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Mayuriben R Tamvar

PG Student, Dept. of Genetics & Plant Breeding, NMCA, NAU, Navsari, Gujarat, India

Sunayan R Patel

Associate Professor, College of Agriculture, Navsari Agricultural University, Bharuch, Gujarat, India

Sunil S Patil

Assistant Professor, College of Agriculture, Navsari Agricultural University, Bharuch, Gujarat, India

Arpan J Naik

Assistant Professor, College of Agriculture, Parul University, Vadodara, Gujarat, India

Harshad N Patel

Associate Professor, College of Agriculture, Navsari Agricultural University, Bharuch, Gujarat, India

Correspondence

Sunil S Patil

Assistant Professor, College of Agriculture, Navsari Agricultural University, Bharuch, Gujarat, India

Diversity study through D² analysis in Chickpea

Mayuriben R Tamvar, Sunayan R Patel, Sunil S Patil, Arpan J Naik and Harshad N Patel

Abstract

A field experiment was conducted during *rabi* 2018 for study of genetic diversity in 60 different genotypes of chickpea using D² statistics method of Mahalanobis (1936) [6]. The 60 genotypes of chickpea were grouped into five clusters suggested the presence of wide genetic diversity among them. The clustering pattern of the genotypes was independent of their geographical distribution. Among different twelve traits studied, protein content, 100-seed weight, number of secondary branches per plant, seed yield per plant, height at first pod, seed volume per weight, days to 50% flowering and number of primary branches per plant contributed very much towards genetic divergence. Based on inter-cluster distance, clusters III and IV followed by IV and V, and II and IV had maximum inter-cluster distance. Therefore, it is concluded that the genotypes belonging to these clusters should be inter-crossed in order to generate more variability and improving seed yield in chickpea.

Keywords: Genetic diversity, D² statistics, cluster analysis, chickpea

Introduction

Chickpea [*Cicer arietinum* L.] (2n=2x=16) is one of the important pulse crop grown during cool season in Asia. It is a self-fertilizing annual grain legume of the family Fabaceae, subfamily Faboideae. It is also known as Gram, Bengal gram, Garbanzo bean, and Egyptian pea. Chickpea is a highly nutritious pulse crop and places second in the importance list of the food legumes that are cultivated throughout the world. Chickpea seeds contain on an average 23% protein, 64% total carbohydrates (47% starch, 6% soluble sugar), 5% fat, 6% crude fiber and 2% ash. It is also reported to contain high mineral content: phosphorus (340 mg/100 g), calcium (190 mg/100 g), magnesium (140 mg/100 g), iron (7 mg/100 g), zinc (3 mg/100 g) by Jukanti *et al.* (2012) [4]. It also plays important role in low input and rainfed agriculture by fixing atmospheric nitrogen. Young plants and pods are eaten like spinach. The green seeds are cooked as a vegetable, mature seeds are used as dry pulse, parched boiled, fried or in various dishes, dhal is the split chickpea seed without the coat and is eaten cooked in thick soup. The flour, known as *besan* is used in many curry products, sweets and ceremonial dishes.

Plant breeders are always fascinated to assess the genetic diversity among the germplasm, varieties or advance breeding material available with them so as to employ them in direct breeding programme because (i) genetically diverse parents are likely to produce high heterotic effects and (ii) the distantly related parents within the same species when utilized in cross breeding programme are likely to produce wider spectrum of variability. A method advised by Mahalanobis (1936) [6] known as "Mahalanobis D² statistics" which is used to know genetic diversity in the available germplasm. This technique measures the force of differentiation at intra cluster and inters cluster levels and thus help in the selection of genetically divergent parents for their exploitation in hybridization programme. The D² statistics also measure the degree of diversification and determines the relative proportion of each component character to the total divergence.

To a plant breeder, single character is not of so much importance as the combined merit of a number of desirable traits become more important when he is concerned with a complex trait like yield. So, for improving yield, selection of parents based on a number of characters having quantitative divergence is required which can have fulfilled by D² statistic developed by Mahalanobis (1936) [6].

Materials and Methods

Description of the study area

The field experiment was conducted at Pulses and Castor Research Station, Navsari Agricultural

University, Navsari during *rabi* season of the year 2018. The place is located 12 km away in the east from the great historical place "Dandi" on the Arabian seashore. Geographically, it is situated at 20°-57'N latitude and 72°-54'E longitude with an elevation of 10.0 meter above mean sea level on the western coastal belt of India. For this study, sixty genotypes of chickpea obtained from Pulses and Castor Research Station, NAU, Navsari (Table 1.) were used. The experiment was laid out in Randomized Block Design (RBD) with three replications. A spacing of 45 cm between rows and 10 cm between plants within the row was maintained. For each genotype five randomly taken plants in each replication were used to record data on number of primary branches per plant, number of secondary branches per plant, pods per plant, plant height (cm), height at first pod (cm), seed yield per plant (g), 100-seed weight (g), seed volume per weight (ml/g), harvest index (%), protein content (%). Days to flowering and days to maturity were recorded on plot basis.

Data analysis

The genetic divergence in sixty genotypes for twelve characters was estimated by using D² analysis given by Mahalanobis (1928) [5]. Grouping of the genotypes into different clusters was done by using Ward's minimum variance method as described by Rao (1952) [9]. For the measurement of intra-cluster distances, sum of distances between all possible combinations of the populations included in a cluster divided by number of cluster was opted. Whereas, for measurement of average inter-cluster distance, clusters were taken one by one and their distances from other clusters were calculated. The distance between two clusters was the sum of D² values between the members of one cluster to each of the members of the other cluster divided by the product of a number of genotypes in both the clusters under consideration. Thereafter, based on D² values (inter-cluster

distance) the scale given by Rao (1952) [9] for a rating of the distance was adopted and the cluster diagram was prepared. Contribution of individual characters towards divergence based on the number of cases where a particular character ranked first, the proportion of this to the total number of combinations expressed in percentage was quantified.

Results and Discussion

The analysis of variance revealed significant differences among the genotypes for all the characters under study *viz.*, days to flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, pods per plant, plant height (cm), height at first pod (cm), seed yield per plant (g), 100-seed weight (g), seed volume per weight (ml/g), harvest index (%), protein content (%) which indicated the existence of variability in the experimental material.

Composition of clusters

Grouping of the genotypes was carried-out by Tocher's method as per suggested by Rao, 1952 Table 1. In all, five clusters were formed from sixty genotypes. The results indicate that a maximum number of diverse genotypes (41 genotypes) appeared in cluster I followed by cluster III (8 genotypes), cluster II, IV and I had 6, 4 and 1 genotypes respectively. The pattern of grouping genotypes in different cluster proved that geographical distribution and genetic divergence did not follow the same pattern and the existence of significant amount of variability. These findings are confirmed by earlier reports of Ram and Trivedi (1991) [8], Biswas *et al.* (1993) [2] and Sreedher *et al.* (2006) [13]. Therefore, it can be concluded that the selection of parents for hybridization should not be based on geographical diversity only, but it should have a base of both geographical origin as well as genetic divergence.

Table 1: Distribution of sixty genotypes of chickpea into seven different clusters on the basis of Mahalanobis D² statistics.

Clusters	No. of genotypes	Genotypes
I	41	NGD-1651, NGD-1652, NGD-1654, NGD-1655, NGD-1657, NGD-1658, NGD-1661, NGDE-1666, NGDE-1667, NGDE-1668, NGDE-1670, NGDE-1673, NGDE-1676, GG-1, GG-6, Dahod Yellow, NG-139, NG-367, NG-461, NG-9, NG-22, NG-24, NG-55, NG-66, NG-71, NG-72, NG-73, NG-74, NG-165, NG-191, NG-206, NG-223, NG-230, NG-305, NG-365, NG-366, NG-493, NG-495, NG-496, NG-94, NG-96
II	6	NGD-1664, NGDE-1665, NGDE-1669, NGDE-1674, NGDE-1678, NGDE-1680
III	8	NGD-1656, NGDE-1675, NGDE-1677, NGDE-1681, NGDE-1682, GG-3, NG-52, NG-113
IV	4	NGD-1663, NGDE-1684, GG-2, GG-5
V	1	NG-323

Intra and inter cluster distances

The intra and inter cluster distances D² between all possible pairs of five clusters were computed and presented in table 2 and depicted in figure 1. The clustering pattern showed that varieties from different source were clubbed into one group and also varieties of same source forming different cluster indicated no relationship between geographical and genetic divergence. The maximum inter-cluster distance (D=66.16) was found between clusters III and IV carrying 8 and 4 genotypes followed by IV and V (D=52.53), and II and IV (D=40.51) indicating that genotypes included in these clusters are genetically diverse and may give rise to high heterotic response. The minimum inter-cluster distance was (D=22.88) found between clusters I and II indicating a close relationship among the genotypes included in these clusters. The lowest intra-cluster distance was in cluster V (D=0.00) indicating that genotypes within this cluster were similar. Whereas, the

highest intra-cluster distance was in cluster IV (D=25.12). In present study, intra-cluster distance values were lower than the inter-cluster distances which indicated substantial diversity present among the genotypes studied. Therefore, for getting more heterotic combination and most promising segregants in segregating generations, selection of genotypes should be from between cluster possessing maximum genetic divergence.

Table 2: Average intra and inter-cluster (D²) values for 60 genotypes of chickpea.

Clusters	I	II	III	IV	V
I	16.93	22.88	34.11	31.82	23.61
II		15.64	33.77	40.51	38.97
III			19.03	66.16	39.77
IV				25.12	52.53
V					0.00

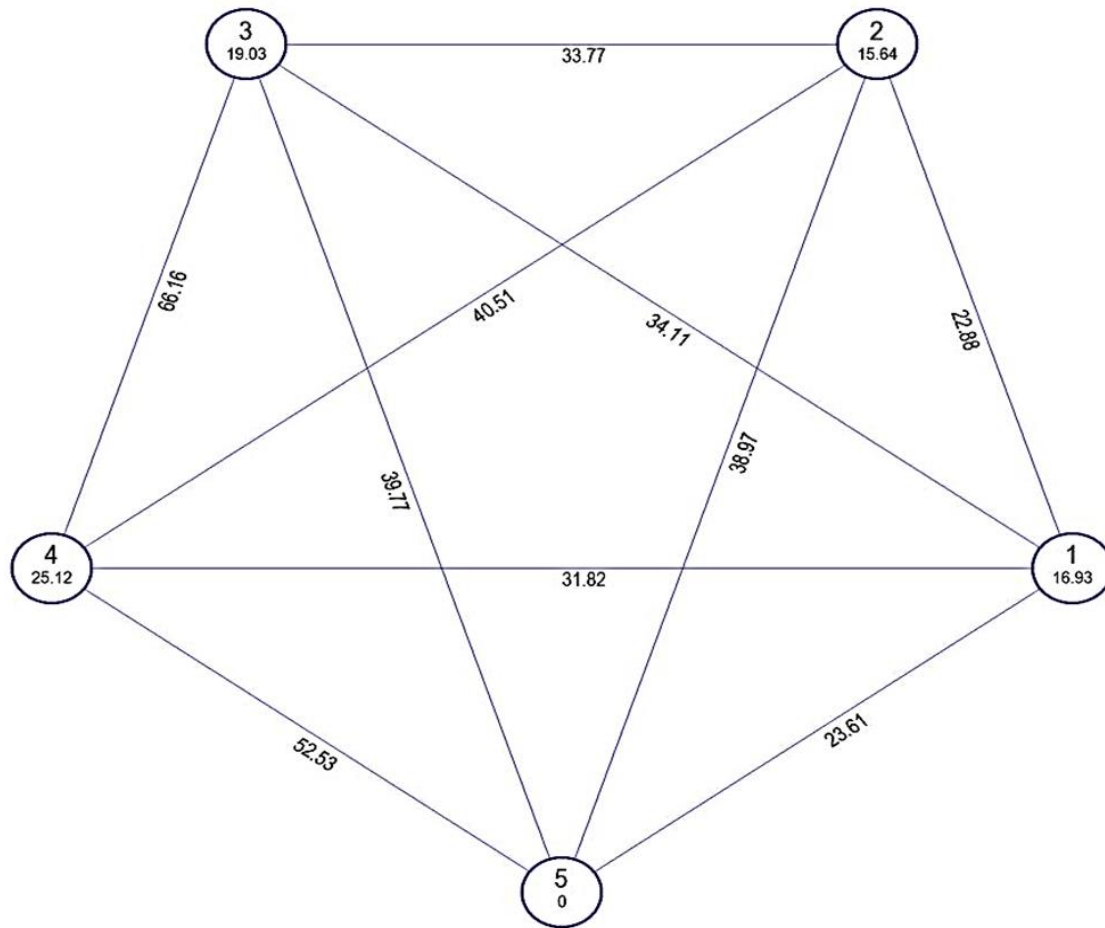


Fig 1: Cluster diagram of 60 genotypes of chickpea

Contribution of various characters towards genetic divergence

The utility of D² analysis is enhanced by its application to estimates the relative contribution of various characters to genetic divergence. The contribution of each character towards total genetic diversity is presented in table 3. The present study revealed that, the characters protein content (36.95 %), 100-seed weight (19.72 %), number of secondary branches per plant (14.18 %), seed yield per plant (9.83 %), height at first pod (9.6 %), seed volume per weight (4.24 %), days to 50 % flowering (2.2 %), number of primary branches

per plant (1.19 %), days to maturity (0.85 %), plant height (0.79 %), pods per plant (0.4 %) and harvest index (0.06) contributed very much towards genetic divergence. Therefore, selection for such traits may give more emphasis hybridization programme to generate large variability and will provide immense scope for the improvement of yield through selection. This type of result were also reported by Jakhar *et al.* (2016) [3] Vijayakumar *et al.* (2017) [15], Saha *et al.* (2018) [10], Shivwanshi and Babbar (2018) [12], Thakur *et al.* (2018) [14] and Vishnu *et al.* (2018) [16].

Table 3: Contribution of twelve characters under study towards total genetic divergence

Sr. No.	Characters	Number of times appearing 1 st in rank	% contribution towards divergence
1	Days to 50 % flowering	39	2.2 %
2	Days to maturity	15	0.85 %
3	No. of primary branches/plant	21	1.19 %
4	No. of secondary branches/plant	251	14.18 %
5	Pods/plant	7	0.4 %
6	Plant height (cm)	14	0.79 %
7	Height at first pod (cm)	170	9.6 %
8	Seed yield per plant (g)	174	9.83 %
9	100-seed weight (g)	349	19.72 %
10	Seed volume per weight	75	4.24 %
11	Harvest index (%)	1	0.06%
12	Protein content (%)	654	36.95%

Cluster means for various characters

The mean performance of cluster values for all characters is presented in table 4. The results clearly indicated appreciable difference among cluster means for most of the characters. As

far as cluster means are concerned, a greater range of mean values among the clusters was recorded for different traits. Based on the mean value of days to flowering and days to maturity genotypes of cluster IV and cluster V, respectively,

proved to be early while, for yield and yield contributing characters like pods/plant, plant height, seed volume/weight, seed yield per plant, number of primary and secondary branches genotypes of cluster IV and cluster V found superior. The cluster II had high mean values for 100-seed weight (31.94) and harvest index (50.08). The cluster III had high mean values for protein content (21.12). Therefore, it is suggested that parent selected for hybridization among the genotypes of above said clusters would produce high heterosis and segregants for more than one economic character. The potential lines are identified from different clusters and used as parents in a hybridization programme. The choice of genotype should be based on genetic distance and depending upon the objective of the breeding programme. Similar finding reported by Agrawal *et al.* (2018) ^[1], Saha *et al.* (2018) ^[10], Sharifi *et al.* (2018) ^[11], Shivwanshi and Babbar

(2018) ^[12].

It could be concluded that high yielding genotypes coupled with other desirable physiological traits like days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, pods per plant, plant height, height at first pod, 100-seed weight, seed volume per weight, harvest index, protein content and seed yield per plant could be selected as parents for hybridization programme from clusters IV, V, II and III. Intercrossing genotypes from these clusters might result in a wide array of variability for exercising effective selection. Patil (2007) ^[7] also indicated that intercrossing genotypes from these clusters might results in hybrids having high vigour and may further results in a wide array of genetic variability for exercising effective selection.

Table 4: Cluster means for twelve characters in sixty chickpea genotypes

Characters	Clusters				
	I	II	III	IV	V
Days to 50 % flowering	79.20	81.28	76.96	74.50	80.00
Days to maturity	106.03	102.89	106.71	110.42	75.33
No. of primary branches / plant	2.24	2.16	2.17	2.03	2.40
No. of secondary branches / plant	10.33	5.88	8.98	9.43	13.87
Pods/plant	28.03	24.58	29.67	36.38	30.00
Plant height (cm)	41.86	35.09	40.85	42.64	39.23
Height at first pod (cm)	18.04	15.13	17.96	15.16	19.67
Seed yield per plant (g)	11.22	9.78	12.50	15.71	11.49
100-seed weight (g)	25.23	31.94	28.48	22.46	17.37
Seed volume per weight (ml/g)	80.66	81.97	81.83	71.90	89.47
Harvest index (%)	45.39	50.08	42.04	42.51	49.20
Protein content (%)	18.32	18.05	21.12	16.88	18.92

Note: Bold figures are minimum and maximum values.

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