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## Genetic divergence for economically important traits of chickpea (*Cicer arietinum* L.)

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### Abstract

The present investigation attempted to understand the genetic divergence among the genotypes for economically important traits. The experiment was conducted in Randomized Complete Block Design (RCBD) with two replications during *rabi* season of 2014-15 at Rahaula farm of Faculty of Agriculture, Mahatma Gandhi Gramodaya Vishwa Vidyalaya Chittrakoot (MGCGV), Satna (M.P.). The results revealed high variability of most of the economically important traits. The diversity analysis revealed grouping of 20 chickpea genotypes in five clusters. The inter- and intra-cluster distances revealed highest intra-cluster diversity in cluster I (13.81) followed by cluster III (9.84). The inter-cluster distance was highest between cluster IV and V (306.92) followed by cluster I and V (252.98), and cluster II and V (142.78). The highest contribution towards genetic variation was reported by hundred seed weight (45.26%) followed by plant height (11.05%), biomass yield per plant (8.95%) and grain yield per plant (7.89%) indicating the greater diversity in the population for these traits. The diverse genotypes identified in this study can be used as parents in the breeding program to develop future varieties.

**Keywords:** Divergence, inter- and intra- cluster distance,  $d^2$  analysis, variability, yield traits, chickpea

### Introduction

Chickpea (*Cicer arietinum* L.) is one of the world's most important grain legumes. It is an annual, self-pollinating, diploid pulse crop with a genome size of ~738 Mbp (Varshney *et al.*, 2013) [22]. Chickpea seeds are major source of plant-based dietary protein (17-23%), carbohydrates (54-60%) and minerals such as phosphorus, magnesium, calcium, iron and zinc (Singh *et al.*, 2008) [18]. It is commonly known as Chana or Bengal gram (India and Pakistan), Garbanzo (Spain), Homes, Amaz (Arab world), Garo (Portugal), Shimbra (Ethiopia) and Nahud, Lablabi (Turkey) is believed to be one of the first legumes cultivated by humans (Loss *et al.*, 1998) [8]. It is originated from South East Turkey and Syria and largely grown in semi-arid regions of the world for over hundreds of years, primarily in India, Pakistan and Middle East (Kumar and Abbo, 2001) [7]. Chickpea contributes significantly towards the agricultural sustainability through its symbiotic nitrogen fixation (Gan *et al.*, 2006) [4].

Chickpea is currently grown at about 14.56 million hectares worldwide with the annual production of 14.78 million tons (FAO stat, 2017) [2]. Among legumes, chickpea ranks third in the cultivated area worldwide. The developing countries share more than 95% of the area, production and consumption of chickpea. In South East Asian countries, chickpea is largely grown with significant cultural, religious and nutritional value. India accounts about 70% in global chickpea production from 9.54 m ha area and an annual production of 9.08 Mt and productivity of 951 kg/ha (FAOstat, 2017) [2]. Six states *viz.*, Madhya Pradesh, Rajasthan, Maharashtra, Uttar Pradesh, Karnataka and Andhra Pradesh together contribute 91% of the total production and 90% area of the country. Madhya Pradesh is leading with 3.01 mha area with production of 3.35 Mt and productivity of 1115 kg/ha (MP Krishi statistics, 2015-16). The chickpea production in India has increased by 77% since 2000 largely due to increase in 55% chickpea cultivation area whereas the only 14% increase in yield has been achieved during this period. Since 2000, production of chickpea across the world has increased by 84% owing to combined effect of increase in area by 43% and yield by 28%. The yield increase in India is low as compared to the world which needs to be increased through intense efforts on developing high yielding improved varieties along with ensuring its availability to the farmers through an active seed system.

Enhancing genetic gains in chickpea for major economically important traits is one of the thrust area for scientist. For enhancing genetic gains, the diverse parents should be used in the crossing with different allele combination to get the transgressive segregants in segregating generations. Estimation of genetic divergence and characterization of genotypes helps breeders to select parents in their breeding programme to create new variability, development of

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superior cultivars and different populations for various genetic studies of economically important traits. The yield is often influenced by a number of traits such as hundred seed weight, number of pods per plant, harvest index, days to maturity and plant height etc. The knowledge on relationship among the traits and its direct or indirect effects on economic yield also helps breeders to make sound breeding and selection strategy for selection of individuals in early generations to enhance genetic gains. Therefore, the present investigation has been planned to assess the genetic diversity among the chickpea genotypes for economically important traits.

### Materials and Methods

The present investigation was carried out with the major aim of to assess the genetic parameters, genetic diversity, the association among the different economic traits, and to assess the stability of chickpea genotypes. The experiment was conducted in Randomized Complete Block Design (RCBD) with two replications during rabi season of 2014-15 at Rahaula farm of Faculty of Agriculture, Mahatma Gandhi Gramodaya Vishwa Vidyalaya Chitrakoot (MGCGV), Satna (M.P.) situated at the latitude of 25.14° N, 80.85 °E, longitude and an altitude of 315 meter above the mean sea level. Four row trial with 4 m row length plots were planted with inter and intra-row spacing of 30 and 10 cm, respectively. Standard agronomic practices were adopted to raise a good crop. The recommended dose of nitrogen and phosphorus per hectare was applied at the time of sowing. Five healthy plants were randomly tagged in each plot to record data on various economic traits from each replication. The data were subjected to analysis of variance, and assessment of genetic diversity for economically important traits using Mahalanobis D<sup>2</sup> analysis (Mahalanobis, 1936) [9].

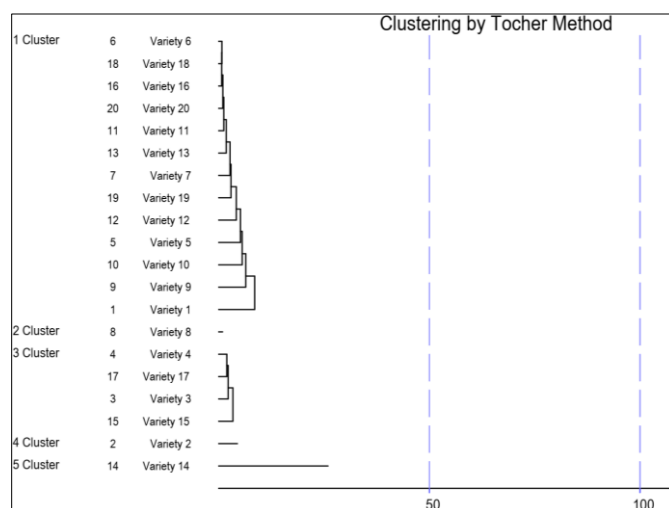
### Results

Analysis of variance for various economic traits of 20 chickpea genotypes evaluated during *rabi* 2014-15 are presented in Table 1. Partitioning of variance using ANOVA indicated that genotypes included in the present study differed significantly for in each individual environment for all the traits except number of pods per cluster and number of seed per pods.

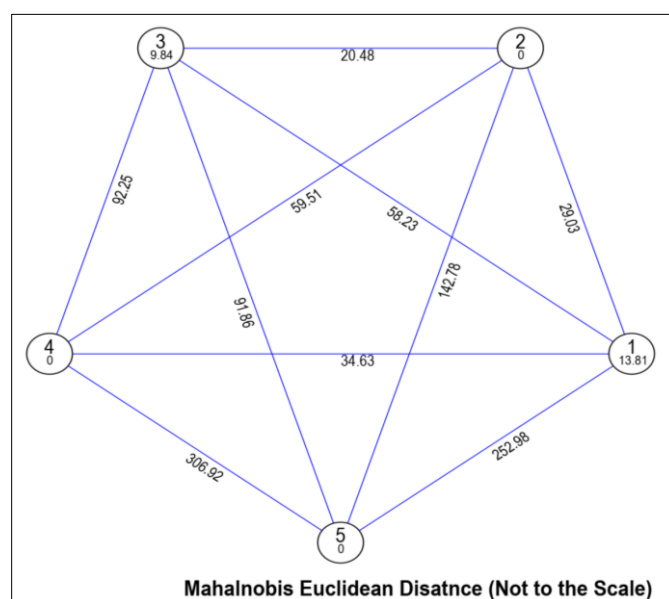
In the present study, hundred seed weight ranged from 13.67 to 54.00 g with an average of 23.63 g. The highest hundred seed weight recorded in PG 0517 (54.00 g) followed by Shubra (37.41 g) and Ujjawala (36.33 g) whereas the lowest hundred seed weight reported in DCP 92-3 (13.67 g) followed by JG 16 and BG 256 (15.00 g) (Table 2). However, harvest index ranged from 34.50 to 51.71% with an average of 41.99%. The highest harvest index was recorded for HK 1 (51.71%) followed by KAK 2 (51.60%) and Shubhra (51.25%) whereas the lowest harvest index was observed in BG 256 (34.50%) followed by GNG 1581 (35.46%) (Table 2).

The grain yield per plant was ranged from 6.57 to 27.87 g with an average of 16.53 g. The maximum grain yield per plant was recorded by Shubhra (27.87 g) followed by PG 0517 (27.33 g) and KAK 2 (25.83 g) whereas minimum grain yield per plant was observed in BG 256 (6.57 g) followed by GNG 1581 (11.83 g) (Table 2). The data collected on chickpea genotypes during Rabi 2014-15 were subjected to genetic diversity analysis that revealed grouping of genotypes in five clusters. Cluster I is the largest clusters with 13 genotypes performing moderately for all the characters.

Cluster III has comprised of four genotypes *viz.*, BGM 547, KAK 2, Shubra and Ujjawala (Table 3). However, three genotypes GNG 469, BG 256 and PG 0517 formed their separate solitary clusters I, IV and V, respectively (Figure 1). The inter- and intra-cluster distances revealed highest intra-cluster diversity in cluster I (13.81) followed by cluster III (9.84). The inter-cluster distance was highest between cluster IV and V (306.92) followed by cluster I and V (252.98), and cluster II and V (142.78) (Table 4). The cluster mean indicates that genotypes of clusters I performed intermediate for all the characters under study whereas cluster II was characterized by highest plant height (51.67 cm) and harvest index (50.60%). The cluster III had highest number of pods per plant (65.77) and number of nodes per plant (82.17). The genotypes of cluster IV had lowest grain yield per plant (6.57 g) and hundred seed weight (15.00 g). However the genotypes of cluster V had highest grain yield per plant (27.33 g), hundred seed weight (54.00 g) and biomass per plant (69.33 g) (Table 5). The highest contribution towards genetic variation was reported by hundred seed weight (45.26%) followed by plant height (11.05%), biomass yield per plant (8.95%) and grain yield per plant (7.89%) (Table 6).



**Fig 1:** Hierarchical cluster analysis (Tocher's Method) of 20 chickpea genotypes evaluated for yield traits during 2014-15



**Fig 2:** Cluster diagram showing inter and intra cluster distances (Tocher's Method) of 20 chickpea genotypes evaluated for yield traits during 2014-15

**Table 1:** Analysis of variance for various agronomic traits of 20 chickpea genotypes evaluated during rainy 2014-15.

Source of Variation	DF	PH	NNPP	NBPP	NPPC	NPOds PP	NSP Plant	NSP Pod	HSW	BIOMPP	HI	GYPP
Replications	2	1.61	848.18	0.39	0.03	97.71	35.37	0.08	1.50	16.19	43.03	12.64
Treatments	19	142.03	280.81	4.77	0.02	244.42	462.20	0.03	345.75	330.44	110.60	98.75
Error	38	14.54	53.82	1.01	0.02	54.29	114.90	0.01	3.00	16.16	20.71	3.49

PH= Plant height (cm); NNPP= Number of Nodes per plant; NBPP= Number of branches per plant; NPPC= Number of pod per cluster; NPOds PP= Number of pods per plant; NSP Plant= Number of seeds per plant; NSP Pod= Number of seeds per pod; HSW= 100 Seed weight (g); BIOMPP=Biomass per plant (g); HI=Harvest Index (%); GYPP=Grain Yield per plant (g)

**Table 2:** Mean performances of genotypes for various agronomic traits of 20 chickpea genotypes evaluated during post-rainy 2014-15

S. No	Genotype	PH	NNPP	NBPP	NPPC	NPOds PP	NSP Plant	NSP Pod	HSW	BIOMPP	HI	GYPP
1	BG 1053	49.44	65.90	6.33	1.00	52.97	70.06	1.32	27.33	35.48	47.91	16.95
2	BG 256	30.00	56.24	4.00	1.00	32.97	37.10	1.12	15.00	19.00	34.50	6.57
3	Shubhra	52.00	76.80	5.83	1.15	71.31	75.84	1.06	37.41	54.33	51.25	27.87
4	BGM 547	48.00	86.66	6.33	1.07	65.10	65.10	1.00	33.67	48.05	46.05	21.91
5	DCP 92-3	37.67	75.85	3.67	1.00	55.67	58.93	1.07	13.67	30.47	39.21	11.92
6	GCP 105	52.33	84.89	3.67	1.00	71.17	83.39	1.17	16.00	38.80	35.95	13.93
7	GNG 1581	42.56	64.04	3.33	1.07	46.33	54.60	1.18	15.00	33.20	35.46	11.83
8	GNG 469	51.67	64.53	6.00	1.07	58.00	67.24	1.20	29.67	37.00	50.60	18.71
9	H.K. 1	50.67	78.19	5.67	1.00	58.75	81.16	1.35	25.33	38.57	51.71	19.95
10	HC-5	33.00	75.96	2.67	1.00	57.60	62.60	1.09	17.33	29.95	39.91	11.86
11	IPC 97-67	53.78	72.32	4.67	1.00	69.01	77.81	1.13	18.00	33.57	39.47	13.14
12	JG 11	55.22	64.62	3.33	1.13	51.83	64.33	1.24	20.67	34.38	37.32	12.67
13	KWR 108	49.89	82.29	4.00	1.00	68.57	95.70	1.40	15.33	41.24	35.55	14.67
14	PG 0517	47.11	61.62	6.33	1.00	64.67	79.71	1.23	54.00	69.33	39.60	27.33
15	Ujjawala	49.89	80.01	5.67	1.07	63.63	70.64	1.10	36.33	43.24	47.34	20.43
16	JG 315	53.11	70.84	4.67	1.07	56.55	69.99	1.22	16.33	35.81	38.90	13.83
17	KAK 2	49.67	85.21	6.00	1.07	63.03	81.86	1.25	32.87	50.08	51.60	25.83
18	JG 14	50.56	74.70	3.67	1.00	61.47	66.59	1.09	17.67	34.73	37.74	13.10
19	JG 16	51.00	94.38	3.33	1.00	59.67	64.73	1.09	15.00	36.13	37.18	13.43
20	CSG 8962	52.33	73.66	3.33	1.33	59.33	64.00	1.07	16.00	34.80	42.60	16.53
	Mean	47.99	74.44	4.63	1.05	59.38	69.57	1.17	23.63	38.91	41.99	16.53
	C.V.	7.94	9.86	21.73	14.15	12.41	15.41	9.33	7.33	10.33	10.84	11.30
	SE±	2.20	4.24	0.58	0.09	4.25	6.19	0.06	1.00	2.32	2.63	1.08
	C.D. 5%	6.30	12.13	1.66	-	12.18	17.72	0.18	2.86	6.64	7.52	3.09

PH= Plant height (cm); NNPP= Number of Nodes per plant; NBPP= Number of branches per plant; NPPC= Number of pod per cluster; NPOds PP= Number of pods per plant; NSP Plant= Number of seeds per plant; NSP Pod= Number of seeds per pod; HSW= 100 Seed weight (g); BIOMPP=Biomass per plant (g); HI=Harvest Index (%); GYPP=Grain Yield per plant (g)

**Table 3:** Distribution of 20 chickpea genotypes into different clusters in D2 analysis during 2014-15

	Number of Genotypes	Name of Genotypes
Cluster 1	13	GCP 105, JG 14, JG 315, CSG 8962, IPC 97-67, KWR 108, GNG 1581, JG 16, JG 11, DCP 92-3, HC-5, H.K. 1, BG 1053
Cluster 2	1	GNG 469
Cluster 3	4	BGM 547, KAK 2, Shubhra, Ujjawala
Cluster 4	1	BG 256
Cluster 5	1	PG 0517

**Table 4:** Average inter- and intra-cluster distances among clusters formed by 20 chickpea genotypes during 2014-15

Clusters	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	13.81				
Cluster 2	29.03	0.00			
Cluster 3	58.23	20.48	9.84		
Cluster 4	34.63	59.51	92.25	0.00	
Cluster 5	252.98	142.78	91.86	306.92	0.00

**Table 5:** Cluster means for different yield and yield contributing traits used for assessment of genetic diversity during 2014-15

Clusters/traits	PH	NNPP	NBPP	NPPC	NPOdsPP	NSPPlant	NSPPod	HSW	BIOMPP	HI	GYPP
Cluster 1	48.58	75.20	4.03	1.05	59.15	70.30	1.19	17.97	35.16	39.92	14.00
Cluster 2	51.67	64.53	6.00	1.07	58.00	67.24	1.20	29.67	37.00	50.60	18.71
Cluster 3	49.89	82.17	5.96	1.09	65.77	73.36	1.10	35.07	48.93	49.06	24.01
Cluster 4	30.00	56.24	4.00	1.00	32.97	37.10	1.12	15.00	19.00	34.50	6.57
Cluster 5	47.11	61.62	6.33	1.00	64.67	79.71	1.23	54.00	69.33	39.60	27.33

PH= Plant height (cm); NNPP= Number of Nodes per plant; NBPP= Number of branches per plant; NPPC= Number of pod per cluster; NPOdsPP= Number of pods per plant; NSPPlant= Number of seeds per plant; NSPPod= Number of seeds per pod; HSW= 100 Seed weight (g); BIOMPP=Biomass per plant (g); HI=Harvest Index (%); GYPP=Grain Yield per plant (g)

**Table 6:** Percent contribution of different traits towards total genetic divergence of 20 chickpea genotypes evaluated during 2014-15

S. No	Traits	No of times ranked 1st	% Contribution towards genetic divergence
1	Plant height (cm)	21	11.05
2	Number of Nodes per plant	12	6.32
3	Number of branches per plant	2	1.05
4	Number of pod per cluster	2	1.05
5	Number of pods per plant	13	6.84
6	Number of seeds per plant	10	5.26
7	Number of seeds per pod	-	-
8	100 Seed weight (g)	86	45.26
9	Biomass per plant (g);	17	8.95
10	Harvest Index (%)	12	6.32
11	Grain Yield per plant (g)	15	7.89

## Discussion

The choice of parents is of paramount importance in any breeding programme. It is rather a difficult task for a plant breeder. Selection of parents on the basis of per se performance is good but there is a possibility of related lines being chosen resulting in limited or no advances under selection and, therefore, there is a need for emphasis on a wide genetic base by the utilization of world collection on genetic criterion. Selection of parents on the basis of geographical diversity is another way of choosing parents and this has led to success in some cases but these needs to be supplemented with genetic diversity. The measures based on genetic criteria qualifying diversity have become important in classifying material for the use by the breeders. Further, the genetic divergence among the parents is important because a cross involving genetically diverse parents is likely to produce high heterotic effect and also a broad spectrum of variability could be expected in the segregating generations. The assessment of divergence for a set of genotypes using multivariate analysis like distance analysis, canonical analysis etc. has been attempted and effectively utilized in a number of crop plants with diverse breeding systems (Murty and Arunachalam, 1966) [10]. Thus, the genetic divergence has a definite role to play for efficient choice of parents for hybridization programme.

The magnitude of  $D^2$  values suggested that there was considerable diversity among the genotypes of chickpea for all the traits under study. The variation allowed grouping of 20 chickpea genotypes into 5 clusters. The trait specific genotypes of different cluster sowing large inter-cluster distance can be used as parent in different breeding programs. The genotypes of clusters with higher intra-cluster can also be considered as parents in breeding program to create future variability and selection opportunities for economically important traits. The findings are in accordance with the earlier genetic diversity studies of Samal and Jagdev (1989) [15], Sandhu and Gumber (1989) [16] and Jeena *et al.* (2005) [6] in which they have highlighted the importance of genetic resources for the breeding programs. The genetic diversity studies of Upadhaya *et al.* (2007) [21], Dwivedi and Gaibriyal (2009) [1] and Hahid *et al.* (2010) [5] also reported clustering of genotypes and its importance in identification best parents of the breeding programs.

The highest contribution towards genetic variation across the environments was reported by hundred seed weight (45.26%) followed by plant height (11.05%), biomass yield per plant (8.95%) and grain yield per plant (7.89%). The highest contribution of hundred seed weight along with other economic traits towards the total genetic divergence has also been reported in earlier studies of Pandey *et al.* (2013) [11] and Parashi *et al.* (2013) [13]. The greater contribution of hundred

seed weight towards total genetic divergence can be attributed to the genotypes of two different groups (Desi and Kabuli) used in the present study (Gaikwad *et al.* 2014) [3]. Estimation of contribution of each trait towards the total genetic variance is also important to understand the population and the traits for which the population has rich diversity to be exploited by the breeders.

The cluster means along with inter- and intra- cluster distances need to be considered for selecting the genotypes as parents in the breeding programs. The findings of cluster mean revealed identification of different trait specific genotypes performed superior during the evaluation. The information of cluster mean along with cluster distance can be used to find superior genotypes to be used as parents in breeding program. The present findings are in accordance with Sial *et al.* (2010) [17], Sreelakshmi *et al.* (2010) [19], Parameshwarappa *et al.* (2012) [12], Prakash and Shekhawat (2012) [14] and Syed *et al.* (2012) [20]. Clustering of genotypes facilitates the grouping of genotypes based on their genetic distance which enables breeders to make selection decisions for parents in the crossing nursery.

## Conclusion

The present investigation attempted to understand the genetic diversity among the economically important traits. The study has identified superior and diverse trait specific genotypes which can be used as parent in future breeding programs. Diversity analysis revealed grouping of 20 genotypes into 5 clusters at individual environment with highest contribution of hundred seed weight (45.26%) followed by plant height (11.05%), biomass yield per plant (8.95%) and grain yield per plant (7.89%) towards total genetic divergence. The cluster means along with inter- and intra- cluster distances need to be considered for selecting the genotypes as parents in the breeding programs. The present study concluded significant variation among the genotypes for different important economic traits with the identification of promising stable genotypes that can be used as a parent in breeding programs.

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