Assessment of genetic diversity among chickpea (*Cicer arietinum* L) genotypes

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ABSTRACT

The present investigations were carried out to study the genetic diversity analysis among 56 diverse genotypes of chickpea (*Cicer arietinum* L) for twelve quantitative characters by using Mahalanobis D^2 statistics during rabi season 2018-19 at Zonal Agricultural Research Station, Ganeshkhind, Pune, Maharashtra. The 56 genotypes of chickpea were grouped into eight non-overlapping clusters. Cluster I with 24 genotypes emerged as the largest cluster followed by Cluster II with 14, Cluster III with 12 and Cluster IV with 2 genotypes. The Cluster V, VI, VII and VIII were monogenotypic containing only one genotype. It was observed that there was a wide diversity among the genotypes with D^2 values ranging from 34.11 to 989.73. The highest D^2 value was observed between the Cluster VI and Cluster VIII having genotypes Phule-G-15109 and Phule-G-0739. This suggested that these genotypes had large source of variation and were useful for future breeding programmes.

Keywords: Chickpea; genetic diversity; cluster analysis; divergence

INTRODUCTION

Chickpea (*Cicer arietinum* L) is one of the most important leguminous crops used for grain as well as green pod vegetable. Chickpea is also known as gram or Bengal gram and dried pulses are called Chana which seems to hold in agriculture to meet out the challenges of under-nutrition to much extent. Chickpea is one of the most important rabi pulse crops in Asia. India is largest producer (25%), importer (14%) and consumer (27%) of pulses in the world (https://journalsofindia.com/pulses-production-and-issues/).

Chickpea is cultivated in diverse agro-climatic conditions in India. The major chickpea producing states of India are Madhya Pradesh followed by Maharashtra, Rajasthan, Uttar Pradesh, Andhra Pradesh and Karnataka. Chickpea is very good source of protein as well as carbohydrates which together constitute 80 per cent of the total dry seed weight. Besides protein and carbohydrates it also contains calcium, phosphorus, iron, essential amino acids and vitamins. The achievement in plant breeding programme largely depends upon the genetic variability available in breeding population and the efficiency of selection technique. The importance of genetic diversity in plant breeding is obvious from results obtained in different crops. The recognition and measurement of such diversity, its nature and magnitude are beneficial, perhaps crucial to any breeding programme. This is particularly important in a crop like chickpea where hybridization is difficult; there being limited scope for making large number of crosses by random mating and hence the information regarding the nature of genetic diversity of the parents to be used in the hybridization is of paramount importance in chickpea breeding programm.

Genetic divergence is a measure of choosing potent parent for crossing. The success of any crossing programme depends on selection of parents having high expression for the economically important characters. Therefore diversity is the basic need of a crop improvement programme. Among the different approaches of selecting parents, selection based on diversity has its own merits. Therefore in the present

study diversity among different genotypes was studied which yielded valuable information that could be useful in suggesting potent parents for crossing. Hays and Johnson (1939) obtained greater heterosis from crosses between diverse parents than those between close related ones. Timothy (1963) found that genetic divergence is one of the criteria for selecting the parents for hybridization which may produce transgressive seggregants in the later generations.

Genetic improvement through conventional breeding approaches depends mainly on availability of the diverse genotypes and the amount of genetic variability present in the population. A method suggested by Mahalanobis (1936) known as Mahalanobis D^2 statistics is a powerful tool for quantifying the divergence between two populations. The present study was undertaken to assess the nature and magnitude of genetic divergence for yield and its component in chickpea.

MATERIAL and METHODS

The experimental material consisted of fifty six genotypes of chickpea collected from Pulses Improvement Project, MPKV, Rahuri, Maharashtra. The experiment was laid out in randomized block design with three replications during rabi season 2018-19. All the recommended agronomic and cultural practices were followed for raising a healthy crop. Data were recorded on five randomly selected plants per replication of each genotype for 12 yield and yield contributing characters viz days to 50 per cent flowering, days to maturity, plant height, plant spread, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100-seed weight, harvest index, protein content and seed yield per plant. The mean data of these five plants were utilized for the statistical analysis. The genetic divergence was computed by using Mahalanobis (1936) D^2 statistics among all the fifty six genotypes. Based on genetic divergence, the cluster formation was done by following Tocher's method as described by Rao (1952).

RESULTS and DISCUSSION

All the 56 genotypes studied under investigations were grouped into eight clusters. Cluster I with 24 genotypes emerged as the largest cluster followed by Cluster II with 14, Cluster III with 12 and Cluster IV with 2 genotypes. The Cluster V, IV, VII and VIII were monogenotypic containing only one genotype. The distribution of 56 genotypes into different clusters is presented in Table 1. Jayalakshmi and Ronald (2011), Singh et al (2012), Parashi et al (2013), Temesgen et al (2015) and Gupta et al (2016) also reported similar results.

The results of average intra- and inter-cluster D and D^2 value are presented in Table 2. The D^2 values varied from 34.11 to 989.73. The lowest value was observed between the pair of genotypes Phule-G-171113 and Phule-G-1107-27-5 and the highest value was between the genotypes Phule-G-15109 and Phule-G-0739. The maximum inter-cluster distance was observed between Cluster VI and Cluster VIII (31.46) followed by Cluster VII and VIII (30.90), Cluster V and VIII (29.46), Cluster III and VI (25.37), Cluster II and VIII (24.61) and Cluster IV and VIII (23.79) indicating that these clusters were more heterogeneous. This also suggests that the genetic architecture of the genotypes in one cluster differred entirely from those included in the other cluster. These results are also in conformity with the findings of Durga et al (2005), Prakash and Shekhawat (2012), Parashi et al (2013) and Naveed et al (2015). The minimum inter-cluster distance was observed between Cluster V and Cluster VI (6.12) indicating proximity with each other.

The maximum intra-cluster distance was found in Cluster III (10.08) followed by Cluster II (9.05) and Cluster I (8.28) suggesting that genotypes included in the clusters might have genetically different architecture and have originated from different genetic pool. However the lowest intra-cluster distance was observed in Cluster IV (5.84) indicating that the strains of this cluster resembled one another genetically and appeared to have evolved from common gene pool. The monogenotypic Clusters V, VI, VII and VIII showed intra-cluster value 0.00. The cluster formation and cluster divergence are used as basis for selection of better parents for hybridization programme. Grouping of genotypes into eight clusters suggested the presence of relatively wide amount of genetic diversity in the material under study.

The results of Table 2 indicate that the genotypes originating in different geographical area could form one cluster while different genotypes evolved in the same area could be grouped into different clusters. Thus clustering pattern of the genotypes in the present study revealed that the genetic diversity was not always related to geographical diversity.

Table 1. Distribution of 56 genotypes of chickpea among different clusters on the basis of D^2 analysis

Cluster	I	II	III	IV	V	VI	VII	VIII
I	68.56 (8.28)	236.85 (15.39)	220.52 (14.85)	437.65 (20.92)	217.27 (14.74)	323.64 (17.99)	246.80 (15.71)	372.10 (19.29)
II		81.90 (9.05)	301.15 (17.44)	166.93 (12.92)	165.63 (12.87)	187.42 (13.69)	178.76 (13.37)	605.65 (24.61)
III			101.61 (10.08)	253.76 (15.93)	543.36 (23.31)	643.64 (25.37)	508.05 (22.54)	211.12 (14.53)
IV				34.11 (5.84)	496.84 (22.29)	499.97 (22.36)	436.39 (20.89)	565.96 (23.79)
V					0.00 (0.00)	37.45 (6.12)	65.61 (8.10)	867.89 (29.46)
VI						0.00 (0.00)	90.25 (9.50)	989.73 (31.46)
VII							0.00 (0.00)	954.81 (30.90)
VIII								0.00 (0.00)

Table 1. contd…..

Cluster	Number of genotypes included	Genotypes
I	24	AKG-1401, Phule-G-1010-14, C-1837, C-1835, Vijay, JAKI-9218, BDNG-797, Phule-G-1005-5-4, RUSSG-64, NBeG-699, RLBG-1, RG-2015-07, Phule-G-16111, CSJ-944, Tembhi Local-1, Phule-G-1022-3, Malavli Local-1, IPC-2013-70, JG-2017-47, C-1827, Phule-G-0819-43, DBGV-214, RCBD-2, RVSSG-54
II	14	Gultekdi Local-2, Gultekdi Local-3, GJG-1509, Shivajinagar Local-1, H-14-21, GCP-101, RVSSG-57, Gultekdi Local-1, Phule-G-1131-31-9, Shivajinagar Local-2, GBM-2, Phule Vikrant, BGD-139, AKG-1303
III	12	CSJ-740, Phule-G-1115-13-16, Phule-G-1131-31-18, PhuleVikram, Digvijay, Phule-G-171104, PDKV Kanchan, Phule G-171101, Phule-G-171105, Malavli Local-2, Phule-G-1131-31-4, Phule-G-171103
IV	2	Phule-G-171113, Phule-G-1107-27-5
V	1	C-1825
VI	1	Phule-G-15109
VII	1	BDNG-2017-21
VIII	1	Phule-G-0739

Table 2. Average intra- and inter-cluster D (in parentheses) and D^2 values in 56 genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII
I	68.56 (8.28)	236.85 (15.39)	220.52 (14.85)	437.65 (20.92)	217.27 (14.74)	323.64 (17.99)	246.80 (15.71)	372.10 (19.29)
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VII							0.00 (0.00)	954.81 (30.90)
VIII								0.00 (0.00)

Mahalanobis (1936) and Jethava et al (1996) revealed from clustering pattern of the genotypes that genetic diversity was not always related to geographical diversity confirming the present findings.

The mean performances for cluster values of twelve characters are presented in Table 3. Based on mean performances of clusters for twelve characters it was found that a wide range of variability among the clusters was present for all the characters. A considerable inter-cluster variation in respect of cluster was observed among the various clusters for twelve characters studied. Cluster means for different characters indicated that none of the clusters contained genotype with all the desirable traits. The genotypes in Cluster IV (48.50) were earliest for days to 50 per cent flowering followed by Cluster VIII (50.00) whereas genotypes in Cluster V (77.67), Cluster VI (76.33) and Cluster VII (75.33) were late for flowering. The highest cluster mean for days to maturity was recorded in Cluster V (120) followed by Cluster VI (118.67) whereas the lowest cluster mean was observed in Cluster IV (83.50) followed by Cluster VIII (89.33) and Cluster III (89.83). The highest cluster mean for number of primary branches per plant was recorded in Cluster IV (6.50) followed by Cluster VI (6.33) whereas the lowest cluster mean was observed in Cluster VIII (3.20). The highest cluster mean for number of secondary branches per plant was recorded in Cluster VII (19.67) followed by Cluster II (18.62) and the lowest cluster mean was observed in Cluster VIII (6.73). Cluster V (54.93) showed maximum plant height followed by Cluster VI (54.58 cm), Cluster II (52.15 cm) and Cluster I (50.82 cm) and minimum plant height was recorded in Cluster VIII (43.93 cm).

Cluster VIII (23.87 cm) showed minimum plant spread whereas maximum plant spread was recorded in Cluster V (39.07 cm) followed by Cluster II (33.78 cm), Cluster IV (33.32 cm) and Cluster I (32.40 cm). The highest cluster mean for number of pods per plant was recorded in Cluster VII (160.60) followed by Cluster VI (160.03). The Cluster VIII (16.77) recorded lowest cluster mean followed by Cluster I (77.34) and Cluster III (81.29).

The highest cluster mean for number of seeds per pod was recorded in Cluster VII (1.90) followed by Cluster I (1.71) and the lowest was observed in Cluster VIII (1.00). The highest cluster mean for 100-seed weight was recorded in Cluster VIII (32.17 g)

Table 3. Cluster mean values for 12 characters in 56 genotypes of chickpea

Cluster	Number of days to 50% flowering	Number of days to maturity	Number of primary branches/plant	Number of secondary branches/plant	Plant height (cm)	Plant spread (cm)
I	69.44	107.44	5.91	15.16	50.82	32.40
II	63.55	100.48	6.10	18.62	52.15	33.78
III	53.00	89.83	5.64	14.79	54.58	31.05
IV	48.50	83.50	6.50	18.13	48.73	33.32
V	77.67	120.00	5.47	18.53	54.93	39.07
VI	76.33	118.67	6.33	17.87	50.60	25.20
VII	75.33	116.33	5.53	19.67	49.67	27.47
VIII	50.00	89.33	3.20	6.73	43.93	23.87

Table 3. contd…..

Cluster	Number of pods/plant	Number of seeds/pod	100-seed weight (g)	Harvest index (%)	Protein content (%)	Seed yield/ plant (g)
I	77.34	1.71	22.10	27.03	25.31	13.79
II	139.13	1.14	19.14	28.44	25.90	13.80
III	81.29	1.68	22.73	30.58	24.93	14.62
IV	151.42	1.10	19.02	24.88	24.38	14.20
V	135.43	1.27	19.07	27.73	26.51	16.60
VI	160.03	1.10	27.47	27.20	27.15	20.73
VII	160.60	1.90	18.03	26.83	23.50	27.03
VIII	16.77	1.00	32.17	36.90	32.96	2.53

followed by Cluster VI (27.47 g) and Cluster III (22.73 g); the lowest was recorded in Cluster VII (18.03 g) followed by Cluster IV (19.02 g) and Cluster V (19.07 g). High cluster mean values for harvest index were recorded by Cluster VIII (36.90%) followed by Cluster III (30.58%) and Cluster II (28.44%) and lower by Cluster IV (24.88%) followed by Cluster VII (26.83%).

The highest cluster mean for protein content was recorded for Cluster VIII (32.96%) followed by Cluster VI (27.15%) and Cluster V (26.51%) and the least was observed for Cluster VII (23.50%) followed by Cluster VI (24.38%). Cluster VIII (2.53 g) exhibited minimum seed yield per plant whereas maximum seed yield per plant was recorded in Cluster VII (27.03 g) followed by Cluster VI (20.73 g), Cluster V (16.6 g) and Cluster III (14.62 g).

Based on the results obtained in the present study, it would be desirable to select the parents based on maximum genetic divergence for most of yield contributing components. The study also envisages the relative importance of the characters like number of pods per plant, days to 50 per cent flowering, seed yield per plant, days to maturity and 100-seed weight in selecting parents for hybridization programme.

CONCLUSION

The study revealed that based on per se performance and intra- and inter-cluster distance genotypes RVSSG-54, AKG-1303, Phule-G-171103, Phule-G-171113, C-1825, Phule-G-15109, BDNG-2017-21 and Phule-G-0739 were found promising for cultivation and could be used as potential parents in future crop improvement programmes. While choosing among the genotypes of a cluster, the per se performance of genotypes for different traits such as number of pods per plant, days to 50 per cent flowering, seed yield per plant, days to maturity and 100-seed weight may be considered so that desirable segregates are obtained after hybridization.

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