



## Elucidating genetic diversity and variability in Chickpea (*Cicer arietinum* L.) using yield attribution traits

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ARTICLE INFO	ABSTRACT
<p>Received : 22 February 2023  Revised : 19 June 2023  Accepted : 04 July 2023</p> <p>Available online: 18 August 2023</p> <p><b>Key Words:</b>  Genetic divergence  Heritability  D<sup>2</sup> analysis  PCA</p>	<p>Fifty-six <i>desi</i> chickpea (<i>Cicer arietinum</i> L.) advance breeding lines were evaluated in order to explore the possibility of genetic divergence for yield and its contributing traits using Mahalanobis's D<sup>2</sup> Statistics and Principal Component Analysis. High estimates of heritability, genetic advance, GCV and PCV were recorded for seed yield per plant (92.2%, 12.4%, 37.1% and 38.7%), biological yield per plant (88.1%, 21.9%, 29.1% and 31.0%) and harvest index (87.3%, 25.0%, 22.7% and 24.3%). All the test genotypes were sort into five discrete clusters. Biological yield/plant (23.5%), days to maturity (17.3%), harvest index (14.6%), seed yield/plant (11.3%), total number of pods/plant (7.4%) and 100 seed weight (6.49%) were found to have highest percentage contributions to genetic diversity in the present research. The first six principal components (PC1 19.7%, PC 16.2%, PC3 11.2%, PC4 9.69%, PC5 7.2% and PC6 6.69%) could explain 70.68% of the total of the interaction variation and have Eigen value more than one. Genotypes JG 2016-1411, JG 2016-9605, JG 2017-46, ICCV 16105, ICCV 16109, ICCV 16112 and ICCV 16116 were present in more than one PCs hence contributed maximum towards yield and can be used in various breeding programmes for yield improvement.</p>

### Introduction

India has gained astounding headway in improving pulse production during last 15 years. Total pulse production in India during 2005-06 was 13.38 million MT, by 2020-21 the production increased to 25.58 million MT (Gaur, 2021). Chickpea had an overwhelming majority share of 49.3% in total pulse production in 2020-21. India had leapfrogged towards attaining self sufficiency in pulses and is essential for supplying reasonably priced protein to the world's expanding population (Bankoliya *et al.*, 2022). Adaptation and implementation of innovative breeding programs has increased the total yield of

chickpea from 1.27 million MT in 1979 to 6.95 million MT in 2019 in central and southern India, which accounts for 445% increase in production. It was possible due to 177% area growth (2.42 to 6.71 million ha) and 97% yield growth (527 to 1036 Kg/ha) over the last 40 years (1979-2019) (Gaur, 2021). Chickpea is a valued crop and possess huge wealth of vitamins, minerals, proteins, fiber and complex carbohydrates. It is consumed all over the world, especially in the Asian and African countries and is referred to as poor man's meat as it contains rich source of protein. Chickpea is grown in rotation

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with cereal crops in India due to its ability to fix areal nitrogen into the soil and intern improves soil fertility. Due to diverse role of this crop in farming system, research on chickpea crop will have significant impact on nutritional security and soil fertility. Narrow genetic base of cultivated chickpea is the major limiting factors for initiating the breeding programme for increasing the yield potential. Understanding genetic variation is crucial for recognize its availability and its potential application in breeding. Improvement in yield can be achieved by selecting the genotypes with desirable characters either alone or in combination with other morphological traits (Shivwanshi and Babbar, 2019).

### Material and Methods

Fifty six genotypes of *desi* chickpea, received from ICRISAT, Patancheru and JNKVV, Jabalpur along with two checks, JG 16 and JG 36, were evaluated during post rainy season, 2018-19, Department of Plant Breeding and Genetics, Seed Breeding Farm, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur. Geographically, the experimental site is located at 23°21'N latitude and 79°94' E longitude at an altitude of 411.8m above the sea level. Tested genotypes were laid out in three replications based on Randomized Complete Block Design (RCBD), with genotypes spaced 30 cm by 10 cm apart on 4.0 m by 1.2 m plot. Weather data such as precipitation, was also obseved throughout the cropping season since weather has profound influence on crop growth, production, pest and disease incidence, irrigation and fertilizer requirement. Throughout the growing season, the chickpea crop was grown according to the prescribed agronomical package of practice of chickpea. Five randomly chosen plants from each plot's were selected to record yield and yield attributing attributes. Mean value of 56 chickpea genotypes were computed for determining principals of variance, Principal Component Analysis (PCA) and cluster analysis were also performed to assess genetic diversity among chickpea accessions.

### Results and Discussion

Throughout the cropping seasons, there was a total of 19.4mm rainfall, a relative humidity range of 31.4

– 82.8% with an average maximum temperature of 27.9°C and lowest temperature of 9.6°C. There was no occurrence of erratic weather change. Hence the weather requirement for crop growth was optimum. For all the parameters considered in the study, the analysis of variance (ANOVA) indicated high significant differences ( $P < 0.001$ ) among the tested genotypes, suggesting presences of genetic variability among the genotypes and revealing the significance of chickpea germplasm in crop improvement programmes. Previous studies (Mohammed *et al.*, 2019) reported presence of variability in similar traits, while some research (Pandey *et al.*, 2013) reported exception for days to maturity and number of seeds/pods.

To assess the level of genetic variability existing in the tested population, the study of phenotypic range of variation alone is insufficient. Both genotypes and the environment in which they are grown play a combine role in determining phenotypic variation. To evaluate genetic variability and to determine the amount of any potential improvement in various traits, one should employ genetic parameters such as heritability, components of variance, coefficient of variation and genetic advance. The traits under research were less influenced by environment since genotypic coefficient of variation (GCV) closely followed phenotypic coefficient of variation (PCV) in all the traits. For seed yield/plant (38.7% & 37.1%), biological yield/plant (31.0% & 29.1%) and harvest index (24.3% & 22.7%), estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were higher, indicating a high level of variability. Rest of the trait (Table 1) showed moderate to low GCV and PCV indicating the need for improvement of based population. The estimated PCV and GCV value simply provides information on the degree of variability present for different traits; it contains no details on heritability component. The information of heritability enables the researcher to choose the selection strategy to attain potential selection gain (Ramanappa *et al.*, 2013). High heritability is also a good indicator for characters inheritance from parents to their off-springs. For seed yield/plant, harvest index, biological yield/plant, number of effective pods/plant and total number of pods/plant, high estimates of heritability were found combined

**Table 1: Estimates of genetic parameters of chickpea genotypes**

Traits	Range	Mean	PCV (%)	GCV (%)	h <sup>2</sup> (%)	GA	GAM (%)
DFI	44-63	52.9	7.2	6.3	77.2	7.7	14.7
D50% F	52-72	60.7	6.3	5.3	72.2	7.3	12.0
DPI	61-77	67.4	5.0	3.8	57.9	5.1	7.6
DM	94-114	105.0	4.3	4.0	87.0	10.4	9.9
PH (cm)	43.5-71.9	53.4	9.5	8.4	77.3	10.4	19.5
HFFN (cm)	15.1-23.1	18.8	14.1	11.1	61.7	4.36	23.1
NPBPP	2.33-3.88	3.09	15.6	6.98	19.8	0.25	8.20
NSBPP	5.33-9.10	7.08	17.0	12.6	55.4	1.76	24.9
TNPPP	35.5-70.0	52.5	18.4	15.9	74.9	19.1	36.4
NEPPP	29.9-69.9	47.6	19.5	17.0	75.5	18.5	19.0
NSPP	1.03-1.24	1.09	5.3	3.3	38.8	0.06	5.48
100 SW (g)	14.8-34.2	26.1	19.2	16.0	69.5	9.23	35.3
BY (g)	15.1-53.4	30.3	31.0	29.1	88.1	21.9	51.2
HI (%)	26.6-76.5	44.6	24.3	22.7	87.3	25.0	46.0
SYPP (g)	6.50-30.3	13.2	38.7	37.1	92.2	12.4	48.2

Where,

PCV- phenotypic coefficient of variation, GCV-genotypic coefficient of variation, h<sup>2</sup>-heritability, GA-genetic advance, GAM-genetic advance as percentage of mean, DFI-Flower initiation, D50%F-Days to 50% flowering, DPI-Days to pod initiation, DM-Days to maturity, PH-Plant height (cm), HFFN-Height of first fruiting node (cm), NPBPP-Number of primary branches/plant, NSBPP-Number of secondary branches/plant, TNPPP-Total number of pods/plant, NEPPP-Number of effective pods/plant, NSPP-Number of seeds/pod, 100SW-100 Seed weight (g), BY-Biological yield (g), HI-Harvest index (%), SYPP-Seed yield/ plant (g).

with moderate to high variation. Similar conclusion was reported by (Mohammed *et al.*, 2019).

Heritability estimates have a limited scope as it varies with change in environment, experimental materials or treatments (Swarup and Chaugale, 1962). Hence, using heritability in association with genetic advance will give an insight into the nature of gene action governing a certain character (Johnson *et al.*, 1955). High broad sense heritability coupled with high genetic advance as percent mean was recorded for biological yield/plant, seed yield/plant, harvest index and total number of pods/plant indicating that these traits were governed by additive gene action and would respond favorably to selection. Conclusion of some researches such as Meena *et al.*, (2014) summarized that traits; seed yield per plant, biological yield, number of pods per plant exhibited high heritability coupled with high expected genetic advance. Findings of Dhuria and Babbar, 2015 and Dehal *et al.*, 2016 also revealed that seed yield per plant is highly heritable coupled with high genetic advance. These results are similar to the present findings. Cluster-IV and cluster-V showed greater divergence, based on the relative divergence of inter-cluster

distance ( $D^2 = 140.0$ ) (Table 2). Genotypes of cluster-IV was characterized by maximum number of primary branches/plant, high biological yield, high number of seeds/pod and low 100 seed weight, whereas short duration advance breeding lines were accommodated in cluster V which was characterized phenological traits such as days to flower initiation, days to 50% flowering, days to pod initiation and days to maturity but has low primary branches per plant. Inter-cluster distance of cluster-III and cluster-V was  $D^2 = 139.5$ . The genotypes of cluster-III were characterized by maximum height for first fruiting node and secondary branches/plant also highest seed yield/plant and harvest index. Based on  $D^2$  statistics, the inter cluster distance suggests hybridization program between genotypes of cluster-IV (JG 24) with cluster-V (JG2016-9218 -14) and cluster-III (JG 2016-1411, JG 2017-50, JG 14) with cluster-V (JG2016-9218 -14) is expected to generate desirable sergeants for various yield attributing traits. Parent line should be chosen from these three different clusters because hybridization between divergent parent is likely to induce variability and transgressive segregants with significant heterotic effect.

**Table 2: Mahalanobiseuclidean inter (diagonal) and intra cluster D<sup>2</sup> values**

Cluster	I	II	III	IV	V
I	27.3	62.2	77.4	69.7	76.7
II		0.0	35.0	111.1	114.9
III			33.0	132.5	139.5
IV				0.0	140.0
V					0.0

The number of contrasting alleles at the desired loci increases with parental distance. These loci will recombine in the F<sub>2</sub> and F<sub>3</sub> generation through successful breeding of unrelated parents, increasing the opportunity for selection of yield related factors. The current study confirmed that any pair of cluster having sufficient genetic variability, could be exploited through hybridization. Similar research was conducted by Jakhar *et al.* (2016), suggesting that, crossing between the genotypes of clusters with high inter cluster would yield good segregates for selection. However, cluster-II and cluster-III had the minimum inter cluster distance (D<sup>2</sup> = 35) followed by cluster-II and cluster-V (D<sup>2</sup> = 114.9). Because the genotypes in these two clusters are relatively closer, breeding between them might not produce high vigor F<sub>1</sub>'s or high yielding segregants. Maximum intracluster distance was recorded for cluster-III (33.0) followed by cluster-I (27.3), whereas cluster-II, cluster-IV were mono-genotypic hence, showed zero value for intra cluster distance, however cluster-III and cluster-I are poly-genotypic with high diversity. Genetic divergence among the parental lines participating in crossing programme is typically credited for heterosis. Less intra-cluster distance than inter cluster distance was also reported by Kujur *et al.*, (2017), indicating homogeneity within the clusters and heterogeneity between the cluster. Cluster-I was largest among all the clusters containing 50 genotypes (Table 3 and Table 4) and have characteristics such as height of plant (53.0 cm), number of primary branches (3.1) and pods per plant (51.1) and test weight (26.2 g). Cluster-III is trigenotypic and has following features: height of first fruiting node (22.4 cm), number of secondary branches (7.29) and number of seeds/pod (1.14) as well as high percentage of harvest index (73.4%) with high seed yield/plant (26.9 g). On the other hand, cluster-II is mono genotypic (JG 2016-9605)

and was characterized by lowest height of first fruiting node (15.1 cm), maximum number of pods (65.5) and effective pods per plant (59.5). Cluster-IV is also mono genotypic (JG 24) and this genotype was characterized by phenological traits such as late emergence of flowers (63 days), delayed 50% blossoming of flowers (72.3 days), delayed pod initiation (77 days), late maturity duration (115 days), tallest plant height (71.9 cm), number of primary branches (3.33), number of seed per pod (1.14), biological yield (53.4 %), test weight (29.8 g) and harvest index (26.6 %). There is only one genotype in cluster V, JG2016-9218 -14, and it was characterized for early flower initiation (50 days), early blooming of 50% flowers (57.6 days), early pod initiation (66 days), early maturity (102 days), number of secondary branches (6.33), effective pods (42.4), number of pods per plant (1.06), biological yield (25.2 g), seed yield/plant (11.3 g) and number of primary branches/plant (3.33). In the present findings days to 50% flowering (0.13%), Days to pod initiation (0.06%), number of primary branches per plant (0.19%) and number of effective pods per plant (0.71%) had minimal contribution towards genetic divergence. However Babbar *et al.* (2015) observed that pod initiation, 100SW (seed weight), days to 50% blossoming of flowers, BW and HI contributed most to divergence. Nevertheless, Shrivastava *et al.* (2012) revealed that days to 50% flower emergence, days to flower commencement, pod initiation, days to maturity, primary branches and seed/pod showed little contribution towards genetic divergence. The fundamental idea of PCA is to eliminate the redundancy in large number of interrelated data set into uncorrelated new set of variables or principal components, and which are arranged, so that the first few components retains most of the variation present in all of the original variables. PCA was used in the current study to analyze fifteen yield and attributing traits in chickpea genotypes. Brejda *et al.* (2000) stated that data were taken into account for each component with an Eigen value greater than 1 which accounts for at least 10% of the variation. Attributes in principal component are most accurately represented by those with higher Eigen values. Six components (PCs) were the only ones to exhibit more than one Eigen value and having cumulative variability of 70.7%, therefore they were given due importance for additional

**Table 3: Clustering of 56 *desi* chickpea genotypes using D<sup>2</sup> statistics**

Cluster	Genotypes (number)	Genotypes (Name)
I	50	ICCV 15117, ICCV 15109, JG 2016-74315, ICCV 15102, ICCV 16111, JG 14, JG 2016-3-1205, ICCV 15115, ICCV 15104, JG 74315-2010-14, JG 2016-14226, ICCV 16101, ICCV 16110, JG 2016-1307, ICCV 16113, JG 2016-45, ICCV 16105, ICCV 16106, ICCV 15105, ICCV 16107, JG 2016-3-1, ICCV 15107, JG2016-16-14, JG 2016-11-1, ICCV 15111, ICCV 16103, ICCV 16114, ICCV 16112, ICCV 16115, ICCV 16117, ICCV 16109, JG 2017-46, ICCV 16118, ICCV 16116, ICCV 15108, JG 2016-44, JG 2016-94, ICCV 15118, JG 2016-11551, JG2016-63-4958, ICCV 16113, ICCV 16104, ICCV 16108, JG 36, ICCV 16102, JG 2017-47, JG 2016-43, JG 2016-1416-11, JG 16, JG 2016-1216
II	1	JG 2016-9605
III	3	JG 2016-1411, JG 2017-50, JG 14
IV	1	JG 24
V	1	JG2016-9218 -14

**Table 4: Cluster mean of 15 quantitative traits of 56 *desi* chickpea genotypes**

Traits	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V
DFF	53	53	56	63**	50*
D50% F	60	59	62	72**	58*
DPI	67	67	70	77**	66*
DM	104	108	112	115**	102*
PH (cm)	53.0*	53.4	53.8	71.9**	53.3
HFFN (cm)	18.7	15.1*	22.4**	22.2	16.5
NPBPP	3.10*	2.55	3.14	3.33**	3.33**
NSBPP	7.09	6.55	7.29**	7.22	6.33*
TNPPP	51.1*	65.5**	61.3	57.1	62.7
NEPPP	47.0	59.5**	54.4	51.4	42.4*
NSPP	1.10	1.10	1.14**	1.14**	1.06*
100 SW (g)	26.2**	24.3	25.7	23.8*	23.9
BY (g)	29.2	48.9	36.8	53.4**	25.2*
HI (%)	43.0	54.9	73.4**	26.6*	44.5
SYPP (g)	12.1	26.8	26.9**	14.2	11.3*

Where, “\*\*\*” and “\*\*” indicates highest value and lowest value, respectively.

explanation. The PC1 had the highest variability of 19.7%, followed by PC2, PC3, PC4, PC5 and PC6 exhibiting 16.2%, 11.2%, 9.69%, 7.20% and 6.69% variability respectively for traits under study (Table 6). Based on rotated component, the PC1 was found to have the highest variability, 19.7% (Table 5) and it was primarily associated with phenological parameters including days to flower initiation, days to 50% flowering, days to pod initiation and days to maturity. When choosing genotypes based on duration, significant difference in flowering time and maturity period can be crucial. The second major component, which make up 16.2% of the overall variability, was highly loaded with yield related characteristics like total of pods/plant, number of effective/per plant, harvest index and seed yield/plant. The genotypes, ICCV 16102, JG 2017-

50, JG 2016-9605, ICCV 15105, ICCV 16110, ICCV 16114, ICCV 16107, JG 2016-94, ICCV 16105, JG JG 2016-1411, ICCV 16108, ICCV 16115, ICCV 15108, ICCV 16112 and ICCV 16116 may be considered as promising advance breeding lines because they have more pods/plant and effective pods/plant, a high harvest index, and increased seed yield per plant. They were found to be better yielding under timely sown condition and may be used further in breeding programme to improve seed yield. The PC3 was highly loaded with number of seeds/pod and exhibited 11.2% of the variability, while PC4 was dominated for seed yield/plant. The PC5 showed 7.2% variability and consisted of trait *viz.* height of first fruiting node indicating usefulness of this PC for mechanical harvesting. The PC6 was dominated for 100 seed

**Table 5: Contribution of different attributes towards clustering**

Traits	Times ranked 1 <sup>st</sup>	Contribution towards divergence (%)
Days to flower initiation	84	5.45
Days to 50% flowering	2	0.13
Days to pod initiation	1	0.06
Days to maturity	270	17.3
Plant height (cm)	61	3.96
Height of the first fruiting node (cm)	52	3.38
No. of primary branches/plant	3	0.19
No. of secondary branches/plant	23	1.49
Total no. of pods/plant	114	7.4
No. of effective pods/plant	11	0.71
No. of seeds/pod	57	3.7
100 seed weight (g)	100	6.49
Biological yield/plant (g)	363	23.5
Harvest index (%)	225	14.6
Seed yield/plant (g)	174	11.3

**Table 6: Eigen value, variability percent and cumulative percent for the principal component axes**

	Principal Components (PCs)					
	1	2	3	4	5	6
<b>Eigen value</b>	2.95	2.43	1.68	1.45	1.08	1
<b>Variability (%)</b>	19.7	16.2	11.2	9.69	7.2	6.69
<b>Cumulative (%)</b>	19.7	35.9	47.1	56.8	64	70.7
Traits	Factor loading after Varimax rotation					
DFI	<b>0.762</b>	-0.496	0.011	0.123	0.003	-0.052
D50% F	<b>0.782</b>	-0.424	0.079	0.102	-0.002	-0.036
DPI	<b>0.752</b>	-0.384	-0.080	0.038	-0.074	0.075
DM	<b>0.741</b>	0.060	0.212	0.080	0.165	0.086
PH (cm)	-0.202	-0.361	-0.258	0.413	-0.050	0.147
HFFN (cm)	-0.052	0.006	-0.119	0.148	<b>0.660</b>	<b>0.690</b>
NPBPP	0.113	0.329	0.353	-0.401	-0.024	0.204
NSBPP	0.319	0.347	0.300	-0.174	-0.425	0.239
TNPPP	0.474	<b>0.572</b>	-0.456	-0.192	0.029	-0.060
NEPPP	0.455	<b>0.539</b>	-0.542	-0.225	0.026	-0.020
NSPP	0.024	0.100	<b>0.656</b>	0.418	0.036	-0.154
100 SW (g)	-0.001	0.185	0.138	0.191	-0.522	<b>0.573</b>
BY (g)	0.184	<b>0.690</b>	0.192	0.390	-0.182	-0.163
HI (%)	-0.101	-0.090	-0.582	0.424	-0.347	0.040
SYPP (g)	0.133	<b>0.593</b>	-0.068	<b>0.637</b>	0.003	-0.083

weight and height of first fruiting node. PC3, PC4 and PC6 are associated to yield related traits. Genotypes JG 2016-1411 was common in PC1, PC2 and PC4. Genotypes JG2016-9605 was common in PC1, PC2 and PC 4, genotype JG 2017-46 was common in PC3, PC5 and PC6 and genotypes ICCV

16105, ICCV 16109, ICCV 16112 and ICCV 16116 was common in PC2, PC3, PC6, and PC1, PC3, PC6 and PC1, PC2, PC3 and PC 2, PC5, PC6 respectively. These genotypes accounts for the entire yield attributing traits. With the help of principal component analysis phenotypic characterization can

be accredited, which is responsible for the observable genetic variation present in each component. Hence, when using these attributes in breeding programmes, characteristics that come together in different principal components, contribute to elucidating the variability, and have a tendency to persist together may be taken into account. Similar analysis was observed in groundnut (Patil *et al.*, 2020) where PC1 was considered as most important component which consists to traits like number of pods per plant, pod yield per plant and seed yield per plant,

### Conclusion

Genotypes JG 2016-1411, JG 2016-9605, JG 2017-46, ICCV 16105, ICCV 16109, ICCV 16112 and ICCV 16116 were common in three PCs. These genotypes contribute maximum towards yield. Genotypes ICCV 16109 performs best in

comparison to other genotypes and can be considered as promising breeding material for precise selection to the development of suitable genotypes and also for the transfer of suitable traits. Five clusters were created out of 56 genotypes. Cluster-IV (JG 24) and cluster-V (JAKI 9218) had the greatest intercluster distance, followed by cluster-III (JG 2016-1411 and JG 2017-50 and JG 14) and cluster-V (JAKI 9218), cluster-II (JG 2016-9605) and cluster-V (JAKI 9218). The chances for the occurrence of a high frequency of heterotic crosses and with high values of heterosis are more when the parent are chosen from these clusters compared to the crosses between parents whose divergence is narrow.

### Conflict of interest

The authors declare that they have no conflict of interest.

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