

Evaluation of Genetic Divergence in Chickpea (*Cicer arietinum* L.) Germplasm

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ABSTRACT

A field experiment was carried out to assess the nature and magnitude of genetic divergence in forty genotypes of desi chickpea using Mahalanobis's D^2 Statistics. High magnitude of heritability (h^2) was recorded for plant height, days to 50% flowering, biological yield, harvest index, number of pods per plant, seed yield per plot, 100 seed weight and seed yield per plant. High heritability coupled with high genetic advance was observed for seed yield per plant, seed yield per plot, number of pods per plant, 100 seed weight, harvest index, biological yield and plant height suggesting that, the role of additive gene effect and possibilities of achieving high genetic progress through selection. The forty chickpea genotypes were grouped into seven clusters suggesting considerable amount of genetic diversity in the material. The cluster III has a total of 10 genotypes, followed by cluster II with nine, cluster VI with seven, cluster IV and V with four, and cluster I and VII with three genotypes,

respectively. The intra-cluster D^2 value ranged from 148.25 to 491.49 while, inter-cluster D^2 value ranged from 386.99 to 2141.49. The maximum intra cluster distance was found in cluster I followed by cluster VII and VI, indicating that cross combinations may occur through hybridization between genotypes from the same clusters. The highest inter-cluster distance was observed between cluster I and V (2141.49), followed by cluster I and IV (1590.64), cluster II and V (1271.17) and cluster I and VII (1184.91) suggesting that the genetic architecture of the genotypes in one cluster differ entirely from those included in other clusters. These lines may be utilized in further breeding programme for the exploitation of hybrid vigour and suggesting wide diversity between them and crossings between genetically diverse lines will result in heterotic segregants, genotypes in these clusters could be employed as parents in a hybridization program to develop desirable plant types. Among the ten traits studied, maximum contribution was made by harvest index (21.28 %) followed by number of pods per plant (19.36%), biological yield (15.13%), plant height (14.87%), days to 50% flowering (12.18%) and seed yield per plant (8.08%). The genotypes ICC15921, ICC15903, K1058 and ICC15926, ICC15226, ICC7549, ICC15855 were identified as genetically diverse parents, which can be utilized for future crop improvement programme in chickpea. The aforementioned findings show that these genotypes contain the greatest genetic diversity and are useful for creating a large number of segregants through a crossing program.

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INTRODUCTION

Chickpea is one of the most important food legumes in the world. Chickpea is the sole cultivated species under the genus '*Cicer*', and has $2n=16$ chromosome with relatively small genome size of 738.09 Mbp (Varshney *et al.* 2011). Globally, it is cultivated in more than 57 countries and rank second in acreage after dry bean. However it stands 3rd in production following dry bean and peas with the productivity of about 913 kg/ha (FAO 2017). South and South-East Asian countries account for more than two third of the total chickpea production. Despite contributing more than 60% of the world's production and area to the chickpea, India continues to be a net importer of the chickpea.

To meet the demands of increasing population, there is need to develop high yielding varieties. Chickpea breeding strategies involves assembling or generating variable germplasm and selection of superior genotype from the germplasm for utilizing them in hybridization program to develop a superior variety. In all these stages, estimation of genetic variability, heritability and genetic advance is necessary. Seed yield is the most important economic character and is a very complex character in nature. It is governed by the polygenes and greatly influenced by the environmental factors. The progress due to selection in nature, in quantitative traits depends on the nature and magnitude of variability present in the populations to be improved. Genetic diversity among parents, which is heritable, is a pre-requisite for any successful breeding program. The proper choice of parents in the breeding program is of paramount importance. Genetic divergence among the parents plays a vital role in cultivar improvement in chickpea because crosses involving genetically diverse parents are likely to produce high heterotic effects and also more variability in segregating generations, which can be exploited for desired improvement. Therefore, there is a need to select diverse parents with desirable characters for further hybridization program for chickpea yield improvement. D^2 statistical analysis is a powerful tool in quantifying the degree of divergence among the population. Multivariate analysis with "Mahalanobis D^2 statistics" is a powerful tool to know the clustering pattern to establish the relation-

ship between genetic and geographic divergence and to determine the role of different quantitative characters towards the maximum divergence. In view of the above facts, the present investigation was undertaken to study the genetic variability and genetic diversity among chickpea genotypes.

MATERIALS AND METHODS

The experimental material consisted of forty genotypes of chickpea grown in *rabi* 2017-18 at field experimentation center of the Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj. The experiment was conducted in a Randomized Complete Block Design with three replications during *rabi* 2017-18. The plot size was 4.8 m², with 1 row of 4.0 m length. Inter row spacing distance was kept 30 cm and plant to plant spacing was 30 x 10 cm. The recommended packages of practices were followed to raise a healthy crop. Data were recorded on ten quantitative traits viz., days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of pods per plant, 100 seed weight (g), biological yield (g), seed yield per plant (g) and seed yield per plot. The days to 50% flowering, days to maturity, and seed yield per plot were recorded on a plot basis and plant height, number of branches per plant, number of pods per plant, 100 seed weight (g), biological yield, harvest index and seed yield per plant were recorded from a random sample of five plants in each plot. Genetic divergence was estimated by using D^2 statistics of Mahalanobis (1936) and clustering of genotypes was done according to Ward's minimum variance method. The per cent contribution of characters towards genetic divergence was estimated according to Singh and Choudhary (1985).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences for all the ten characters studied indicating that significant amount of genetic variability present in the material (Table 1). Estimates of genetic parameters of variability are presented in Table 2. Coefficient of variation at phenotypic and genotypic levels was observed relatively high for seed yield per plant, seed

Table 1. Analysis of variance for ten quantitative characters of chickpea germplasm.

Sl. No.	Characters	Mean sum of squares		
		Replication (df = 02)	Treatment (df = 39)	Error (df = 78)
1	Days to 50% flowering	0.80	56.78**	0.59
2	Days to maturity	1.29	16.38**	0.87
3	Plant height (cm)	0.12	201.12**	1.15
4	No. of primary branches per plant	0.12	0.33	0.27
5	No. of pods per plant	3.31	522.15**	8.13
6	Biological yield per plant (g)	0.18	92.72**	1.11
7	Harvest index (%)	0.70	80.63**	1.08
8	100 seed weight (g)	0.01	18.11**	0.92
9	Seed yield per plant (g)	0.06	20.05**	1.10
10	Seed yield per hectare (q)	1.14	79.04**	1.13

*, ** = Significant at 5% and 1% levels of significance, respectively.

yield per plot, biological yield and number of pods per plant indicating the presence of high amount of variation in these traits. The magnitude of PVC was higher than GCV for all the characters indicating the influence of environment of these traits. The highest heritability was observed for plant height followed by days to 50% flowering, biological yield, harvest index, number of pods per plant, seed yield per plot, 100 seed weight and seed yield per plant. The genetic advance under selection was observed high for number of pods per plant. The present study for high heritability for these characters was confirmed to those observed by Jain *et al.* (2023), Mohan and Thiyagarajan (2019), Kishore *et al.* (2018), Kumar *et al.* (2017) and Hussain *et al.* (2017) in different chickpea trials. High heritability coupled with high genetic advance as percent of mean were recorded for seed yield per plant, seed yield per plot, number of pods per plant, 100 seed weight, harvest index,

biological yield and plant height indicating that these characters were governed largely through the additive gene effect as reported by Sharma *et al.* (2019), Chopdar *et al.* (2017), Kumar *et al.* (2017) and Jakhar *et al.* (2016) also observed high genetic coefficient of variation in chickpea, which was in conformity with the present study.

All the genotypes were grouped into seven clusters as per Ward minimum variance method, with cluster III containing the maximum of 10 genotypes followed by nine genotypes in cluster II, 7 genotypes in cluster VI, 4 genotypes in cluster IV and V and 3 genotypes in cluster I and VII (Table 3). It means the overall genetic similarity was found in the germplasm were presented within the cluster and the pattern of distribution of genotypes in different clusters exhibited that geographical diversity was not related to genetic diversity as genotypes of same

Table 2. Estimates the genetic parameters for ten quantitative characters of forty chickpea genotypes.

Sl. No.	Characters	Range	σ^2g	σ^2p	GCV	PCV	Heritability (h ² bs)	GA as % of mean
1	Days to 50% flowering	85.16-102.50	18.73	19.32	4.51	4.58	96.94	9.15
2	Days to maturity	118-127	5.17	6.04	1.84	1.99	85.58	3.51
3	Plant height (cm)	38.82-74.45	66.65	67.80	14.35	14.47	98.30	29.31
4	No. of primary branches per plant	1.70-3.20	1.01	0.29	5.41	22.41	05.84	2.69
5	No. of pods per plant	21.42-76.59	171.34	179.47	23.98	24.55	95.47	48.28
6	Biological yield per plant (g)	12.08-37.71	30.53	31.65	23.28	23.70	96.47	47.10
7	Harvest index (%)	29.13-51.74	26.51	27.60	11.83	12.07	96.05	23.89
8	100 seed weight (g)	11.40-21.56	5.73	6.65	15.62	16.83	86.12	29.87
9	Seed yield per plant (g)	2.62-13.66	6.31	7.42	28.76	31.10	85.06	54.65
10	Seed yield (q/ha)	4.25-27.00	25.97	27.10	30.05	30.70	95.82	60.60

Table 3. Distribution of forty chickpea genotypes in various clusters.

Cluster	No. of genotypes	Name of genotypes
I	03	ICC15921, ICC15903, K1058
II	09	ICC1608, ICC15857, IPC09-21, IPC06-0127, Pusa372, ICC15896, ICC7356, GPF02, JG09-21
III	10	ICC17007, ICC16020, ICC15683, ICC10489, Sadha Bahar, ICC15680, IPC05-74, ICC15911, ICC21170, ICC4648
IV	04	BKG21176, ICC6117, RSG945, BKG21204
V	04	ICC15926, ICC15226, ICC7549, ICC15855
VI	07	ICC15928, ICC15226, BKG26212, BKG21164, ICC1877, IPC05-59, JBT34166
VII	03	BKG21191, ICC9311, ICC15561

geographical region were grouped into different cluster and vice-versa, as supported by earlier finding Parashi *et al.* (2013), Kumar *et al.* (2017) and Agrawal *et al.* (2018). The possible reason for grouping of genotypes of different places into one cluster could be free exchange of germplasm among the breeder of different region or unidirectional selection practiced by breeder in tailoring the promising cultivar for selection of different region.

The intra-cluster D^2 value ranged from 148.25 to 491.49 while, inter-cluster D^2 value ranged from 386.99 to 2141.49 (Table 4) in Ward minimum variance method. The highest intra-cluster distance was exhibited by cluster I (491.49) followed by cluster VII (440.53) and cluster VI (279.30). The intra cluster

distance was maximum in cluster I followed by cluster VII and VI which indicated that hybridization involving genotypes within the same clusters may result in cross combinations. The highest inter-cluster distance was observed between cluster I and V (2141.49), followed by cluster I and IV (1590.64), cluster II and V (1271.17) and cluster I and VII (1184.91) suggesting that the genetic architecture of the genotypes in one cluster differ entirely from those included in other clusters. These lines may be utilized in further breeding programme for the exploitation of hybrid vigour and suggesting wide diversity between them and genotypes in these clusters could be used as parents in hybridization programme to develop desirable type because crosses between genetically divergent lines will generate heterotic segregants. As heterosis can be best exploited and chances of getting transgressive segregants are maximum when generating diverse lines are crossed (Raj *et al.* 2018, Agrawal *et al.* 2018, Kumar *et al.* 2017, Jayalakshmi *et al.* 2014 and Parashi *et al.* 2013). Therefore, crosses between the members of clusters separated by inter-cluster distances are likely seemed to be beneficial for further improvement. Significant differences among the genotypes for different characters indicated variations among the genotypes favorable for their use in the breeding programs. Crosses between parents with maximum divergence would be more responsive to improvement since they are likely to produce higher heterosis and desirable genetic recombination.

A comparison of the mean values of different

Table 4. Average intra and inter cluster distance values among seven clusters for forty genotypes of chickpea.

Cluster	I	II	III	IV	V	VI	VII
I	491.49 (22.16)	536.68 (23.16)	935.54 (30.58)	1590.64 (39.88)	2141.49 (46.27)	1062.01 (32.58)	1184.91 (34.42)
II		241.01 (15.52)	386.99 (19.67)	766.78 (27.69)	1271.17 (35.65)	680.87 (26.09)	906.35 (30.10)
III			235.60 (15.34)	404.23 (20.10)	593.11 (24.35)	401.96 (20.04)	670.86 (25.90)
IV				148.25 (12.17)	512.49 (22.63)	760.12 (27.57)	739.50 (27.19)
V					209.54 (14.47)	591.88 (24.32)	945.02 (30.74)
VI						279.39 (16.71)	650.50 (25.50)
VII							440.53 (20.98)

Table 5. Mean values of clusters of different characters towards genetic divergence in forty chickpea genotypes.

Sl. No.	Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
1	Days to 50% flowering	92.66	96.07	97.10	91.75	99.50	97.26	92.38
2	Days to maturity	125.55	121.95	122.40	121.62	125.20	123.97	123.83
3	Plant height (cm)	69.49	65.38	56.41	49.35	45.34	55.90	48.15
4	No. of primary branches/plant	2.08	2.42	2.60	2.20	2.40	2.63	2.06
5	No. of pods per plant	51.66	53.21	55.27	46.45	67.98	64.82	28.18
6	Biological yield per plant (g)	23.66	25.02	24.14	18.58	23.50	28.72	14.08
7	Harvest index (%)	34.56	44.78	45.33	49.36	48.10	41.36	33.67
8	100-seed weight (g)	16.38	16.98	14.10	14.66	13.23	16.07	15.17
9	Seed yield/ plant (g)	8.33	9.84	8.59	6.64	9.18	10.53	4.29
10	Seed yield (q/ha)	24.22	20.02	17.63	15.50	12.64	16.17	7.75

clusters for ten traits has been presented in Table 5. Cluster VI had exhibited highest cluster mean value for seed yield per plant, biological yield and number of branches per plant. Cluster V had highest mean value for number of pods per plant and dwarfness. Cluster II showed high mean value for 100 seed weight and earliness while, cluster I exhibited highest mean value for seed yield per plot. Seed yield is highly complex trait, thus indirect selection based on major component trait may increase the efficiency of breeder. The percent contribution of nineteen traits towards total genetic divergence is listed in Table 6. Among the ten traits studied, maximum contribution was made by harvest index (21.28 %) followed by number of pods per plant (19.36), biological yield (15.13%), plant height (14.87%), days to 50% flowering (12.18%) and seed yield per plant (8.08%). These findings are in accordance with the results of Janghel *et al.* (2020), Shivwansh and Babbar (2019), Agrawal *et al.* (2018), Raj *et al.* (2018), Kumar *et al.* (2017) and Jayalaksh-

Table 6. Contribution of different characters towards genetic divergence of forty chickpea genotypes.

Sl. No.	Characters	Per cent contribution (%)
1	Days to 50% flowering	12.18
2	Days to maturity	1.03
3	Plant height (cm)	14.87
4	No. of branches/plant	0.66
5	Number of pods/ plant	19.36
6	Biological yield (g)	15.13
7	100 seed weight (g)	0.26
8	Harvest index (%)	21.28
9	Seed yield per plant (g)	8.08
10	Seed yield/hectare (q/ha)	7.82

mi *et al.* (2016). Therefore, during the hybridization programme, these characters may be given importance. The genotypes ICC15921, ICC15903, K1058 and ICC15926, ICC15226, ICC7549, ICC15855 were identified as genetically diverse parents, which can be utilized for future crop improvement program in chickpea. The aforementioned findings show that these genotypes have maximum genetic diversity and useful for developing a large number of segregants through crossing program by using maximum diverse genotypes.

CONCLUSION

The genotypes ICC15921, ICC15903, K1058 and ICC15926, ICC15226, ICC7549, ICC15855 were identified as genetically diverse parents, which can be utilized for future crop improvement program in chickpea. The study of diversity index reflects that in present set of germplasm, ample genetic variation exists for seed yield per plant, therefore a direct selection based on seed yield can be done to develop high yielding varieties. However, after further evaluation, some genotype may be used as parents in the crossing program to create the better genetic recombinants for improving yield *per se*. The above results indicate that the genotypes, viz., ICC15921, ICC15903, K1058 and ICC15926, ICC15226, ICC7549, ICC15855 have maximum genetic diversity and useful for developing a large number of segregants through crossing program by using maximum diverse genotypes.

REFERENCES

- Agrawal T, Kumar Anand, Kumar A, Kumar S, Kumar RR (2018) Exploring genetic diversity for heat tolerance in chickpea (*Cicer arietinum* L.) genotypes. *Fronti Crop Improve* 6 (1): 23-27.
- Agrawal T, Kumar Anand, Kumar S, Kumar A, Kumar M, Perveen Sadia (2018) Assessment of genetic diversity in chickpea (*Cicer arietinum* L.) germplasm under normal sown condition of Bihar. *Int J Curr Microbiol Appl Sci* 7(4): 3552-3560. <https://doi.org/10.20546/ijemas.2018.704.400>
- Chopdar DK, Bharti B, Sharma PP, Dubey RB, Meena BB (2017) Studies on genetic variability, character association and path analysis for yield and its contributing traits in chickpea (*Cicer arietinum* L.). *Leg Res-An Int J* 40: 824-829. DOI:10.18805/lr.v0i0.8395.
- FAO (2017) Statistical Database. Food and Agriculture Organization of the United Nations, Rome, Italy (<http://www.apps.fao.org>).
- Hussain Q, Ahmad NA, Khan R, Asim M, Adnan M, Aziz T, Muhammad A (2017) Assessment of genetic variability and heritability for quantitative traits between desi and kabuli chickpea genotypes. *Pure Appl Biol* 6: 1111-1118. <http://dx.doi.org/10.19045/bspab.2017.600119>
- Jain SK, Sharma LD, Gupta KC, Kumar V, Yadav MR (2023) Variability and character association for yield and quantitative traits under late sown condition in chickpea (*Cicer arietinum* L.). *Leg Res* 46(4): 408-412. doi.10.18805/LR-4432.
- Jakhar DS, Kamble MS, Singh A, Raj P (2016) Genetic variability, character association and path coefficient analysis in chickpea (*Cicer arietinum* L.). *EM Int* 22: 239-244.
- Janghel DK, Kumar K, Sunil R, Chhabra AK (2020) Genetic diversity analysis, characterization and evaluation of elite chickpea (*Cicer arietinum* L.) genotypes. *Int J Curr Microbiol Appl Sci* 9: 199-209. DOI: <https://doi.org/10.20546/ijemas.2020.901.023>
- Jayalakshmi V, Kiran Kumar, Reddy C, Jyothirmayi G, Trivikram Reddy A (2016) Studies on genetic diversity in chickpea utilizing morphological and total protein markers. *J Leg Res* 39: 323-325. doi.10.18805/lr.v0i0F.6769
- Jayalakshmi V, Ronald RG, Lakshmana K (2014) Diversity analysis of chickpea germplasm in scarce rainfall zone of Andhra Pradesh, India. *J Leg Res* 37: 682-684. doi.10.5958/0976-0571.2014.00697.3
- Kishore L, Swarup I, Nehra A, Kirar G, Jeeterwal RC (2018) Genetic variability, heritability and genetic advance analysis in chickpea (*Cicer arietinum* L.). *Int J Pure Appl Biosci* 6: 141-144. DOI: <http://dx.doi.org/10.18782/2320-7051.6494>.
- Kumar Anand, Agrawal T, Kumar Sanjay, Kumar A, Kumar RR, Kumar M, Kishore C, Singh PK (2017) Identification and evaluation of heat tolerant chickpea genotypes for enhancing productivity in rice fallow area of Bihar and mitigating impacts of climate change. *J Pharmacog Phytochem* SP1: 1101113.
- Kumar Sanjay, Kumar A, Kumar A, Kumar RR, Roy RK, Agrawal T (2017) Genetic variability of chickpea genotypes under heat stress condition: Character association and path coefficient based analysis. *Ind J Ecol* 44 (SI 4): 59-64.
- Mahalanobis PC (1936) On generalized distance in statistics. *Proc Nat Institute Sci* 2: 49-55.
- Mohan S, Thiagarajan K (2019) Genetic variability, correlation and path coefficient analysis in chickpea (*Cicer arietinum* L.) for yield and its component traits. *Int J Curr Microbiol Appl Sci* 8:1801-1808. DOI : <https://doi.org/10.20546/ijemas.2019.805.209>.
- Parashi VS, Lad DB, Mahse LB, Kute NS, Sonawane CJ (2013) Genetic diversity studies in chickpea (*Cicer arietinum* L.). *Bioinfolet* 10 (1): 337-341. <https://doi.org/10.21921/jas.5.4.4>
- Raj Prince, Kumar Anand, Perween Sadia (2018) Exploring genetic diversity in chickpea (*Cicer arietinum* L.) under normal sown condition of Bihar. *Curr J Appl Sci Technol* 31(4):1-5. DOI: 10.9734/CJAST/2018/45989
- Sharma RN, Johnson PL, Nanda HC, Sao A, Sarawgi AK, Verma SK, Prabha N, Singh AK (2019) Genetic variability, character association and coheritability for yield traits over the locations in chickpea (*Cicer arietinum* L.). *Leg Res* 41: 501-505. Doi:10.18805/LR-4150.
- Shivwansh R, Babbar A (2019) Genetic divergence analysis in chickpea germplasm. *Leg Res* 42: 715-718. Doi.10.18805/LR-3921
- Singh RK, Chaudhary BD (1985) Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi, pp 266. DOI: 10.4236/aid.2015.54017
- Varshney RK, Bansal KC, Aggarwal PK, Dutta SK, Craufurd P. (2011) Agricultural biotechnology for crop improvement in a variable climate: Hope or hype? *Trends Pl Sci* 16: 363—371. DOI: 10.1016/j.tplants.2011.03.004