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Short Communication

Genetic diversity studies in chickpea (*Cicer arietinum* L.) germplasm

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ABSTRACT

The present experiment was carried out with thirty five genotypes of Chickpea in Rabi 2017-18 at field experimentation centre of the Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad to assess the nature and magnitude of genetic divergence using Mahalanobis's D^2 Statistics. Analysis of variance revealed highly significant differences among the thirty two genotypes for fifteen characters studied indicating that significant amount of genetic variability present in the material. Seed yield per plant had maximum Phenotypic and Genotypic Coefficient of Variation (PCV and GCV), followed by, 100-seed weight and number of pods per plant. High magnitude of heritability (broad sense) was recorded for seed yield per plant, number of pods per plant and harvest index. High heritability coupled with high genetic advance was observed for seed yield per plant, number of pods per plant, harvest index and biological yield per plant suggesting that, the role of additive gene effect and possibilities of achieving high genetic progress through selection. The twenty five Chickpea genotypes were grouped into six clusters clusters suggesting considerable amount of genetic diversity in the material. The cluster VI had maximum ten genotypes followed by cluster I (08 genotypes), cluster II and V having five genotypes, while cluster IV had four genotypes and cluster III having three genotypes, respectively. The intra-cluster D^2 value ranged from 11.17 to 49.53 while, inter-cluster D^2 value ranged from 32.01 to 152.13. The maximum intra cluster distance was exhibited by cluster IV followed by cluster V and cluster VI. The maximum inter-cluster distance was observed between cluster II and V(152.13), followed by cluster V and VI(146.93) and cluster II and VI (143.60) suggesting that the genetic architecture of the genotypes in one cluster differ entirely from those included in other clusters. Cluster IV had exhibited highest cluster mean value for seed yield per plant and seed index. Cluster V has highest mean value for number of pods per plant, biological yield per plant and days to maturity. Cluster VI showed high mean value number of primary branches per plant and harvest index. Cluster III exhibited highest mean value for number of secondary branches per plant and lowest mean value for plant height and days to maturity. Maximum contribution toward the total divergence was exhibited by 100-seed weight followed by seed yield per plant, biological yield, number of pods per plant and harvest index. The genotypes BCG101, BCG708, PBC37, IC275313, Phule G Vikram ICC144, IC275326, ICC3812, ICC303 and PKV4 were identified as genetically diverse parents, which can be utilized for future crop improvement programme in Chickpea. The above results indicated that these genotypes have maximum genetic diversity and useful for developing a large number of segregants through crossing programme by using maximum diverse genotypes.

Key words: Chickpea, Cluster analysis, D^2 statistics, Genetic variability

Chickpea is one of the most important food legumes in the world. Chickpea is the only 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. India remains a net importer of chickpea despite contributing to more than 60% to global chickpea in area and production. 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 programme 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. (Vaghela *et al.* 2009). Genetic diversity among parents, which is heritable, is a pre-requisite for any successful breeding programme. The proper choice of parents in the breeding programme is of paramount importance. Genetic divergence among the parents plays a vital role in cultivar improvement 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 programme for chickpea yield improvement. D^2 statistical analysis is a powerful tool in quantifying the degree of divergence among the population. Murthy and Arunachalam (1966) stated that multivariate analysis with “ Mahalanobis D^2 statistics” is a powerful tool to know the clustering pattern to establish the relationship 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.

The experimental material consisted of thirty five genotypes of chickpea grown in Rabi 2017-18 at field experimentation centre of the Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad. The experiment was laid out in a randomized complete block design with three replications during Rabi 2017-18. The plot size was 4.8 m^2, 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 primary branches per plant, number of secondary branches per plant, number of pods per plant, 100 seed weight (g), biological yield (g) and seed yield per plant (g).The days to 50% flowering, days to maturity, and seed yield per plant were recorded on a plot basis and plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, 100 seed weight (g), biological yield and harvest index 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 Tocher’s method. The per cent contribution of characters towards genetic divergence was calculated according to Singh and Chaudhary (1985).

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

S. No.	Characters	Mean sum of squares		
		Replications (df= 2)	Treatments (df= 34)	Error (df= 68)
1	Days to 50% flowering	1.03	19.14**	8.18
2	Days to maturity	0.88	19.57**	6.89
3	Plant height (cm)	1.18	187.27**	47.09
4	No. of primary branches/plant	0.016	0.83**	0.23
5	No. of secondary branches/plant	1.39	13.69**	3.02
6	No. of pods/plant	103.50	350.00**	33.72
7	100-seed weight (g)	7.65	19.03**	9.31
8	Biological yield (g)	713.71	3022.48**	381.08
9	Seed yield per plant(g)	148.30	964.75**	65.25
10	Harvest Index (%)	97.64	358.35**	35.71

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

The analysis of variance revealed significant differences for all the ten characters studied (Table 1) indicating that significant amount of genetic variability present in the material. Estimates of genetic parameters of variability are presented in Table 2. Coefficient of variation at phenotypic and genotypic levels was observed relatively high in for seed yield per plant, biological yield, Number of pods per plant and secondary branches per plant indicating the presence of high amount of variation in these traits. The magnitude of PVC was higher than GVC for all the characters indicating the influence of environment of these traits. The highest heritability was observed in seeds per pod followed by pod length, days to 50% flowering, days to first flowering, seed yield per plant and dry matters of plant. These traits showed high habitability indicating additive gene effect. The genetic advance under selection was low. The present study for high habitability for these characters was conformed to those observed by Kumar *et al.* (2017), Chandra (1968), Joshi (1972) and Indu (1985) in different chickpea trials. The highest heritability was observed for seed yield per plant, number of pods per plant and harvest index. High genetic advance was recorded by biological yield. High heritability coupled with high genetic advance were recorded for seed yield per plant, biological yield per plant, harvest index and number of pods per plant indicating that these characters were governed largely through the additive gene effect as reported by Kumar *et al.* (2017), Parshuram *et al.* (2003), Chavan (1994), Joshi (1972) and Chandra (1968). Asawa *et al.* (1977) also observed high genetic coefficient of variation in chickpea, which was in conformity with the present study.

All the genotypes were grouped into six clusters as per Tocher’s method, with cluster VI containing the maximum of 10 genotypes followed by eight genotypes in

Table 2. Genetic parameters of variability in thirty five genotypes of chickpea

S. No.	Characters	Mean	Range	$\sigma^2 g$	$\sigma^2 p$	GCV	PCV	Heritability ($h^2 bs$)	Genetic advance	GA as % of mean
1	Days to 50% flowering	71.15	66.00-75.66	3.65	11.84	2.69	4.84	31.00	2.19	3.07
2	Days to maturity	120.48	115.33-125.33	4.23	11.12	1.71	2.77	38.00	2.61	2.71
3	Plant height (cm)	52.34	34.46-68.46	46.73	93.82	13.06	18.50	50.00	9.94	18.99
4	No. of primary branches/plant	2.46	1.26-3.60	0.20	0.43	18.07	26.75	46.00	0.62	25.42
5	No. of secondary branches/plant	8.56	5.00- 13.26	3.56	6.58	22.2	35.08	54.00	2.86	33.50
6	No. of pods/plant	44.18	25.93- 66.66	105.43	139.15	23.24	26.69	76.00	18.41	41.66
7	100-seed weight (g)	20.42	17.33-27.66	3.24	12.55	8.81	17.34	26.00	1.88	9.22
8	Biological yield (g)	123.38	76.00-212.33	880.47	1261.55	23.99	28.72	70.00	51.07	41.29
9	Seed yield per plant (g)	62.97	36.33-125.33	299.83	365.09	27.50	30.43	82.00	32.33	51.33
10	Harvest Index (%)	53.99	32.81-76.47	107.54	143.26	19.21	22.17	75.00	18.51	34.28

Table 3. Distribution of thirty five chickpea genotypes in various clusters

Cluster	No. of Genotypes	Name of Genotypes
I	08	ICC807, PG739, BCG944, PG12310. BCH902, BDNGK798, VIRAT, PKV2
II	05	BCG101, BCG708, PBC37, IC275312, PhuleG VIKRAM
III	03	IC275347, JAKI9218, SAKI9516
IV	04	KRIPA, VIJAY, IC275321, IC275322
V	05	ICC144, IC275326, ICC3812, ICC303, PKV 4
VI	10	PBC1103, IC275341, Digvijay, Vishal, IC275323, IC275340, IC275339, BDNG797, IC275329, IC275338

Table 4. Average intra and inter cluster D2 values among six clusters for thirty five genotypes of chickpea

Clusters	I	II	III	IV	V	VI
I	**27.84**	32.01	44.05	79.60	120.50	115.95
II		**11.17**	48.56	129.53	152.13	143.60
III			**11.32**	123.26	139.92	124.91
IV				**49.53**	132.10	146.93
V					**29.14**	44.30
VI						**28.29**

cluster I, five genotypes in cluster II and V, 4 genotypes in cluster IV and 3 genotypes in cluster III. (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 geographical region were grouped into different cluster and vice-versa, as supported by earlier finding of Lal *et al.* (2001), Raval *et al.* (2004), Paramesharappa *et al.* (2011), Parashi *et al.* (2013) 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 11.17 to 49.53 while, inter-cluster D^2 value ranged from 32.01 to 152.13 (Table 4) in Tocher's method. The highest intra-cluster distance was exhibited by cluster IV (49.53) followed by cluster V (9.14) and cluster VI (28.29). The intra cluster distance was maximum in cluster IV followed by cluster V which indicated that hybridization involving genotypes within the same clusters may result in cross combinations. The highest inter-cluster distance was observed between cluster II and V (152.13), followed by cluster IV and VI (146.93), cluster II and VI (143.60) and cluster III and V (139.92) 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 (Kumar *et al.* 2018). 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.

Cluster IV had exhibited highest cluster mean value for seed yield per plant and seed index. Cluster V has highest mean value for number of pods per plant, biological yield per plant and days to maturity (Table 5). Cluster VI showed high mean value number of primary branches per plant and harvest index. Cluster III exhibited highest mean value for number of secondary branches per plant and lowest mean value for plant height and days to maturity. Among the ten traits studied, maximum contribution was made by 100-seed weight (51.18 %) (Table 6), followed by seed yield per plant (9.75%), biological yield (9.45%), number of pods per plant (9.24%) and harvest index (8.07%). These findings are in accordance with the results of Kumar *et al.* (2018) and Agrawal *et al.* (2018). Therefore, these characters may be given importance during hybridization programme. The genotypes BCG101, BCG708, PBC37, IC275313, Phule G Vikram ICC144, IC275326, ICC3812, ICC303 and PKV4 were identified as genetically diverse parents, which can be utilized for future crop improvement programme in Chickpea.

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

Cluster	Days to 50% flowering	Days to maturity	Plant Height (cm)	No. of primary branches / plant	No. of secondary branches / plant	No. of pods per plant	100- seed weight (g)	Biological yield/plant (g)	Harvest index (%)	Seed yield per plant (g)
I	70.62	120.95	51.42	2.48	7.78	46.34	21.41	116.45	54.13	60.66
II	69.13	120.40	63.33	1.98	6.28	42.38	19.33	103.20	49.55	50.86
II	72.66	118.22	40.00	2.73	11.44	33.31	18.77	111.55	39.89	40.22
IV	72.83	119.91	53.28	2.43	9.91	53.58	23.00	192.50	54.06	98.33
V	73.40	121.53	51.68	2.10	7.96	53.85	18.66	135.33	52.18	65.53
VI	70.33	120.53	51.47	2.80	9.11	37.04	20.63	110.00	61.02	62.26

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

SI.No.	Source	Contribution %
1	Days to 50% Flowering	1.21
2	Days to maturity	0.84
3	Plant height (cm)	2.02
4	No. of primary branches/plant	3.03
5	No. of secondary branches/plant	5.21
6	Number of pods/ plant	9.24
7	100 -seed weight (g)	51.18
8	Biological yield (g)	9.45
9	Harvest index (%)	8.07
10	Seed yield per plant (g)	9.75

The above results indicate that these genotypes have maximum genetic diversity and useful for developing a large number of segregants through crossing programme by using maximum diverse genotypes.

The genotypes BCG101, BCG708, PBC37, IC275313, Phule G Vikram ICC144, IC275326, ICC3812, ICC303 and PKV4 were identified as genetically diverse parents, which can be utilized for future crop improvement programme in Chickpea. The above results indicate that these genotypes have maximum genetic diversity and useful for developing a large number of segregants through crossing programme by using maximum diverse genotypes.

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