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Genetic divergence in Chick pea (*Cicer arietinum* L.)

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Abstract
D^2 Statistics grouped 50 genotypes of chickpea into 8 clusters. The clustering pattern of the genotypes did not confirm to the geographical distribution. The maximum inter cluster distance was observed between cluster V and VIII followed by cluster V and VI. The minimum inter cluster was found between cluster II and III. The cluster VIII was the best for days to maturity, number of secondary branches per plant, number pods per plant, number of seeds per pod, biological yield per plant, 100-seed weight, seed yield per plant and harvest index. The luster VI was the best for days to 50% flowering while cluster VII was the best for number of primary branches per plant. Therefore, inter crossing of such genotypes involved in these clusters would be useful for inducing variability in the respective characters and their rational improvement for increasing the seed yield.

Keywords: Chickpea, cluster analysis, D^2 statistics, inter cluster distance and intra cluster distance

Introduction

Chickpea (*Cicer arietinum* L.) is an important winter-season food legume having extensive geographical distribution. Its 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) [13]. 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 Gujarat, area under chickpea was 173.00 thousand hectares with a total production of 235.00 thousand tonnes and 1358 kg/ha productivity. 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 chickpea (Ramanujam, 1975) [7]. 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) [6]. 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) [5]. 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) [12, 1]. The present study aims to find out the genetic diversity among 100 promising chickpea genotypes.

Materials and Methods

The present investigation was conducted to assess the genetic variability, correlation co-efficient of fifty genotypes of chickpea were sown in pots of randomized block design replicated thrice at the oil Seed Research Station, Junagadh Agricultural University, Manavadar during Rabi 2021-2022. Each entry was recommended in a single row of 4 meter length with a spacing of 60cm between rows and 10 cm between plants. All the recommended agronomical practices along with necessary plant protection measures were followed timely for the successful raising of the crop.

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Observations were recorded on five randomly selected plants in each entry and replication for 11 characters *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, biological yield per plant(g), 100-seed weight (g), seed yield per plant (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) [8]. Contribution of individual characters towards divergence was estimated according to the method described by Singh and Choudhary (1979) [10]. Grouping of variety into various clusters was done and average intra and inter cluster distance were estimated.

Results and Discussion
Grouping of the genotypes was carried out by following Tocher's method (Rao, 1952) [8] with the assumption that the genotypes within the cluster have smaller D^2 values among themselves than those from groups belonging to different clusters. In all, 8 clusters were formed from 50 genotypes. The composition of cluster is given in Table 1. The maximum numbers of accessions were grouped in cluster I (43 accessions). The clusters II, III, IV, V, VI, VII and VIII are solitary cluster containing single genotype from different geographical regions. The cluster I was the largest having 43 genotypes from different geographical regions of the India, among them fourteen from ICRISAT (Hyderabad), six from Junagadh (Gujarat), four from Akola (Maharastra), three each from Nandyal (Andhra Pradesh) and IARI (New Delhi), two each from Raipur, Badnapur, Jabalpur and Arnej (Gujarat) and one each from Gulbarga, USA (Dharwad), Ganganagar (Rajasthan), AGRISAT and Kanpur (Uttar Pradesh). Cluster II & Cluster III and Cluster V from ICRISAT (Hyderabad), Cluster IV from Sehore (Madhya Pradesh), Cluster VI & Cluster VII from Kanpur (Uttar Pradesh) and Cluster VIII from IARI (Dharawad), respectively.

In general, intra-cluster distances were lower than the inter-cluster distance (Table 2). The maximum inter-cluster distance (D=31.88) was found between cluster V and VIII followed by that between V and VI (24.59). The minimum inter-cluster distance was found between cluster II and III (D=7.21). The intra-cluster distance (D=10.91) and remaining seven clusters contained only one genotype hence its intra-cluster distance was zero. The genotypes belonging to the clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates.

Wide range of variation for several characters among single as well as multi-genotypic clusters was observed. However, the most important trait causing maximum genetic divergence was observed in number of pods per plant (46.29%) and was responsible for differentiating the genotypes studied (Table 3). Days to 50% flowering was the next important trait contributed to total genetic divergence. Hence, selection for Discussion divergent parents based on these two characters would be useful for heterosis breeding in chickpea. Dwevedi and Lal (2009) [2] and Santosh *et al.* (2017) [9] also reported higher genetic diversity due to number of pods per plant and Tamver *et al.* (2019) [11] reported higher genetic diversity due to days to 50% flowering. The number of seeds per pod, days to maturity, number of primary branches and 100-seed weight contributed 15.43%, 6.86%, 5.63% and 5.47 % towards total genetic divergence, respectively. The harvest index, biological yield per plant, number of secondary branches per plant and plant height contributed negligible toward the total divergence in yield.

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. The genotypes with high values of any cluster can be used either for direct adoption or for hybridization followed by selection. In the present study, the cluster VI was the best for days to 50% flowering. The cluster VII was the best for number of primary branches per plant. The cluster VIII was the best for days to maturity, number of secondary branches per plant, number pods per plant, number of seeds per pod, biological yield per plant, 100-seed weight, seed yield per plant and harvest index. Therefore, intercrossing of such genotypes involved in these clusters would be useful for inducing variability in the respective characters and their rational improvement for increasing the seed yield.

It has been well established fact that more the genetically diverse parents used in hybridization programme, the greater will be the chances of obtaining high heterotic hybrid and broad-spectrum variability in segregating generations (Arunachalam, 1981) [14]. It has also been observed that the most productive hybrids may come from high yielding parents with a high genetic diversity. Therefore, in the present investigation, based upon high yielding genotypes and large inter-cluster distance, it is advisable to attempt crossing of the genotypes from cluster VI and VIII with the genotypes of cluster VII, which may lead to broad spectrum of favorable genetic variability for yield improvement in chickpea.

Table 1: Grouping of 50 genotypes of chickpea in various clusters on the basis of D^2- statistic

Cluster	Number of genotypes	Name of genotypes	Place of origin
I	43	ICC-1813, ICCV 1305, ICCV 97024, ICC 2263, ICC 12715, ICCV 13104, ICCV 92944, ICCV 13107, ICC 6926, ICC 4958, ICCV 14106, ICCV 1118, ICCV 181668, ICCV 14108	ICRISAT (Hyderabad)
		IG 9868, IG 73545	Raipur
		BDNG- 2016-2, BDGG-219	Badnapur
		Annigeri- 1	Gulbarga
		PG-216, PG 15109, PG 92926, AKG-1303	Akola (Maharastra)
		Dahod yellow, GG-1, GG-3, GG-4, GG-5, GJG-6	Junagadh (Gujarat)
		BGD-103	UAS, Dharwad
		JG-315, JG-16	Jabalpur (Madhya Pradesh)
		GAG-0514, GAG 1620	Arnej (Gujarat)
		GNG-2064	Ganga Nagar (Rajasthan)
		NBeG-47, NBeG-778, NBeG 798	Nandyal (Andhra Pradesh)
		SA-1	AGRISAT
		Pusa-256, MABC-66-266, BGM-202-11	IARI, New Delhi

		DGM-810	Kanpur (Uttar Pradesh)
II	1	ICCV 11108	ICRISAT (Hyderabad)
III	1	ICC 6553	ICRISAT (Hyderabad)
IV	1	SAKI- 9516	Sehore (Madhya Pradesh)
V	1	IPCCL-19-1	ICRISAT (Hyderabad)
VI	1	IPC-14-39	Kanpur (Uttar Pradesh)
VII	1	DCP-35	Kanpur (Uttar Pradesh)
VIII	1	BGD-112	IARI, Dharwad

Table 2: Average inter and intra- cluster distance ($D = \sqrt{D^2}$) values in chickpea.

	I	II	III	IV	V	VI	VII	VIII
I	10.91	14.98	15.21	15.19	14.69	15.34	14.33	21.63
II		0.00	7.21	10.42	23.75	12.28	21.20	15.77
III			0.00	11.69	23.22	12.75	19.45	17.11
IV				0.00	23.63	12.16	18.77	13.71
V					0.00	24.59	18.12	31.88
VI						0.00	14.30	13.68
VII							0.00	23.42
VIII								0.00

Table 3: Cluster mean for eleven characters of chickpea.

Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches per plant	No. of secondary branches per plant	No. of pods per plant	No. of seeds per pod	Biological yield per plant (g)	100 seed weight (g)	Seed yield per plant (g)	Harvest index (%)
I	43.51	88.48	46.78	1.97	7.90	62.29	1.55	38.18	19.53	19.54	47.81
II	52.33	82.67	40.69	1.40	7.53	83.08	1.27	33.06	21.86	19.20	47.73
III	55.67	88.33	44.99	2.20	8.23	82.14	1.23	35.05	11.58	21.43	36.63
IV	43.00	78.00	41.89	1.80	6.80	83.58	2.23	48.00	15.60	23.68	45.80
V	34.33	89.00	44.73	1.73	8.37	45.42	1.20	36.76	10.70	17.24	45.27
VI	56.67	89.33	41.34	1.73	5.23	75.18	2.37	38.98	21.72	17.23	37.37
VII	51.33	88.00	45.81	3.43	7.63	52.93	2.37	46.68	18.24	18.53	46.73
VIII	49.33	102.33	42.50	1.67	8.47	91.36	2.43	52.16	28.31	25.16	56.12
Mean	44.27	88.44	46.26	1.97	7.83	63.84	1.59	38.64	19.35	19.65	47.42
S.Em	1.11	1.55	2.79	0.14	0.57	1.13	0.07	3.20	1.17	1.70	3.72
% Contribution towards total genetic divergence	18.94%	6.86%	0.08%	5.63%	0.08%	46.29%	15.43%	0.41%	5.47%	0.16%	0.65%
No. of times ranked 1st	232	84	1	69	1	567	189	5	67	2	8

Conclusion

Study of genetic divergence indicate that the number of pods per plant, days to 50% flowering, number of seeds per pod, days to maturity, number of primary branches per plant and 100-seed weight were given maximum contribution towards total genetic divergence.

Therefore, selection for number of pods per plant, days to 50% flowering, number of seeds per pod, days to maturity, number of primary branches per plant and 100-seed weight would offer this scope for stimulations improvement contributing characters for improving the yield potential in chickpea.

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