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Assessment of Genetic Diversity using D^2 Statistics in Chickpea (*Cicer arietinum* L.) under Late Sown Conditions

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Authors' contributions

This work was carried out in collaboration among all authors. Author VPR designed the study, performed the statistical analysis, wrote the protocol and wrote the first draft of the manuscript. Authors SP and JMR managed the analyses of the study. Author JMR managed the literature searches. All authors read and approved the final manuscript.

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ABSTRACT

An experiment was conducted during *Rabi*, 2019-20 at Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj (Allahabad) consisting of 36 chickpea genotypes obtained from ICAR-Indian Institute of Pulses Research, Kanpur, U.P in RBD with three replications. The data was recorded on 13 traits to study the genetic divergence. Analysis of variance revealed that there was considerable genetic variability in the available germplasm for all the characters studied. Divergence analysis revealed that highest inter cluster distance (1505.25) was found between clusters I and V indicates that there is ample scope for selection of better parents.

Keywords: Chickpea; genetic divergence; mahalnobis D^2 statistic.

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1. INTRODUCTION

Chickpea *(Cicer arietinum* L.) is a self - pollinated diploid (2n= 2x=16) with genome size of 732 Mbp. It belongs to the sub-family papilionaceae of family leguminoceae, is an important and unique food legume. It is an imperative pulse crop of the world occupying third position amongst pulses. It is known to be originated in western Asia and then dispersed in two diverse directions. Large seeded chickpea, referred to as *Kabuli* type, are well adapted to spring sowing. Small seeded cultivars of different colors are known as *Desi* types and are mostly planted in winter from Pakistan Eastward and also in Ethiopia, Sudan, Mexico, Chile [1] (Springer, Boston, MA. https://doi.org/10.1007/978-1-4684-2886-5_9).

In India the area under chickpea was 9.539 million ha with a production of 90.75 million tons while the productivity was 951kg/ha. In Utter Pradesh, it is grown on 5.89 lakh ha area with total production of 5.967 lakh tons and average productivity of 1013 kg/ha during 2018-19 (ICAR-Directorate of pulses Development - Annual Report, - Indian Institute of Pulses Research E-pulses Data Book). It occupies 61 per cent of total area under pulses producing about 65 per cent of total production in Uttar Pradesh. Chickpea contains about 17.7 to 38.5 per cent protein and 56.5 per cent carbohydrates besides ash, calcium, phosphorus and iron. Chickpea has got special importance in diet and is consumed in a variety of ways. Chickpea is one of the most important Rabi pulse crops in Asia. India is largest producer (25%), importer (20%) and consumer (20%) of pulses in the world [2].

Though India is the largest producer of this crop, it imports 25% chickpea because its productivity is low as compared to countries like Italy, Turkey, Iron, etc. There is a good scope to improve the productivity of this crop by varietal improvement and adopting the improved production technology on larger areas of the country. Mahalnobis D^2 statistic has proved to be a powerful tool for quantifying the genetic divergence in a given population in respect of characters considered together. The crosses between the genotypes with maximum genetic divergence would be utilized for improvement as they are likely to yield desirable recombinants in the progeny.

2. MATERIALS AND METHODS

The experimental materials comprising of 36 genotypes including check (Pusa 362) were laid out under Randomized Block Design (RBD) with three replications. The row to row and plant to plant distance was kept at spacing of 30×10 cm^2. Total number of rows was 36 and the row length was 47.1m. The nitrogen was applied in two splits, one at the time of sowing and other at 25 days after sowing. Entire Phosphorus was applied as basal dose. All recommended practices were followed and timely plant protection measures were taken to avoid damage through insect-pests and diseases. Observations for different quantitative traits were recorded on five randomly selected competitive plants for each treatment in each replication, except days to flowering and days to maturity which was recorded on a plot basis. Analysis of variance was worked out to test the significance of F and T-tests. It was carried out according to procedure of RBD analysis for each character as per methodology suggested by Panse and Sukhatme [3]. A measure for group distance based on multiple characters given by Mahalanobis (1936) D^2 technique with the help of which genetic diversity between genotypes was estimated (AS Jeena, PP Arora, 2002). The analytical tool used for this work was the Multivariate analysis.

3. RESULTS AND DISCUSSION

The genetic improvement in a crop species is inevitable and continuous process to meet the future challenges. For this the strengths of available germplasm has to be evaluated to identify potential genotypes which ultimately leads to food and nutritional security of the country. Success of the breeding programme largely depends upon the knowledge of genetic variability present in a given crop species for the characters under improvement. As such, before launching any breeding programme it is necessary to have thorough knowledge on variability present in the available genetic material.Analysis of variance showed there is significant difference among the genotypes for thirteen characters under the study (Table 1). This indicated that there is ample scope for selection of genotypes for yield and its components.

Further, the diversity of parents used in hybridization programme is of utmost importance (Murthy and Arunachalam, 1966). Since the

crosses between the parents with maximum genetic divergence are likely to yield desirable recombinants in their progenies. However, it is a difficult task for the plant breeder to select the most suitable and genetically divergent parents, unless he is provided with necessary information about the genetic variability and genetic diversity present in the available germplasm.

The data collected on thirteen yield and yield contributing characters for 36 genotypes of chickpea were subjected to multivariate analysis and genetic divergence by using Mahalanobis D^2 statistic. The magnitude of D^2 values suggested that there was considerable variability in the material studied, which led to genetic diversity. Kumar and Arora [4], Gupta and Krishna [5], Jethava et al. [6], Thripathi [7], Sirohi et al. [8], Khan [9], Sivakumar and Muthiah [10], Lal et al. [11], Nimbalkar and Harer [12], Jivani et al. [13], Khan et al. [14], Thakur et al. [15] reported wide genetic diversity in chickpea genotypes.

Thirty six chickpea genotypes were grouped into 5 clusters following Mahalanobis's D^2 analysis [16] (Table 2). Clustering pattern indicated that cluster I is the largest cluster comprising 29 out of 36 genotypes. On the other hand, cluster II comprised of 4 genotypes, cluster III, IV and V comprised of one genotype each. The pattern of group constellation proved the existence of significant amount of variation. The distribution of genotypes indicated that the geographical diversity and genetic diversity were not related and there are forces other than geographical separation which are responsible for diversity such as natural and artificial selection, exchange of breeding material, genetic drift and environmental variation.

Table 1. ANOVA for thirteen characters in chickpea (*Cicer arietinum* L.)

S. No.	Characters	Mean Sum of Squares		
		Replication (d.f=2)	Treatments (d.f=35)	Error (d.f=70)
1	Days to 50% flowering	141.89	3.241 **	1.564
2	Days to 50% pod setting	20.731	4.910 **	1.864
3	Days to maturity	18.753	19.916 **	43.628
4	Plant height	22.752	39.423 **	5.816
5	No. of primary branches	0.199	0.729 *	0.063
6	No. of secondary branches	0.059	12.060 **	0.092
7	No. of pods per plant	15.390	269.80 **	9.662
8	No. of seeds per pod	0.0518	0.848 *	0.0325
9	No. of seeds per plant	19.237	3210.94**	6.935
10	Seed Index	6.361	104.19 **	5.503
11	Biological yield per plant	9.514	103.51 **	6.711
12	Harvest index	106.76	73.551 **	112.28
13	Seed yield per plant	0.634	28.349 **	0.446

,Indicates significant at 5 &1 % level of significance*

Table 2. Distribution of 36 chickpea genotypes into different clusters based on D^2 statistic

Clusters	No. of genotypes	Genotypes
I	29	ILC 585, IPC 10-116, PG 0517, ILC 1202, IPC 14-112,ILC 166, IPC 08-83, ICC 595468, ILC 12-238, ICPK 9-40, ICC 15117, Flip 09-162 C, ILC 3518, IPC 14110,JAKI 9218, IPC 97-67, IPC 11-09, ICC 30-20, IPC 08-11,IPC 09-50, Pusa 362, GNG 469, IPC 06-11, ICC 20-80,IPC 14-86, ICC 26, ICCV15614, BPM, Flip 9-130c.
II	4	IPCK 11-239, JG 36, ICC 21170, 9-145
III	1	JG 315IV 1 RSG 931V 1 IPC 0524
IV	1	RSG 931
V	1	IPC 0524

3.1 Intra and Inter Cluster Distance (D^2) of Eight Clusters

Highest intra cluster distance was observed for cluster I (67.07) which comprised of twenty nine genotypes (Table 3). Hybridization programme involving genetically diverse parents belonging to different distant clusters would provide an opportunity for bringing together gene constellations of diverse nature. Promising hybrid derivatives may resulted probably due to complementary interaction of divergent genes in parents (Anand and Murthy, 1968).In the present study the highest inter cluster distance (1505.25) was found between clusters I and V followed by clusters II and V (729.21), cluster I and cluster IV (657.69), cluster I and cluster III(633.34), cluster IV and cluster V (594.34).

The genotypes of the most distant clusters I and V were quite contrasting in performance with respect to days to 50% flowering, number of primary branches per plant, Days to maturity, number of seeds per pod, number of seeds per plant, biological yield per plant, 100-seed weight, and seed yield per plant. The smallest inter cluster distance (194.17) was observed between cluster II and cluster III. The smallest inter cluster distance indicates less diversity between the genotypes contained in these clusters. It indicates close relationship and similarity of the genotypes for most of the characters. However, these genotypes can be undertaken for hybridization in order to exploit variation for the specific characters for which the genotypes of the two clusters shown marked difference. For successful breeding program, selection of genetically diverse parents is an important prerequisite so as to obtain better and desirable recombinants.

3.2 Cluster Mean

Mean performance of a cluster is the mean of overall values of individual correlated variables of all genotypes included in that cluster. The cluster mean was presented in Table 4. It was depicted that there was considerable difference in the cluster mean for different characters. Cluster IV recorded maximum values for days to 50% flowering, days to 50% pod setting, plant height, number of secondary branches per plant and days to maturity. Cluster V recorded maximum values for Number of primary branches per plant, number of seeds per pod, number of seeds per plant, biological yield per plant, seed index, seed yield per plant. Cluster III recorded maximum value for number of pods per plant. Cluster II recorded maximum value for Harvest index.

Table 3. Intra (bold) and inter cluster average divergence (D2) values of 5 clusters from 36 genotypes of chickpea (*Cicer arietinum* L.)

Clusters	I	II	III	IV	V
I	67.07	205.63	633.34	657.69	1505.25
II		67.05	194.17	294.64	729.21
III			0	332.37	209.48
IV				0	594.34
V					0

Table 4. Cluster means for various characters in 5 clusters

Cluster	DF 50%	DP 50%	PH (cm)	PBPP	SBPP	DM	NPPP	NSPP	NSPPI	BYLD PP	HI (%)	SI (g)	SYLD PP (g)
Cluster 1	81.33	101.30	59.29	2.26	3.74	122.09	21.40	1.36	56.37	12.26	50.45	19.48	6.05
Cluster 2	81.92	101.58	61.14	2.45	5.65	121.17	23.39	1.96	97.42	16.33	53.72	15.75	8.50
Cluster 3	82.00	102.67	58.59	2.00	5.40	122.00	29.11	2.03	146.33	25.33	51.68	17.00	12.96
Cluster 4	81.00	100.33	65.99	4.00	12.33	119.33	13.31	1.03	104.47	30.13	51.55	12.00	15.50
Cluster 5	83.00	103.33	59.06	3.20	7.40	119.70	24.84	2.05	199.07	31.40	50.95	20.00	15.70

DF: Days to 50% flowering, DP: Days to 50% pod setting, PH: Plant height, PBPP: Primary branches per plant, SBPP: Secondary branches per plant, DM: Days to maturity, NPPP: Number of pods per plant, NSPP: Number of seeds per pod, NSPPL: Number of seeds per plant, BYLDPP: Biological yield per plant, HI: Harvest Index, SI: Seed Index, SYLDPP: Seed yield per plant.

Table 5. Percentage contribution of individual characters towards total divergence

Source	Contribution %	Times ranked 1st
Days to 50% flowering	3	19
Days to 50% pod setting	2	13
Plant height	3	19
Primary branches per plant	4	25
Secondary branches per plant	13	81
Days to maturity	4	25
Number of pods per plant	12.43	78
Number of seeds per pod	6	38
Number of seeds per plant	9	56
Biological yield per plant	18	113
Harvest index	0.16	1
Seed index	3.81	24
Seed yield per plant	18	113

3.3 % Contribution

The utility of D^2 analysis, which is a potent tool to quantify the extent of divergence in biological populations at genetic level, is further enhanced by its applicability to estimate the relative contribution of the various plant characters to genetic divergence. The selection and choice of parents mainly depends upon contribution of characters towards divergence (Nayak et al*.,* 2004). The more the number of times that each of the 13 characters appeared in first rank the more it contributed towards diversity. The present study revealed that seed yield per plant (18%), biological yield per plant (18%), secondary branches per plant (13%), number of pods per plant (12.43%), number of seeds per plant (9%), number of seeds per pod (6%), number of primary branches (4%),Days to maturity (4%), contributed to 84.43% of total divergence followed by 100 seed weight (3.81%), days to 50% flowering (3%), days to maturity (3%) and days to 50% pod setting (2%) (Table 5).

3.4 Genotypes Included into the Clusters

The genotypes contained in cluster I, IV, and V seem to be quite promising for many of the characters like days to 50% flowering, days to 50% pod setting, plant height, number of primary branches per plant, number of secondary branches per plant, days to maturity, number of seeds per pod, number of seeds per plant, 100 Seed weight, biological yield per plant and seed yield per plant.

Cluster I : ILC 585, IPC 14-112, ILC 3518, Pusa 362, GNG 469, BPM.
Cluster IV : RSG 931
Cluster V : IPC 0524

4. CONCLUSION

It is concluded that on the basis of Analysis of variance significant difference was recorded for all the seed yield and its components indicating presence of large amount of variability in the genotypes. Maximum numbers of genotypes were grouped into cluster I which included 29 genotypes. In the present study the highest inter cluster distance (1505.25) was found between clusters I and V. Genotypes belongs to these clusters may be used as parents to produce transgressive segregants.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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