GENETIC DIVERGENCE ANALYSIS IN CHICKPEA (*CICER ARIETINUM* L.)

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Abstract: Genetic divergence analysis is a powerful tool in quantifying the degree of divergence between biological populations and to assess the relative contribution of different components to the total divergence. The present investigation aimed at ascertaining the nature and magnitude of genetic diversity among a set of chickpea genotypes. The genetic divergence were estimated in 30 elite genotypes for characters by using Mahalanobis D^2 statistic. The genotypes were grouped into four clusters. Cluster IV had maximum intra cluster distance while inter cluster distance was highest between clusters II and IV. Cluster means indicated that none of the clusters was superior for all characters studied. Therefore hybridization between genotypes belonging to different clusters is suggested for development of superior genotypes.

Keywords: D^2 static, Genetic divergence, Chickpea

INTRODUCTION

The genus *Cicer* consists of 43species, chickpea belonging to legume Family and highly self pollinated crop Chickpea is one of the earliest cultivated legumes crop (Redden and Berger 2007). According to Food and Agriculture Organization statistics (FAOSTAR 2001) the cultivated chickpea in India covering 10.4 million hectares and contributing 5.6 produces million tones. with the productivity of 808 kg per hectares (Anonymous, 2007). It is grown in Rabi season in irrigated as well as rainfed areas of the country. In India it occupied first rank of both in production and productivity among the pulse crops (FAO, 2008). Chickpea with 17-24% proteins, 41-50% carbohydrates and high percentage of other mineral nutrients and unsaturated fatty acids is one of the most important legumes crop for human consumption (Kerenetal 2007). Chickpea has high variation for different qualitative and quantitative traits *viz.* shape and color of grain, flower color, podding, color of seed coat, earliness resistance to insect and diseases. However, development of new varieties largely depends on the amount of genetic diversity in the germplasm. Success of the hybridization followed by selection depends largely on the selection of parents with high genetic diversity for traits of interest (Murthy and Arunachalon 1968). The importance of genetic diversity has been emphasized by several workers (Kumar and Arora 1992). The Analysis D^2 statistic (Mahalanobis 1936) is apowarful tool in the degree of divergence at genotypic level in respect of several traits considered together. Therefore an effort was mode to estimate the nature and magnitude of genetic diversity in a set of 30 elite genotypes of chickpea.

MATERIAL AND METHOD

The present investigations was conducted at Department of Crop Science, Mahatma Gandhi Chitrakoot Gramodaya Vishwavidyalaya, Chitrakoot, Satna (M.P.) during *Rabi* season of 2009-10. The experimental material comprised of 30 genotypes IC-12701, KAK-2, ICC-327344, ICC-484, EC-848098, IC-266738, ICC-5780, IC-269529, HC-5, ICC-5373, ICC-11316, DCP-92-3, ICC-10389, IC-327664, IC-424320, ICC-486, ICC-511, ICC-8933, ICC-10130, IC-424345, ICC-10459, ICC-14880, JG-63, ICC-5742, ICC-10819, ICC-485, ICCV-10, ICC-970, ICC-5337 and IC-424299. The experiment was laid out fallowing Randomized Block Design (RBD) with three replications during *Rabi* 2009-10. The experiment was shown on 20 October, 2009-10. Each treatment was grown in 3 meter long single row plot spaced 30 cm apart. The plant to plant distance was maintained 10 cm by thinning. The recommended agronomic practices and plant protection measures were adopted to raise a good crop. All the recommended cultural practices and plant protection measures were followed, data were recorded for eight quantitative characters *viz* Day to first flowering, Number of branches per plant, plant height (cm), Number of pods per plan, Number of seeds per pod, Days to 80 % maturity, Seed yield per plant(g), 100-seed weight, Observations were recorded for sow yield its camplet on five competitive plants in each genotype per replication and mean value plant basis were obtained. Were data used to carry out divergence analysis using Mahalanobis D2 statistic (1936) and the genotypes were grouped into different clusters as a described by Rao (1952).

Table 1. Distribution of 30 Chickpea genotypes in different clusters basis of D^2 statistic.

Cluster number	Number of genotypes	genotypes
I	**20**	IC-12701, ICC-485, EC-848098, ICC-5373, ICC-970, ICC-484, JG-63, ICC-10130, ICC-10389, IC-269529, ICC-5742, ICC-486, HC-5, ICC-511, DCP-92-3, ICC-5780, ICC-11316, ICCV-10, ICC-10459, ICC-8933,
II	**5**	KAK-2, IC-424320, ICC-5337, IC-424345, IC-266738,
III	**4**	ICC-327344, ICC-14880, ICC-10819, IC-424299.
IV	**1**	IC-327664,

Table 2. Intra and inter-cluster D2 d values among 4 clusters in chickpea

Cluster number	I	II	III	IV
I	**52.98 (7.28)**	574.61 (23.97)	175.03 (13.23)	166.62 (12.91)
II		**61.16 (7.82)**	157.96 (12.57)	689.29 (26.25)
III			**21.44 (4.63)**	280.52 (16.75)
IV				**0.00 (0.00)**

Table 3. Cluster means for eight quantitative characters in chickpea.

Cluster number	Day to first flowering	Number of branches per plant	plant height (cm)	Number of pods per plan	Number of seeds per pod	Days to 80 % maturity	Seed yield per plant(g)	100-seed weight (g)
I	59.48#	6.09	38.95	36.57	1.25	130.82#	6.26	15.83#
II	60.00	5.80	36.15#	28.56	1.04#	131.93	7.37+	26.73+
III	60.75	5.65#	36.40	26.27#	1.08	132.00	5.83#	21.42
IV	90.67+	7.47+	44.27+	37.63+	1.47+	134.00+	6.73	17.00

#, + indicates lowest and highest values, respectively

Table 3. Per cent character contribution in chickpea

characters	Day to first flowering	Number of branches per plant	plant height (cm)	Number of pods per plan	Number of seeds per pod	Days to 80 % maturity	Seed yield per plant(g)	100-seed weight (g)
Per cent contribution	15.63	0.00	0.69	1.84	2.53	0.69	1.61	77.01

RESULT AND DISCUSSION

The study of genetic divergence of 30 chickpea germplasm for eight quantitative characters was done through Mahalanobis's D^2 statistics as described by (Rao, 1952).The results have been described as under. Thirty chickpea genotypes were grouped in to four clusters (Table-1) Cluster I had highest number of genotypes (20) followed by cluster II and cluster III which had 5, and 4 genotypes, respectively. The genotypes IC-327664 could not be grouped together and formed separate cluster IV.

The intra and inter-cluster distance among different clusters are given in (Table-2)**.** The intra cluster D^2 values ranged from 0.00 (Cluster IV) to 61.16 (Cluster II). The inter-cluster D^2 value indicated that the most diverged clusters were II and IV followed by cluster I and II. The minimum inter- cluster values was between cluster II and III (157.96) followed by cluster I and IV (166.62) which indicated that these group were less diverged.

The mean performance of all the characters in different cluster is presented in (Table-3), Cluster IV showed high mean Variance for days to first flowering (90,67), number of branches per plant (7.47), plant height (44.27), number of pods per plant (37.63), number of seeds per pod (1.47) and days to 80% maturity (134.00). Cluster I had lower mean for days to first flowering (59.48), days to 80% maturity (130.82) and seed yield per plant (5.83) while cluster

III had lower mean for number of branches per plant, number of pods per plant and 100-seed weight. Cluster II had high mean for 100-seed weight (7.37) and seed yield per plant (26.73) while low mean for plant height (36.15) and number of seeds yield per (1.04).

The per cent character contribution ranged from 0.00 to 77.01 (Table-4)**.** The contribution of seed yield per plant (77.01%) and days to first flowering (15.63%) was highest whereas, the contribution of number of seeds per pod (2.53%), number of pods per plant (1.81%), 100-seed weight (1.61%), plant height and days to maturity (0.69%) was very low. Number of branches per plant contribution nothing towards genetic divergence.

The genotypes are the reservoir of genetic diversity, which is exploited to meet the changing needs for developing improved varieties of a crop. It is also important that considerable variability for economic traits must exist in the genotypes for profitable exploitation following recombination during of selection. The need of parental diversity in optimum magnitude to obtain superior genotypes for recovering transgressive segregates had also been repeatedly emphasized (Griffing and Lindstrom, 1954; Moll *et al.*, 1962; Arunachalam, 1981). Earlier workers considered distance in place of origin as index of genetic diversity and used it for selection of parents for hybridization. However, the genetic diversity of selection parents is not always based on factors such as geographic diversity/ place of release or ploidy level (murty and Arunachalam, 1966; Bhatt, 1970; Malhotra and Singh, 1971; Solh and Erskine, 1982; Balyan and Singh 1986; Gupta *et al*., 1996). Thus, for characterization of genotypes for genetic divergence selection, suitable and diverse genotypes should be based on sound statistical procedures, such as D^2 statistics and Non-hierarchical Euclidean cluster analysis. These procedures characterize genetic divergence using the criteria of similarity or dissimilarity based on the aggregate effect of a number of agronomically important characters.

The concept of D^2 introduced by Mahalanobis (1936) is neither restricted to population nor to the previously known population and the pattern obtained by D^2 analysis substantially changes with the addition of more characters. The technique is based on self-weighing on genetic variability (Rao, 1952). Obviously, among several techniques, Mahalanobis generalized distance has occupied a unique place in the plant breeding.

Earlier workers have also reported existence of high degree of genetic diversity in chickpea material evaluated by them (Narayana and Reddy 2001, Jeena and Arora 2002, Raval and Dobariya 2004, Jeena *et al.* 2005 and Gumber *et al.* 2006). Presence of substantial genetic divergence among the germplasm line screened in present investigation suggested that this material serve as good source for selecting the diverse parents for hybridization programme aimed at isolating desirable combination for seed yield as well as other characters.

An examination of clustering pattern of the 30 chickpea genotypes into 4 clusters revealed that genotypes of heterogeneous origin were frequently present in same clusters. Cluster I had highest number of genotypes (20) followed by cluster II and cluster III which had 5, and 4 genotypes, respectively. The genotypes IC-327664 could not be grouped together and formed separate cluster IV. The finding is in conformity with the previous reports advocating lack of parallelism between genetic and geographic diversity in chickpea (Shiv Kumar and Muthiah 2000, Nimbalkar and Harer 2001, Jeena and Arora 2002, Raval and Dobariya 2004, Srivastava *et al*. 2005 and Gumber *et al*. 2006).

The intra cluster D^2 values ranged from 0.00 (cluster IV) to 61.16 (cluster II). The inter cluster D^2 value indicated that most diverged cluster were II and IV (689.29) followed by Cluster I and II (574.61). The minimum inter-cluster values was between cluster III and II (157.96) followed by Cluster I and IV (166.62) which indicated that these group were less diverse.

The mean performance of all the characters in different cluster is presented in (Table -3) Cluster IV showed high mean for days to first flowering (90.67), number of branches per plant (7.47), plant height (44.27), number of pods per plant (37.63), number of seeds per pod (1.47) and days to 80% maturity (134.00). Cluster I had lower mean for days to first flowering (59.48), days to 80% maturity and seed yield per plant (15.83) while, cluster III had lower mean for number of branches per plant, number of pods per plant and 100-seed weight. Cluster II had high mean for 100-seed weight (7.37) and seed yield per plant (26.73) while low mean for plant height (36.15) and number of seeds per pod (1.04).

Per cent character contribution ranged from 0.00 to 77.01 (Table-4). The contribution of seed yield per plant (77.01%) and days to first flowering (15.63%) was highest whereas, the contribution of number of seeds per pod (2.53%), number of pods per plant (1.84%), 100-seed weight (1.61%), plant height and days to 80% maturity (0.69%) was very low. Number of branches per plant contributed nothing towards genetic divergence.

The genotypes included in the same cluster with minimum intra-cluster distances may not necessarily closely relate. Similarly, the cluster with maximum intra-cluster distances also. Although, the genotypes included in a cluster with minimum intra-cluster distance would mean comparatively more morphological similarity. During the present study it was noticed that reliable information about diversity will be available in a rich and productive environment for fullest expression of genotypes for most of the characters It has also been suggested by several workers (Patel *et al*. 2006) that reliable

information about diversity will be available in a rich and productive environment. An examination of the estimate within and between clusters, genetic diversity revealed that the genotypes of the same cluster had little divergence from each other with respect to the aggregate effect of the character studied. The hybridization between the genotypes of the same cluster thus, may not provide good segregants. The crosses may be attempted between the genotypes of the cluster separated by large inter-cluster distance (Table-4). This can give desirable transgressive segregants.

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