Assessment of Genetic Diversity of Chickpea Genotypes (*Cicer arietinum* L.) Using D^2 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.

Original Research Article

ABSTRACT

An experiment using twenty genotypes of chickpea (*Cicer arietinum* L.) was conducted during Rabi season of 2019-2020, to find the genetic diversity using D^2 statistics. The experiment was laid out in randomized block design with three replications at the experimental field of Himgiri Zee University, Dehradun. The observations was recorded on nine quantitative characters where five randomly selected plants were taken the average was computed while the traits days to 50 % flowering and days to 100 % maturity was taken from plot basis. Results revealed that the genotypes were grouped into 4 clusters where Cluster-I had fifteen genotypes and cluster II had three genotypes while one genotype each was present in cluster III and IV. The seed yield per plant contributed maximum towards genetic diversity (32.00 %) followed by plant height at maturity (14.00 %) and number of secondary branches (9.00 %). The maximum intra cluster distance was found in cluster II (164.691) indicating that the 15 genotypes including in the cluster II were most divergent. However, maximum inter cluster distance was noticed between cluster I and cluster II (313.247) which could be used in hybridizing program.

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1. INTRODUCTION

Chickpea (*Cicer arietinum* L. 2n=2x=16) is an important winter-season food legume having extensive geographical distribution and the third most important rabi food legume after dry beans and field pea [1]. Its nutritional value and ecological adaptability make it an important crop globally. A chickpea seed contains 17-24% proteins, 41- 51% carbohydrates and high percentage of other mineral nutrients and unsaturated linoleic and oleic acid and is one of the most important crops for human consumption [2]. India being the largest producer of chickpea, with about 8 million tons, accounting of about 70% of total world production is an important country to the contribution of pulse production world-wide [3].

There are mainly two types of chickpea i.e, Desi and Kabuli. The production is high in desi type around 80 percent and 20 percent in kabuli. Desi chickpea is mostly produced in countries like India, Pakistan, Myanmar, Australia, Bangladesh while kabuli chickpea is mostly produced in Iran, Mexico, Ethiopia, Turkey and Canada. In India area under chickpea was 94.85 lakh hectares with a production of 93.80 lakh tonnes and productivity of 979 kg/ha during 2017-2018, [4]**.** Limited or lack of genetic variability is one of the important factor for the limited progress achieved in increasing the productivity of grain legumes including chickpea [5]**.** Genetic divergence among the parents plays an important role in cultivar improvement which can be exploited for crop improvement [6]. The knowledge of genetic diversity has a significant impact on the improvement of crop plants and helps in genotype selection [7]**.** The use of diverse parents in hybridization helps in isolation of superior recombinants. [8]. Multivariate analysis through Mahalanobis statistics is an essential tool for variability at the genotype level and also in the selection of genetically diverse parents to acquire recombinants in the segregating generations.

2. MATERIALS AND METHODS

The germplasm was evaluated at the experimental field, Himgiri Zee University, Dehradun during Rabi 2019-20. Dehradun is located at the foot of the Himalayas and has an altitude of 960 meters (2100 ft) above sea level with 30.31° north latitude and 78.03° east longitude with annual average rainfall of 2073.3 mm mostly received during June to September. The annual average temperature of the study area is 20°C with maximum and minimum temperature of 27.8 ° C and 13.3 ° C respectively. The relative humidity is around 76 % and the soil type is classified as sandy loam soil with a pH of 7.20 and found under normal range. The experimental material consisted of 20 lines of chickpea (*Cicer arietinum* L.) which were obtained from IIPR, Kanpur, Uttar Pradesh and VNMKV, Prabhani, Maharashtra. The chickpea was grown in Randomized Block Design with three replicate with three rows of each entry and was planted at a row to row distance of 50 cm and plant to plant distance of 10cm. The sowing was done in the first week of December 2019. The recommended dose of nitrogen, phosphorus and potassium was applied @20kg/ha, 60kg/ha, 20kg/ha. Thimet 10-G was applied at the border of the field to prevent from entry of some predators like rabbit, rat etc. All the necessary agronomic practices were followed to raise a healthy crop. Five randomly selected plants from each plots were taken to record data on viz., number of primary branches, number of secondary branches, plant height (cm), number of pods per plants, 100 seed weight (g), seed yield per plant (g) and protein content (%), while days to 50% flowering, and days to maturity was taken in plot basis. Genetic divergence was estimated by using D2 statistics by [9] and grouping of the genotypes in different clusters were done by using Tocher's method [10]. The percent contribution of characters towards genetic divergence was calculated [11].

3. RESULTS AND DISCUSSION

The knowledge regarding the extent of variability and genetic diversity is of much importance while making improvement in a complex trait such as seed yield. In the present study, 20 genotypes were grouped into four clusters (Table 1). The clustering pattern could be utilized in hybridization program and deciding the cross combinations, which would generate the highest variability for various characters. The superior genotypes for breeding program could also be selected on the basis of cluster mean and inter cluster distance.

3.1 Composition of Clusters

The grouping of genotypes was carried out by following the Tochers method with the

assumption that the genotypes within the cluster have smaller D^2 values among themselves than those from genotypes belonging to different clusters. In all, 4 clusters were formed from 20 genotypes. The composition of clusters is given in Table 1. The cluster I was the largest cluster with 15 genotypes. Cluster II was the second largest with 3 genotypes. While Cluster III and Cluster IV comprised of one genotype each (i.e. Monogenic cluster). The mono genotypic cluster indicated that genotypes belonging to these clusters had wide diversity from the rest and as well as from each other. Genetic diversity studies

were earlier reported in chickpea [12]. Another study revealed from the study on 70 elite lines of desi chickpea, eleven clusters were formed [13]. Genetic divergence study in 25 genotypes of chickpea and grouped them into seven clusters using Tocher's method [14]. The clustering pattern indicated that the genetic diversity was not fully associated with geographical and genetic diversity. This could be due to other forces than geographical separation such as natural and artificial selection, exchange of breeding material genetic drift and environmental variation responsible for genetic diversity.

Table 1. Composition of D^2 clusters for chickpea genotypes

Cluster No	Genotypes	Number of genotypes
Cluster – I	ICCS-439, ICC-244263, ICC-5335, JG-16, JG-130,JG-3-14-16,JG-315, BG-212, GG-2, KWR-108, IPC-07-56, DCP-92-3, RUG-203, NBEG-47, SUBHRA	15
Cluster – II	VISHAL, VIRAT and VIJAY	03
Cluster – III	PKV-4	01
Cluster – IV	PKV-2	01

Table 2. Average inter and intra cluster values for chickpea genotypes

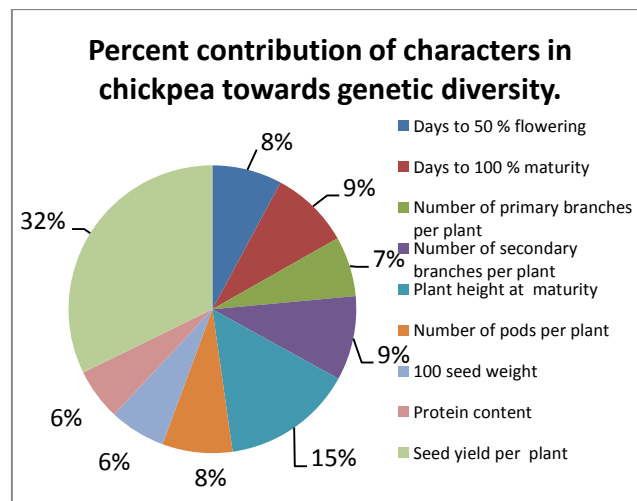| Clusters No	Cluster – I	Cluster –II	Cluster – III	Cluster – IV
Cluster – I	9763.707 (98.811)	98123.625 (313.247)	31292.396 (176.897)	138387.813 (372.005)
Cluster – II		27123.076 (164.691)	4638.352 (273.200)	19771.359 (140.611)
Cluster – III			0.000 (0.000)	122462.789 (349.947)
Cluster – IV				0.000 (0.000)

Fig. 1. Contribution of different characters towards genetic divergence of 20 chickpea genotypes for nine characters

Table 3. Cluster means of chickpea genotypes for various character

Clusters	Characters								
	Days to 50 % flowering	Days to 100 % maturity	Number of primary branches per plant	Number of secondary branches per plant	Plant height at maturity (cm)	Number of pods per plant	100 seed weight (g)	Protein content (%)	Seed yield per plant (g)
Cluster – I	92.841	142.847	2.540	9.001	51.558	54.863	24.869	19.847	8.631
Cluster – II	87.547	138.927	2.800	7.844	47.330	37.657	21.712	22.987	9.807
Cluster – III	82.413	134.183	3.160	7.080	49.440	58.330	12.960	23.503	8.600
Cluster – IV	87.187	139.980	2.407	7.200	44.890	25.377	14.000	21.310	8.730
Mean	87.497	138.984	2.726	7.781	48.304	44.056	18.385	21.911	8.942

Table 4. Percentage contribution of nine characters towards genetic divergence of 20 chickpea genotypes

S.No	Characters	Contribution (%)
1	**Days to 50 % flowering**	7.86
2	**Days to 100 % maturity**	8.93
3	**Number of primary branches per plant**	6.75
4	**Number of secondary branches per plant**	9.47
5	**Plant height at maturity**	14.74
6	**Number of pods per plant**	7.89
7	**100 seed weight**	6.32
8	**Protein content**	5.79
9	**Seed yield per plant**	32.25
Total		100

3.2 Inter and Intra Cluster Distances

The inter-cluster and intra cluster distances are shown in Table 2. The experimental results revealed that the inter cluster distance was greater than the average intra cluster distances, denoting wide genetic diversity among the genotypes of different groups. The intra cluster distance ranged from 9763.707 to 27123.076 respectively, remaining two clusters were recorded 0.00, which means mono-clustering among the genotypes. Cluster I indicated the minimum intra cluster distance (9763.707) and maximum intra cluster distance was indicated by cluster II (27123.07). The maximum inter cluster distance was found between cluster I and cluster IV (138387.813). Maximal inter cluster distance amidst two clusters indicates the maximal divergence amidst the clusters. By virtue of this, in the hybridization program the clusters I and II may be used because those clusters have a maximal inter cluster distance amidst two clusters indicates the maximum divergence amidst the clusters. The clustering pattern could be utilized in selection of parents for crossing and deciding the best cross combinations which may generate the highest possible variability for various traits. Genetic diversity studies in 60 chickpea genotypes was earlier conducted and found considerable inter cluster distances between Cluster III and IV [15].

3.3 Cluster means of Various Characters

The cluster mean values for 9 characters are presented in Table 3. Wide range of mean values among the clusters was recorded for different traits. Maximum cluster mean value was present for seed yield per plant in clusters II (9.80 g) followed by Cluster IV (8.73g). Cluster I exhibited highest means values for 100 seed weight (24.87 g), number of pods per plant (54.86), plant height (51.56 cm), number of secondary branches per plant (9.00), days to maturity (142.84) and days to 50 % flowering (92.84). Similar results were recorded earlier [16].

3.4 Characters Contribution towards Genetic Divergence

The analysis of variance for each character was carried out using mean of the 20 chickpea genotypes. Estimation of inter and intra cluster variance, along with ratio of inter cluster variance to the total variance (R^2) and inter cluster coefficient of variation (CV_b) for nine characters were worked out and presented in Table 4. The relative ranking of contribution of nine characters towards genetic divergence based on D^2 statistic revealed that seed yield per plant contributed maximum towards genetic diversity (32.25 %) followed by plant height at maturity (14.73 %), number of secondary branches (9.47 %), days to maturity (8.93 %) and number of pods per plant (7.89 %). Similar results were obtained by earlier workers [17].

4. CONCLUSION

In the present study, the genetic divergence was assessed by Mahalanobis D^2-statistic grouped 20 genotypes into four clusters. Maximum genetic divergence was observed between clusters I and IV. The characters seed yield per plant, plant height at maturity, number of secondary branches per plant, days to 100 % maturity and number of pods per plant contributed much to the total divergence. On the basis of cluster mean values, Cluster II (Vishal, Virat and Vijay) was superior for grain yield per plant, while cluster III (PKV-4) was good for protein content, number of pods per plant and primary branches and Cluster I (ICCS-439, ICC-244263, ICC-5335, JG-16, JG-130,JG-3-14-16,JG-315, BG-212, GG-2, KWR-108, IPC-07-56, DCP-92-3, RUG-203, NBEG-47, SUBHRA) was good for 100 seed weight. From the D^2 analysis of genetic diversity, based high yielding genotypes and large inter cluster distances, it is advisable to attempt crossing of the genotypes from cluster I and IV which may lead to broad spectrum of favorable genetic variability for yield improvement in chickpea.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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