

GENETIC DIVERSITY STUDIES IN CHICKPEA (*CICER ARIETINUM* L.) IN KOLHAPUR REGION OF MAHARASHTRA

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Abstract

Genetic diversity was assessed in 40 genotypes of chickpea using Mahalanobis's D^2 statistics. Ten quantitative characters including grain yield were considered for the study. D^2 values between all possible pairs of 40 genotypes ranged from 23.23 to 1654.86 and seven clusters were formed with cluster II accommodating maximum 23 genotypes followed by cluster I with 11 genotypes and cluster IV with 2 genotypes. However, the cluster III, V, VI and VII were mono-genotypic indicating wide divergence from other clusters. The character 100 seed weight was the maximum contributor towards divergence (61.54%) followed by number of pods/plant (15.00%), days to 50 per cent flowering and seed yield/plant (6.92%), number of secondary branches (4.23%), number of seeds/pod (2.18%), protein content (1.55%) and number of primary branches (0.64%). The days to maturity and height of the plant (0.51%) were the lowest contributor towards divergence. On the basis of inter cluster distances, cluster means, *per se* performance observed in the present study the six genotypes *viz.*, IC-83429, Vishal, Vijay, IC-83397, IC-83340 and IC-83523 were found to be superior genotypes for further breeding programme.

Introduction

Chickpea (*Cicer arietinum* L.) commonly known as Chana, Gram or Bengal gram. It belongs to the sub-family *Papilionaceae* of family *Leguminosae*, is an important and unique food legume. It is an important pulse crop of the world occupying third position amongst pulses.

Chickpea is a self-pollinated crop. Cross pollination is rare; only 0 - 1 per cent is reported. It is generally grown on heavy or red soils of pH 5.5 - 8.6. Frost, hailstones and excessive rains damage the crop. It is one of the most important *Rabi* pulse crops in Asia. India is largest producer (25%), importer (20%) and consumer (27%) of pulses in the world. In India the area under chickpea was 8.75 million ha. Production was 8.25 million tons and productivity 943 kg/ha.

The D^2 statistics is a tool which helps in the identifications of genetically divergent parents for their exploitation in hybridization programmes; as hybrids between lines of diverse origin display a greater heterosis than those between closely related strains. 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. The knowledge about the source of genetic diversity for the different characters is of considerable importance, since the prime aim of the plant breeder is to improve the yield and the quality by evolving superior varieties. An investigation into the nature and the degree of divergence is useful for an understanding of the course of evolution and for classifying population into groups on the basis of diversity, particularly, when they are overlapping for one or more characters.

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Materials and Methods

The experimental material comprising 40 genotypes were raised in randomized block design in three replications during *Rabi* 2013, at College of Agriculture, Kolhapur. Each entry was represented by a double row of 4.00 m length with a spacing of 30 cm between rows and 10 cm between plants within a row. Two grains were dibbled/hill to ensure better crop stand and a single seedling was kept/hill after thinning. Observations on following 10 quantitative characters were recorded on five randomly selected plants from each plot in each replication. These plants were tagged before flowering. The data were recorded on days to 50 per cent flowering, days to maturity, height of the plant (cm), number of primary branches, number of secondary branches, number of pods/plant, number of seeds/pod, 100 seed weight (g), seed yield/plant (g) and protein content (%). The analysis for divergence was done by following Mahalanobis (1936) D^2 statistic. Tocher's method as described by Rao (1952) was followed for cluster formation.

Results and Discussion

The analysis of variances revealed the presence of significant variability among chickpea genotypes. On the basis of Mahalanobis D^2 statistics and Tocher method the 40 chickpea genotypes were grouped into 7 clusters. Cluster I consisted of 11 accessions, cluster II consisted of 23 genotypes, cluster IV consisted of 2 genotypes and remaining clusters (III, V, VI and VII) were mono-genotypic (Table 1 and Fig. 1). The clustering pattern of the accessions showed that geographical diversity was not related with genetic diversity. Kumar (1997), Prakash (2006) and Thakur *et al.* (2009) reported that there is no association between genetic diversity and geographical diversity.

Table 1. Distribution of 40 genotypes of chickpea in to different clusters.

Cluster No.	Number of genotypes	Genotypes Included
I	11	IC-83343, IC-83353, IC-83428, IC-83443, IC-83319, IC-83486, IC-83345, IC-83327, IC-83415, IC-83348, IC-83452
II	23	IC-83346, IC-83565, IC-83466, IC-83367, IC-83563, IC-83374, IC-83329, IC-83411, IC-83357, IC-83370, IC-83338, IC-83435, IC-83406, IC-83383, IC-83368, IC-83335, IC-83372, IC-83523, IC-83510, IC-83360, IC-83391, IC-83465, IC-83321
III	1	IC-83524
IV	2	IC-83340, IC-83397
V	1	IC-83429
VI	1	Vijay
VII	1	Vishal

Intra-cluster distance was highest in cluster IV (44.62) and followed by cluster II (26.52) and cluster I (23.23). The intra cluster distance was not observed in cluster III, V, VI and VII as these clusters had only one genotype each (Table 2 and Fig. 2). These results are in general agreement with the findings of Lal *et al.* (2001), Harisatyanarayana and Reddy (2001), Nimbalkar and Harer (2001), Adhikari and Pandey (1983). The high intra cluster distance values revealed the presence of genetic diversity between the genotypes which were grouped together in those clusters. Hence, there is a lot of scope for exchange of genes among genotypes within these clusters. With regard to inter cluster distance the Cluster III and cluster VII were most diverse with each other as distance

between them was 1654.86. It can be inferred that crossing between these genotypes may result in good recombinants for successful breeding programme. As indicated by inter cluster D^2 values the cluster II and cluster III were closest (82.81) which revealed that those genotypes were not very distant but could not be grouped together based on these traits. Several authors have suggested that the crossing between the genotypes of clusters with high inter cluster would yield good segregates for selection.

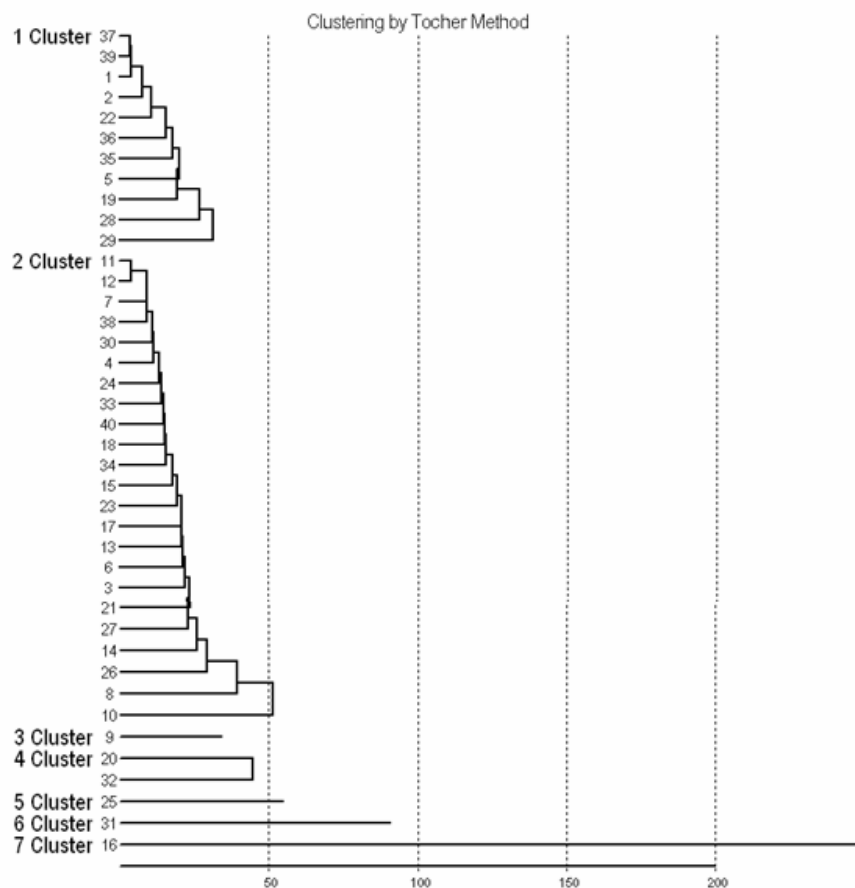


Fig. 1. Clustering of 40 genotypes of chickpea by Tocher method.

The best combination of parents for improvement in various characters can be recommended on the basis of *per se* performance of the genotypes and inter cluster divergence. Based on mean performance of 10 characters (Table 3), Cluster VI exhibited higher seed yield/plant (20.74 g). It contained one genotype, *viz.*, Vijay having medium maturity and height of the plant, higher number of pods/plant, highest number of primary branches and number of secondary branches.

Cluster III was found to be the least yielder. It comprised of single genotype, *viz.*, IC-83524 having very less number of primary branches and secondary branches and very low 100 seed weight. Per cent contribution of characters towards divergence was analysed and it was found that 100 seed weight contributed highest for divergence followed by number of pods/plant, days to 50 per cent flowering, seed yield/plant, number of secondary branches, number of seeds/pod, protein

content and number of primary branches. The traits days to maturity and height of the plant contributed least for genetic divergence (Table 4). Khan *et al.* (1987) observed that the characters like days to 50 per cent flowering, number of effective branches, seed size contributed more to divergence. Jethava *et al.* (1996) observed that the characters like seed yield/plant, number of pods/plant and 100 seed weight contributed to diversity. Samal *et al.* (1989) reported the contribution of 100 seed weight, seed yield/plant and days to 50 per cent flowering to the total divergence. Nimbalkar and Harer (2001) reported maximum genetic divergence due to plant height and 100 seed weight.

Table 2. Average intra and inter cluster D^2 and D (in parentheses) values of seven clusters formed from 40 genotypes of chickpea.

Clusters	I	II	III	IV	V	VI	VII
I	23.232 (4.82)	87.048 (9.33)	273.24 (16.53)	101.002 (10.05)	135.955 (11.66)	147.622 (12.15)	641.102 (25.32)
II		26.522 (5.15)	82.81 (9.10)	255.36 (15.98)	202.492 (14.23)	306.95 (17.52)	1085.043 (32.94)
III			0.000 (0.000)	523.036 (22.87)	379.860 (19.49)	582.739 (24.14)	1654.862 (40.68)
IV				44.622 (6.68)	295.496 (17.19)	128.368 (11.33)	406.022 (20.15)
V					0.000 (0.000)	137.827 (11.74)	691.164 (26.29)
VI						0.000 (0.000)	341.510 (18.48)
VII							0.000 (0.000)

Figures in the parentheses indicate 'D' values.

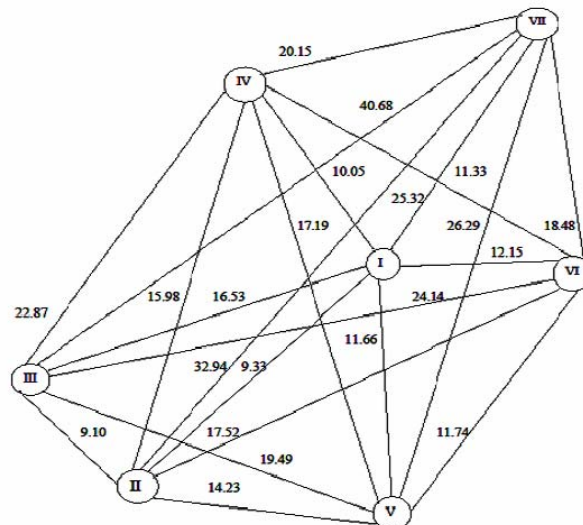


Fig. 2. Cluster diagram: Clusters and their interrelationships.

Table 3. Cluster means for different traits in chickpea.

Characters	Days to 50 per cent flowering	Days to maturity	Ht. of the plant (cm)	No. of primary branches	No. of secondary branches	No. of pods / plant	No. of seeds / pod	100- seeds weight (g)	Seed yield /plant (g)	Protein content (%)
I	57.94	113.12	43.47	3.99	11.45	61.33	1.33	15.42	8.63	21.12
II	64.29	114.62	41.97	3.81	12.19	53.58	1.45	11.53	7.37	21.05
III	77.33	116.00	43.07	3.53	12.73	51.87	1.33	7.61	5.59	19.08
IV	78.83	122.17	44.05	4.23	14.60	46.30	1.37	18.46	9.27	18.33
V	51.67	121.00	48.03	3.73	11.93	118.00	1.09	14.75	15.52	23.03
VI	66.00	118.33	46.97	4.73	17.73	76.13	1.12	17.65	20.74	19.34
VII	57.33	116.33	56.60	4.13	15.33	83.40	1.23	26.99	20.49	23.51
Population mean	64.77	117.37	46.31	4.02	13.71	70.09	1.27	16.06	12.51	20.78

Table 4. Per cent contribution of different characters to genetic diversity.

Sl. No.	Characters	No. of times appearing Ist in Ranking	Per cent contribution
1.	Days to 50% flowering	54	6.92
2.	Days to maturity	4	0.51
3.	Height of the plant	4	0.51
4.	No. of primary branches	5	0.64
5.	No. of secondary branches	33	4.23
6.	No. of pods/plant	117	15.00
7.	No. of seeds/pod	17	2.18
8.	100-seed weight	480	61.54
9.	Seed yield/plant	54	6.92
10.	Protein content	12	1.55
	Total	780	100.00

The D^2 analysis thus proved to be a very useful technique in isolating diverse groups from the germplasm under study. On the basis of inter cluster distances, cluster means, *per se* performance observed in the present study the six genotypes *viz.*, IC-83429, Vishal, Vijay, IC-83397, IC-83340 and IC-83523 were found to be superior and can be used as a potent parents for improvement of chickpea.

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