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Studies on Genetic Diversity in Desi Chickpea (*Cicer arietinum* L.) using D2 Statistics

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

A trail was conducted during *rabi* 2020 to study genetic diversity among 36 favorable genotypes of chickpea (*Cicer arietinum* L.) with help of Mahalanobis D^2 statistics. On the basis of D^2 values, 36 genotypes were arranged into 5 clusters. The intra cluster distances were lower than inter-cluster distances, specifying that genotypes comprised within a cluster shows tendency to vary less apart from each other. Out of thirteen characteristics considered, secondary branches per plant, number of pods per plant, seed yield per plant, harvest index and plant height, contributed very much in relation to genetic divergence. Wide range of variability was noticed for quantitative traits. This suggested that the selection based on these characteristics would be valuable in improving the grain yield. Therefore, a direct selection based on seed yield and component traits may be practiced to choose superior genotypes which could be utilized in breeding program for the development of high yielding chickpea genotypes.

Keywords: Chickpea; genetic divergence; percent contribution; inter and intra cluster distance; Genetic advance; variability.

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1. INTRODUCTION

Among the cultivated pulses, one of the important pulse crop is chickpea (*Cicer arietinum* L.). Chickpea is a self-pollinated diploid (2n= 2x=16) with a genome size of 732 Mbp. It belongs to the sub-family Papilionaceae of the family Leguminosae, which is an important and unique food legume. It is an important pulse crop of the world occupying the third position amongst pulses. It is known to be originated in western Asia and then dispersed in two diverse directions.

In India, the area under chickpea was 9.539 million hectares with a production of 90.75 million tons and productivity of 951 kg/ha during 2018-19 (ICAR- Directorate of pulses development- Annual Report- Indian Institute of Pulses Research E- Pulses Data Book).In Uttar Pradesh, the area under chickpea was 5.89 lakh hectares with a total production of 5.967 lakh tones and productivity of 1013 kg/ha during 2018-2019. It occupies 61 percent of the total area among pulses and about 65 percent of total production is from Uttar Pradesh. The protein percent in the chickpea is about 17.7 to 38.5 percent and the carbohydrate is about 56.5 percent besides ash, calcium, phosphorus, and iron (K Desai *et al*.,2015). Chickpea has got special importance in diet and is consumed in a variety of ways. It is mostly used in the form of dal (flour or parched). Dal obtained after milling from chickpea forms a major part of the regular diet of vegetarians. Though India is a large producer of chickpea, it imports 25% because of the low productivity when compared to other countries like Italy, Turkey, Iran, Ethiopia etc.,. There is adequate opportunity to raise the productivity of chickpea by varietal improvement and adopting the improved production technology on larger areas of the country.

Yield is a complex character governed by several factors inherent in the plant as well as the environment in which the plant grows. Thorough knowledge of the nature and magnitude of genetic variability present in a crop species is essential to plant breeders before launching any breeding program [1]. Heritability of a metric character is a parameter of particular significance to the breeder as it measures the degree of resemblance between the parents and the offspring and its magnitude indicates the chances with which a genotype can be identified by its phenotypic expression. While genetic advance aids in exercising the necessary selection pressure. Genetic diversity is a powerful tool for the determination of genetic discrimination among the genotypes which is used to select appropriate plant genotype(s) for hybridization to develop high- yielding potential variety [1]. Genetic diversity can be evaluated with morphological traits, seed protein, isozymes, and DNA markers. With the development of advanced biometrical methods such as Multivariate analysis [2] based on Mahalanobis's D^2 statistics, it has become possible to quantify the magnitude of genetic diversity among the germplasm for their utilization in respect of the breeding program with high probability of bearing potential hybrid vigor. This is important as for the development of any genotype with desirable traits, it is necessary to include diverse parents in the hybridization program.

2. MATERIALS AND METHODS

The present work was conducted during *rabi* 2020-2021 at field experimentation center, Department of Genetics and Plant Breeding, Naini Agriculture Institute, SHUATS, Prayagraj (Allahabad) U.P., India. The experimental material consists of 36 desi genotypes including one check which was grown in RBD with 3 replications. The experimental field was divided into 36 blocks of equal size and each block consists of one genotype. The inter and intra row spacing was kept 30x10cm to maintain the standard plant density. The experiment was conducted following the recommended package of practices. Observations for different quantitative traits were recorded on five randomly selected competitive plants from each treatment in each replication, except for days to flowering and days to maturity which were recorded on a plot basis. The data on various quantitative characters were subjected for analysis as per the Mahalanobis D^2 (1936) statistics. Mahalanobis D^2 (1936) statistics is a powerful tool for quantifying genetic divergence. Grouping of genotypes in different clusters was done by using Tocher's method [2]. The percent contribution of different quantitative characters towards divergence was calculated according to Singh and Choudhary [3].

3. RESULTS AND DISCUSSION

The Knowledge regarding the extent of variability and genetic diversity is of much importance while improving a complex trait like yield. Therefore, the selection of parents having a wide genetic divergence for a number of characters is of prime

importance, which is assessed by D^2 statistics developed by Mahalanobis (1936). The diversity of the parents is of utmost importance since the crosses made between the parents with maximum genetic divergence are more likely to yield desirable recombinants in the segregating progenies. The selection of the superior parents for hybridization is based on the inter-cluster distance and cluster mean.

3.1 Composition of Clusters

Thirty-six genotypes were grouped into five clusters following Tocher's method (Table-1). It indicates that the genotypes within the cluster have smaller D^2 values while genotypes among the clusters have larger D^2 values. Cluster I was the largest cluster with 32 genotypes followed by II, III, IV, V which comprises a single genotype. There is a wide diversity between the genotypes of these single-genotypic clusters. 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 variations.

3.1.1 Inter and intra cluster distances

The highest inter-cluster distance (3352.85) was found between cluster II and IV followed by cluster II and V (2239.1) and cluster I and IV (1794.33) (Table-2). The highest intra-cluster distance was observed for cluster I (144.69). The smallest inter-cluster distance indicates that less diversity among the genotypes contained in these clusters. It indicates a close relationship and similarity of the genotypes for most of the characters. The genotypes belong to clusters that show high genetic distance can be undertaken for hybridization to exploit variation for the specific characters for which the genotypes of the clusters shown the marked difference. For a successful breeding program, the selection of genetically diverse parents is an important prerequisite to obtain better and desirable recombinants.

3.1.2 Cluster mean of various characters

The cluster mean was presented in the Table-3. It was depicted that there was a considerable difference in the cluster mean for different characters. Cluster II recorded minimum values for days to 50% flowering and days to 50% pod setting [4], while maximum values was recorded for no of pods per plant and seed index. Cluster III recorded maximum value for no of primary branches per plant and no. of seeds per pod. Cluster IV recorded maximum values for plant height, no of seeds per pod, no of seeds per plant, biological yield per plant and seed yield per plant. Cluster V recorded maximum value for no. of secondary branches per plant and harvest index. Therefore, the genotypes belonging to these clusters would be subjected to intercrossing [5] and thus creating variability for respective characters and their sensible improvement for raising the seed yield.

3.1.3 Characters contributed towards genetic divergence

The present study revealed that maximum contribution towards the total divergence was of the no of secondary branches per plant (35%), no of pods per plant (14.5%), seed yield per plant(10%), harvest index(9%), plant height(6.53%) which contributed to 75% of the total divergence followed by no of seeds per plant (6%), days to maturity (5%), seed index(3.2%), days to 50% pod setting(3%), biological yield per

Table 1. Distribution of genotypes into various clusters

Cluster	No. of genotypes	Genotypes
I	32	BDNGK-798, IPC 19-12, 1CCC-37, 1CC 11019, ICC 257, PG 06102, ICC 190, IPC 18-103, 04-01A, IPC 11-85, C-1044, ICC 752, IPC 2K-2000-25, DCP 92-3, ICC-11847, IPC 18-120, IPC-21170, ICC 4958, CSQ 89-62, Flip 09-1306, ICC 5439, RVS 5949, WBG-29, WCK-3, IPC 04-98, PG-96006, IPC 12-100, C-207, PG-05, ICC 731, CSJ 512, ICC 762
II	1	Pusa 362
III	1	Indira Chana-1
IV	1	C-1027
V	1	GIURI-K-499

Table 2. Intra (bold) and inter cluster distances from 36 genotypes of chickpea (*Cicerarietinum* L.)

Clusters	**I**	**II**	**III**	**IV**	**V**
I	144.69	422.21	658.22	1794.33	934.99
II		0	1572.35	3352.85	2239.1
III			0	361.21	430.26
IV				0	551.8
V					0

Table 3. Cluster mean value for 13 characters in Chickpea germplasm

	DF 50%	**DP 50%**	**DM**	**PH cm**	**NPBPP**	**NSBPP**	**NPPP**	**NSPP**	**NSPPl**	**BYPP (g)**	**Hl (%)**	**Sl (g)**	**SYPP (g)**
Cluster 1	84.09	101.4	123	59.7	2.62	6.17	19.82	1.4	62.29	12.8	46.2	18.9	5.93
Cluster 2	80	100	120.3	62.3	2	2.27	31	1	31	11.33	49.8	22	5.6
Cluster 3	84.67	102.7	123	58.7	4.17	5.87	27.87	2	146.33	25.33	49.5	17	12.53
Cluster 4	84	103.3	120	65.9	3.17	8.13	23.6	2	199.07	31.4	48.8	20	15.27
Cluster 5	82.67	100.7	120.7	58.4	3.67	12.2	12.07	1	104.47	30.13	49.9	12	15.06

DF50%:Days to 50% flowering ,DP50%:Days to 50% pod setting, DM:Days to maturity, PH:Plant height (cm), NPBP:No. of Primary Branches per plant, NSBP:No. of Secondary Branchesper plant ,NPPP: No. of pods per plant, NSPP:No ofsee ds per Pod, NSPPl:No ofseeds per Plant, BYPP: Biological yield per plant (g), HI:Harvest index %; SI:Seed index , SYLDPP:Seed yield per plant (g)

Table 4. % Contribution of individual characters towards total divergence

S.NO	**Source**	**% Contribution**	**Times ranked 1st**
1	Days to 50% flowering	2	12.50
2	Days to 50% pod setting	3	18.75
3	Days to maturity	5	31.25
4	plant height	6.53	40.81
5	No. of primary Branches per Plant	2.34	14.63
6	No. of secondary Branches per Plant	35	218.75
7	Number of pods per plant	14.5	90.63
8	Number of seeds per pod	0.95	5.94
9	Number of seeds per plant	6	37.50
10	Biological yield per plant (g)	2.48	15.50
11	Harvest index (%)	9	56.25
12	Seed index (g)	3.2	20.00
13	Seed yield per plant (g)	10	62.50

plant(2.45%), no of primary branches per plant (2.34%), days to 50% flowering(2%) and no of seeds per pod (0.95%) [4]. The more no. of times a characters appeared at the first rank, the more it contributed towards diversity [6]. It is well-known fact that to obtain the high heterotic hybrids and variability in the segregating generations, there is a need of using genetically divergent parents in the breeding program [7].

4. CONCLUSION

The genetic divergence grouped 36 genotypes into 5 clusters using Mahalanobis D^2 statistics. Cluster II and IV shows the highest inter-cluster distance followed by cluster II and V. Cluster II recorded minimum values for days to 50% flowering and days to 50% pod setting, while maximum values for no of pods per plant and seed index. Cluster III recorded maximum value for no of primary branches per plant and no. of seeds per pod. Cluster IV recorded maximum values for plant height, no of seeds per pod, no of seeds per plant, biological yield per plant and seed yield per plant. Cluster V recorded maximum value for no. of secondary branches per plant and harvest index. A total of 75.03% of variability towards divergence was mainly contributed by characters such as no of secondary branches per plant, no of pods per plant, seed yield per plant, harvest index, and plant height. Based upon the larger inter-cluster distance and high yielding superior genotypes, it is recommended for crossing between the genotypes of the cluster II and IV, and cluster II and V. Hybridization between the elite genotypes belonging to these clusters may leads to the creation of genetic variability for raising the yield in chickpea.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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