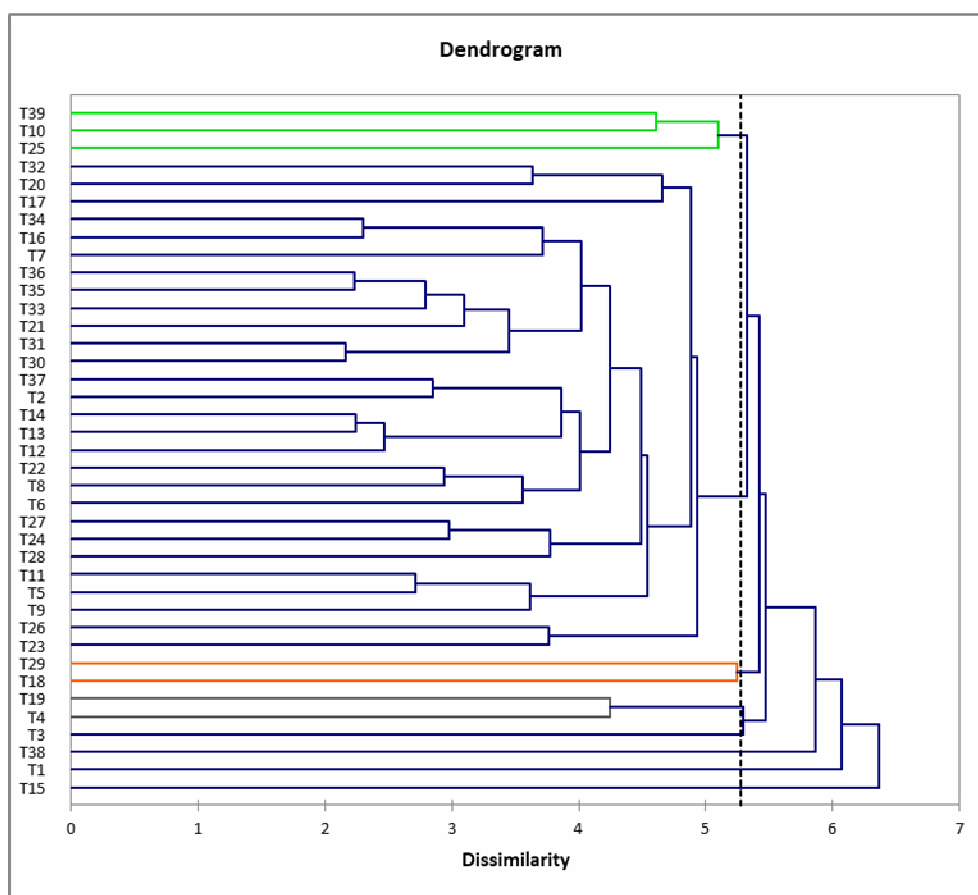
DTF = Days to flowering; DM = Days to maturity; PH = Plant height (cm); HOFP = Height of first pod (cm); PB = Primary branches; SB = Secondary branches; PPP = Pods per plant; SPP = Seeds per pod; HSW = Hundred seed weight (g); BY = Biological yield (g); SYP = Seed yield per plant (g); HI = Harvest index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

[illegible]

**Table 6:** Cluster mean for quantitative characters in 39 genotypes of chickpea

Cluster	DTF	DM	PH	HOFP	NPB	NSB	PPP	SPP	HSW	BY	HI	SYP	PYG
I	59.50	109.50	45.90	<b>35.40</b>	3.10	7.50	30.30	1.10	<b>27.89</b>	18.70	45.65	41.16	343.14
II	56.93	108.50	49.75	27.48	2.58	6.54	24.98	1.04	23.43	12.92	37.95	34.47	385.27
III	60.00	<b>114.50</b>	55.20	30.05	3.20	<b>9.60</b>	32.10	1.35	26.16	20.40	<b>64.68</b>	31.33	<b>533.00</b>
IV	55.50	113.50	50.20	27.60	2.05	5.30	19.35	1.35	22.28	<b>12.05</b>	35.00	34.58	487.94
V	53.83	107.50	43.10	24.20	2.67	7.03	26.93	1.07	20.67	13.53	29.03	36.98	321.17
VI	<b>52.50</b>	<b>106.50</b>	54.80	30.00	<b>4.50</b>	7.70	30.30	<b>1.40</b>	<b>20.05</b>	14.80	49.05	30.18	245.12
VII	55.50	109.25	<b>58.05</b>	29.65	3.00	9.45	<b>44.70</b>	1.05	20.72	<b>18.90</b>	37.32	<b>46.71</b>	416.02
VIII	<b>60.50</b>	<b>106.50</b>	35.40	20.50	2.40	5.70	15.90	1.10	22.20	15.65	60.35	27.47	186.50

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. 1 :** Dendrogram of 39 chickpea genotypes derived by UPGMA from 13 yield traits

### References

- Aswathi, P.V., Ganesamurthy, K. and Jayamani, P. (2019). Genetic variability for morphological and biometrical traits in chickpea (*Cicer arietinum* L.). *Electronic Journal of Plant Breeding*, **10**(2), 699-705.
- Babbar, A., Pandey, S. and Singh, R. (2015). Genetic studies on chickpea genotypes grown in late sown under rice fallow conditions of Madhya Pradesh. *Electronic Journal of Plant Breeding*, **6**(3), 738-748.
- Basha, S.J., Jayalakshmi, V., Khayum, A.S., Kamakshi, N. (2020). Studies on growth and yield characters of chickpea (*Cicer arietinum* L.) varieties suitable for mechanical harvesting. *J. Soc. Trop. Plant Res.* **7**(3), 634-637.
- Biru, A., Kassahun, T., Teklehaimanot, H. and Dagnachew, L. (2017). Broad sense heritability and genetic advance for grain yield and yield components of chickpea (*Cicer arietinum* L.) genotypes in western Ethiopia. *International Journal of Genetics and Molecular Biology*, **9**(4), 21-25.
- Dasgupta, T., Islam, M.O., Gayen (1992). Genetic variability and analysis of yield components in chickpea (*Cicer arietinum* L.). *Annals Agric. Res.*, **13**, 157-160.
- Dewey, D.R. and Lu, K.H. (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.*, **51**, 511-518.

- Hagos, A.A., Desalegn, T. and Belay, T. (2018). Genetic variability, correlation and path analysis for quantitative traits of seed yield, and yield components in chickpea (*Cicer arietinum* L.) at Maichew, Northern Ethiopia. *African Journal of Plant Science*, **12**(3), 58-64.
- Jadhav, P.S., Rathore, A.H., Lipane, R.R., Berad, P.B., Suresh, B.G. (2014). Selection of promising lines generation of chickpea genotypes through correlation and path coefficient analysis. *Supplement on Genetics and Plant Breeding*, **9**(4), 1769-1771.
- Lenka, D. and Mishra, B. (1973). Path coefficient analysis of yield in rice varieties. *Ind. J. Agric. Sci.*, **43**, 376- 279.
- Malik, S.R., Shabbir, G., Zubir, M., Iqbal, S.M. and Ali, A. (2014). Genetic diversity analysis of morpho-genetic traits in desi chickpea (*Cicer arietinum* L.). *International Journal of Agriculture and Biology*, **16**(5), 956-960.
- Miller, P.A., Williams, J.E., Robinson, H.F. and Comstock, R.E. (1958). Estimates of variance and co-variance in upland cotton and their implications in selection. *Agron J.*, **50**, 126-131.
- Padmavati, P.V., Murthy, S.S., Rao, S.V. and Ahamed, L.M. (2013). Correlation and path coefficient analysis in kabuli chickpea (*Cicer arietinum* L.) *International Journal of Applied Biology and Pharmaceutical Technology*, **4**(3), 107-110.
- Parhe, S.D., Harer, P.N. and Nagawade, D.R. (2014). Investigation of genetic divergence in chickpea (*Cicer arietinum* L.) genotypes. *Bioscan*, **9**(2), 879- 882.
- Puri, M.K. and Johnson, P.L. (2013). Study of variability, diversity and association analysis of Chickpea (*Cicer arietinum* L.) germplasm under normal and late sown conditions of Chhattisgarh state. *Trends in Biosc.*, **6**(6), 723-731.
- Ramanappa, T. M., Chandrashekara, K., Nuthan, D., Krishi, G., Kendra, V., Krishi, G., and Kendra, V. (2013). Analysis of Variability for Economically Important Traits in Chickpea (*Cicer arietinum* L.). *International Journal of Research in Applied, Natural and Social Sciences*, **1**(3), 133-140.
- Shafique, M.S., Ahsan, M., Mehmood, Z., Abdullah, M., Shakoor, A., Ahmad, M.I. (2016). Genetic variability and interrelationship of various agronomic traits using correlation and path analysis in chickpea (*Cicer arietinum* L.). *Academia Journal of Agricultural Research*.
- Sheoran, O.P., Tonk, D.S., Kaushik, L.S., Hasija, R.C. and Pannu, R.S. (1998). Statistical Software Package for Agricultural Research Workers. Recent Advances in information theory, Statistics and Computer Applications by D.S. Hooda and R.C. Hasija Department of Mathematics Statistics, CCSHAU, Hisar (139-143).
- Sreelakshmi, C.H., Shivani, D. and Sameer, K.C.V. (2010). Genetic divergence, variability and character association studies in Bengal gram (*Cicer arietinum* L.). *Electronic Journal of Plant Breeding*, **1**(5), 1339-1343.
- Vishnu, B., Veera, J. and Rani, M. (2018). Genetic diversity studies among chickpea (*Cicer arietinum* L.) genotypes under rainfed and irrigated conditions for yield attributing and traits related to mechanical harvesting. *Legume Research - An International Journal*.