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Original Research Article

Genetic Diversity Analysis in Chickpea (*Cicer arietinum* L.)

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Keywords

Chickpea, Cluster analysis, D^2 statistics, Inter cluster distance and Intra cluster distance

A B S T R A C T

Genetic diversity study was conducted in 100 promising chickpea (*Cicer arietinum* L.) genotypes using Mahalanobis D^2 Statistics. Based on D^2 values, 100 genotypes were grouped into twelve clusters. The cluster I consisted of maximum 49 genotypes, followed by Cluster III, cluster VII and cluster IX, which had 16, 12 and 12 genotypes, respectively. The maximum intra cluster distance was found in cluster IX (7.72) followed by cluster VIII (6.65), VII (6.52), cluster III (6.14) and cluster I (5.46). Inter cluster values varied from 2.75 to 14.95. However, maximum inter cluster distance was noticed between cluster VII and cluster X (14.95), followed by cluster XI and cluster XII (14.08), cluster VI and cluster XI (13.43) and cluster II and cluster XI (13.22). whereas, days to 50 % flowering (22.89 %) followed by 100 seed weight (21.29 %), total number of seeds per plant (14.16 %) and plant height (13.80 %) contributed maximum towards diversity. Based on inter cluster distances and *Per se* performance PG 0749, BCG 79, ICC 5003, ICC 1058, HK 06-171 and PKV KABULI 4 were identified for inclusion in hybridization programme for realizing desirable transgressive segregates.

Introduction

Chickpea (*Cicer arietinum* L.) is an important winter-season food legume having extensive geographical distribution. It's nutritional value and ecological adaptability make it an important crop globally. A chickpea seed contains 17-24% proteins, 41-50.8% 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 (Farshadfar and Farshadfar, 2008). It makes up the deficiency of cereal diets. India is the largest producer, with about 8 million tons, accounting of about 70% of total world production. In Maharashtra, production of 1058 thousand tones were recorded with productivity of 844 kg/ha on area of 1314 thousand hectares. Maharashtra is the second largest producing state in the country after Madhya Pradesh with share of 14% (www.mahaagri.gov.in, 2015). However; its productivity is less as compared to that in other countries due to cultivation of chickpea on marginal lands. Limited or lack of genetic variability is important factor for the limited progress achieved in increasing the productivity of grain legumes including schickpea (Ramanujam, 1975). Genetic diversity is the base for survival of plants in nature and for crop improvement. Genetic divergence among the parents plays a vital role in cultivar improvement due to more

variability in segregating generations, which can be exploited for improvement (Nimbalkar *et al.,* 2017). Inclusion of diverse parents in hybridization helps in isolation of superior recombinants. Mahalanobis's D^2 statistics is a powerful tool in quantifying the degree of variability at the genotype level. The utility of multivariate analysis has greatly been emphasized (Murty and Arunachalam, 1966). Several workers studied the genetic diversity, clustering pattern, relative contribution of different characters towards divergence and effectiveness of selection (Venkateswarlu, 2001; Manivannan *et al.*, 2002; Bisht *et al.*, 2005). The present study aims to find out the genetic diversity among 100 promising chickpea genotypes.

Materials and Methods

The experimental material comprising 100 genotypes of chickpea including 75 desi and 25 kabuli, were grown during *Rabi* 2016-2017 in a Randomized Complete Block Design with two replications at the Experimental Farm, Department of Genetics and Plant Breeding, College of Agriculture, Latur. Data were recorded on five randomly tagged plants for days to 50% flowering, days to maturity, plant height (cm), number of primary branches, number of secondary branches, total pods plant^{-1}, total number of seeds plant^{-1}, 100 seed weight (g), seed yield plant^{-1} (g), and harvest index (%).

Data were calculated by Mahalanobis D^2 statistics (1936) and the genotypes were grouped into different clusters according to Tocher's method as described by Rao (1952). Contribution of individual characters towards divergence was estimated according to the method described by Singh and Choudhary (1979). Grouping of variety into various clusters was done and average intra and inter cluster distance were estimated.

Results and Discussion

Based on the D^2 values the 100 genotypes were grouped into twelve clusters (Table 1 and Fig. 1) which revealed that the genotypes varied significantly for all the characters studied indicating considerable variable in the germplasm. Cluster I consist of maximum 49 genotypes, followed by cluster III, cluster VII, cluster IX which had 16, 12 and 12 genotypes, respectively, while remaining all clusters possessed one genotype in each except cluster VIII which had 4 genotypes. Cluster I consisted maximum forty-nine genotypes indicating that the genotypes had narrow genetic divergent among them. The similarity in the base population, from which they had been evolved, might be the cause of genetic uniformity. However, the unidirectional selection potential for one particular trait or a group of linked traits in several places may produce similar phenotypes which can be aggregated into one cluster irrespective of their geographic origin (Joshi *et al.*, 2006 and Parashi *et al.*, 2013). The intra cluster distance ranged from 0.00 to 7.72 (Table 2). The maximum intra cluster distance was found in cluster IX (7.72) followed by cluster VIII (6.65), VII (6.52), cluster III (6.14) and cluster I (5.46) indicating that the 12 genotypes including checks, Virat and BDNGK 797 in the cluster IX were most divergent. However, maximum inter cluster distance was noticed between cluster VII and cluster X (14.95), followed by cluster XI and cluster XII (14.08), cluster VI and cluster XI (13.43) and cluster II and cluster XI (13.22) indicating that these clusters are quite divergent from each other and the genotypes belonging to them can be used for hybridization programme as crosses between genotypes belonging to the clusters with maximum inter cluster distance, may give high heterotic response resulting in better recombinants.

Table.1 Grouping of 100 chickpea genotypes into 12 clusters by Tocher's method

Cluster No.	Number of Genotypes	Genotypes
I	49	PBC 1103-2, BCG 54-1, BCG 10-11, GJG 0906, GNG 2058, G 84, GJG 0814, Digvijay, B 45, ICC 5034, ICC 1142, B 49, G 57, ICC 7117, B 24, BCG 902, BCG 78, BCG 36, BCG 1917, IC 22, BCG 85, PKV Kabuli 2, PBC 37-1, ICC 110, ICC 1696, ICC 85, ICC 2444, BCG 1316, BCG 2023, GNG 0904, GCP 101, GJ 25, BDNG 797, ICC 45033, ICC 12654, Vijay, BCG 10-4, RSG 143-1, PBC 1103-1, ICC 867, BCG 64, RVSGS 11, ICC 101, PG 12310, ICC 4958, ICC 117, IPCK 08-130, ICC 111 and ICC 15105.
II	1	HK 08-206.
III	16	G 97, B 768, ICC 113, ICC 0918, ICC 11027, NO. 115, G 45, IPCK 0762, ICC 104, RKG 153, JS 06, BCG 75, ICC 303, JGK 1, G 94 and PG 09305.
IV	1	BDNGK 807.
V	1	BGC 10-1.
VI	1	PG 0749.
VII	12	GNG 2064, B 611, PBC 37-2, BCG 79, BGD 1070, G 87, GK 23, ICC 5003, HK 06-171, ICC 1058, HK 06-163 and ICC 1433.
VIII	4	ICC 33103, ICC 33229, PKV Kabuli 4 and JG 23.
IX	12	JG 11, Green Chana, ICC 932, Virat, ICC 8111, ICC 13812, IC 261, ICC 16-348, ICC 11775, ICC 107, BCG 15-44 and BDNG 798.
X	1	G 20.
XI	1	ICC 14346.
XII	1	ICC 14333.

Table.2 Average intra and inter cluster D^2 and D value of 12 clusters from 100 chickpea genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	29.81 (5.46)	48.30 (6.95)	50.97 (7.14)	43.69 (6.61)	51.12 (7.15)	52.70 (7.26)	61.51 (7.82)	55.95 (7.48)	66.26 (8.14)	109.41 (10.46)	87.04 (9.33)	70.39 (8.39)
II		00.00 (0.00)	67.24 (8.20)	25.70 (5.07)	121.22 (11.01)	7.56 (2.75)	87.98 (9.38)	33.87 (5.82)	107.32 (10.36)	122.32 (11.06)	174.76 (13.22)	77.79 (8.82)
III			37.69 (6.14)	74.47 (8.63)	81.72 (9.04)	87.98 (9.38)	110.25 (10.50)	72.93 (8.54)	107.32 (10.36)	67.89 (8.24)	88.17 (9.39)	81.72 (9.04)
IV				00.00 (0.00)	94.09 (9.70)	31.13 (5.58)	85.19 (9.23)	65.12 (8.07)	76.56 (8.75)	109.62 (10.47)	159.51 (12.63)	61.46 (7.84)
V					00.00 (0.00)	120.56 (10.98)	78.67 (8.87)	129.96 (11.40)	48.86 (6.99)	117.28 (10.83)	62.25 (7.89)	83.35 (9.13)
VI						00.00 (0.00)	86.86 (9.32)	40.57 (6.37)	94.28 (9.71)	147.13 (12.13)	180.36 (13.43)	84.82 (9.21)
VII							42.51 (6.52)	85.37 (9.24)	107.32 (10.36)	223.50 (14.95)	153.76 (12.40)	96.62 (9.83)
VIII								44.22 (6.65)	128.14 (11.32)	165.89 (12.88)	143.28 (11.97)	117.28 (10.83)
IX									59.59 (7.72)	131.56 (11.47)	101.40 (10.07)	101.60 (10.08)
X										00.00 (0.00)	132.25 (11.50)	93.50 (9.67)
XI											00.00 (0.00)	198.24 (14.08)
XII												00.00 (0.00)

Table.3 Percent contribution of 10 characters for diversity in chickpea

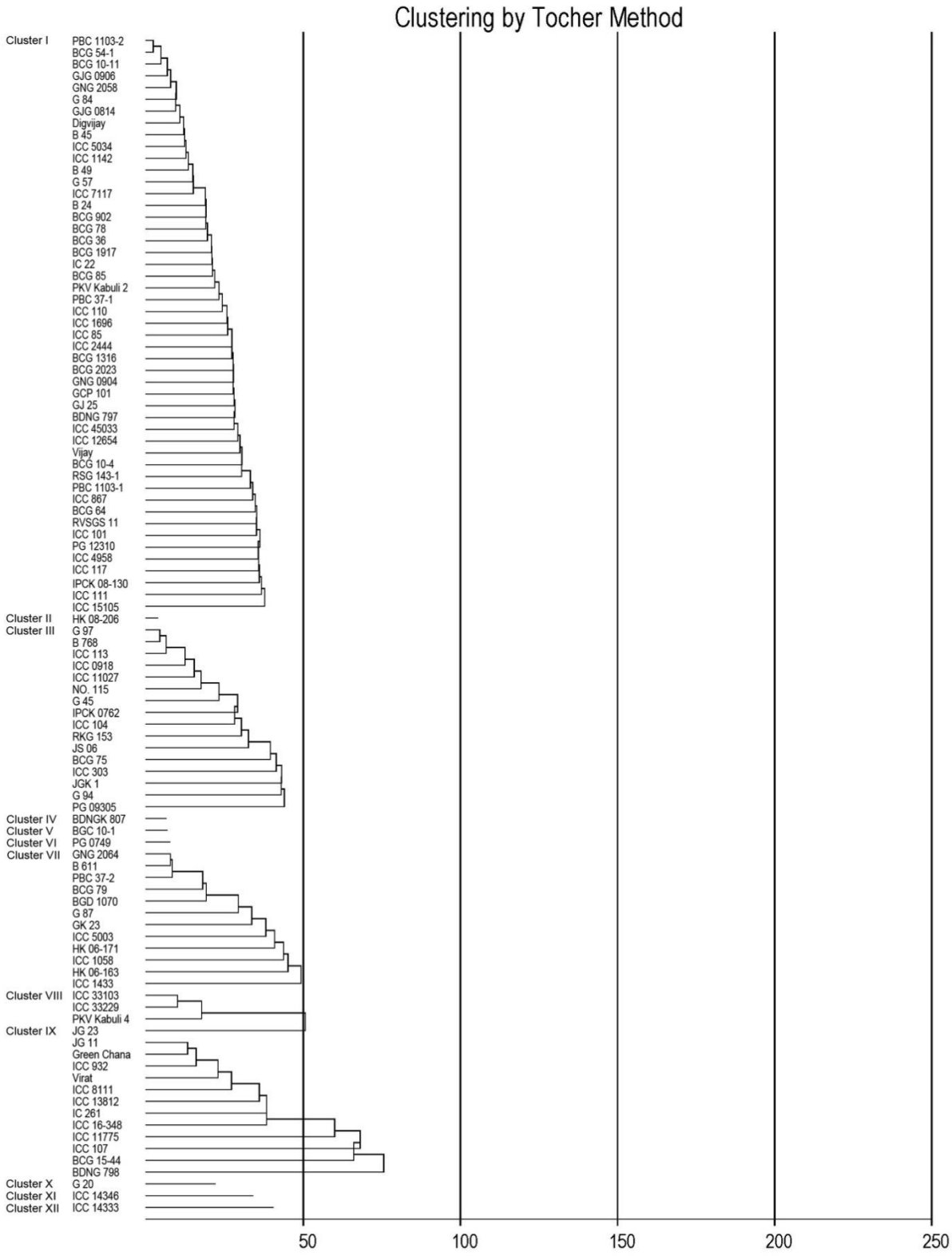
Sr. No.	Characters	Times ranked 1st	Contribution (%)
1	Days to 50% flowering	1133	22.89
2	Days to maturity	157	3.17 %
3	Plant height (cm)	683	13.80
4	No. of primary branches	182	3.68
5	No. of secondary branches	471	9.52
6	No. of pods per plant	504	10.18
7	Total number of seeds per plant	701	14.16
8	Test weight (gm)	1054	21.29
9	Harvest index (%)	20	0.40
10	Seed yield per plant (gm)	45	0.91
	Total	4950	100

Table.4 Cluster mean performance for 10 characters of 100 chickpea genotypes

Clusters	DF	DM	PH	NPB	NSB	NPP	TNSP	TW	HI	SYP
I	46.94	107.10	46.62	3.20	6.05	30.76	31.24	26.29	50.78	8.20
II	44.50	105.50	40.79	3.30	8.70	28.13	29.03	43.50	56.37	11.93
III	42.16	105.53	40.93	2.62	4.18	23.17	22.29	25.53	48.88	5.88
IV	45.00	110.50	39.44	3.10	9.40	44.50	39.50	33.50	59.16	12.91
V	48.00	103.50	49.90	2.50	6.90	31.00	37.60	8.50	47.50	3.40
VI	46.00	107.00	42.50	4.00	9.20	28.75	34.80	43.50	52.58	12.80
VII	58.46	110.21	49.22	3.35	5.97	31.22	30.14	26.33	49.38	7.52
VIII	45.75	107.88	49.63	3.57	5.77	23.94	23.03	41.75	50.39	10.54
IX	45.71	105.71	46.33	3.67	7.53	38.63	45.70	18.42	46.59	7.73
X	33.00	101.00	26.40	2.80	5.90	26.25	28.74	17.00	51.09	4.30
XI	39.00	100.00	58.00	2.90	0.00	30.50	33.71	15.50	38.74	4.10
XII	51.50	112.50	28.36	3.64	10.41	28.63	27.37	16.50	42.07	4.15

DF = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), NPB = Number of primary branches, NSB = Number of secondary branches, NPP = Number of pods per plant, TNSP = Total number of seeds per plant, TW = Test weight (gm), HI = Harvest index (%), SYP = Seed yield per plant.

Fig.1 Grouping of 100 genotypes into 12 clusters by Tocher's method



Similar findings have been reported by Lal *et al.,* (2001) and Dwevedi and Lal (2001).

Maximum expression of genotypes (Table 3) towards diversity was observed for days to 50 % flowering (22.89 %) followed by 100 seed weight (21.29 %), total number of seeds per plant (14.16 %), plant height (13.80 %) and pods per plant (10.18%). Parashi *et al.,* (2013) reported those days to 50 % flowering and number of seeds per plant contributed maximum towards genetic diversity. Pahre *et al.,* (2014) and Kuldeep *et al.,* (2015) reported that 100 seed weight and number of pods per plant contributed maximum towards genetic diversity.

The average cluster mean of ten characters revealed that none of the clusters contained genotype with all the desirable characters and so recombinant breeding between genotypes of different clusters is needed (Table 4). The genotypes in cluster IV recorded highest cluster mean for seed yield per plant (12.91), number of pods per plants (44.50) and harvest index (59.16) followed by cluster VI with highest cluster mean recorded for seed yield per plant (12.80), harvest index (52.58), test weight (43.5) and secondary branches (9.20). The cluster XI shows the least value to the days to maturity. However, cluster X showed least value to days to 50% flowering (33.0) with least plant height (26.40).

Genetic diversity analysis within and between cluster revealed that the genotypes of the same cluster had little divergence from each other with respect to the character studied. The hybridization between the genotypes of the same cluster thus, may not provide good sergeants. Based on inter cluster distances and *Per se* performance PG 0749, BCG 79, ICC 5003, ICC 1058, HK 06-171 and PKV Kabuli 4 were identified for inclusion in hybridization programme for realizing desirable transgressive segregates. This finding is in accordance with that of Dwevedi and Lal (2009) and Gaikwad *et al.,* (2014).

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