Genetic diversity studies in chickpea (*Cicer arietinum* L) genotypes under late sown condition

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ABSTRACT

This study aimed to assess the genetic diversity among 50 chickpea genotypes using Mahalanobis D^2 statistics to identify potential parents for breeding programmes during rabi 2022-23 at Zonal Agricultural Research Station, Ganeshkhind, Pune, Maharashtra. The experiment was conducted in a randomized block design with three replications and data were collected for 11 yield and yield-contributing traits. Genetic divergence was determined using Mahalanobis D^2 statistics and cluster formation was done using Tocher's method. The genotypes were grouped into 11 clusters, with Cluster I being the largest, containing 35 genotypes. The clusters II, III, IV, VI, VII, VIII, IX, X and XI were monogenotypic containing only one genotype. Significant inter-cluster distances were observed, indicating substantial genetic divergence. There was wide diversity observed among the genotypes with D^2 values ranging from 28.70 to 585.64. The highest D^2 value was observed between the Clusters IV and X having genotypes Phule G-1424-4-2 and Vijay. This suggested that these genotypes had large source of variation. Based on per se performance and intra- and inter-cluster distance genotypes Jaki-9218, Phule Vikram, Vishal, TRCH-4, Local Gawadevadi, Local Awasari-3, Phule G-1424-4-2, Phule G-14481, C-2266, C-2265, Phule G-1403-18-14, Vijay and Digvijay were found promising for cultivation and could be used as potential parents in future crop improvement programmes.

Keywords: Chickpea; genetic diversity; cluster analysis; divergence

INTRODUCTION

Pulses play a vital role in various cropping systems across the country, with specific preferences and suitability varying by region. Chickpea (*Cicer arietinum* L) is the most favoured pulse for consumption. According to Aggarwal et al (2015), it comes in third place after field pea (*Pisum sativum* L) and common bean (*Phaseolus vulgaris* L). It is annual, temperate, predominantly self-pollinating leguminous crop of family Fabaceae. During 2020-2021, chickpea production in India was 11.91 million tonnes from an acreage area of 10.00 million ha with a productivity of 1,192 kg per ha (Anon 2023). Chickpea solely contributes nearly 50 per cent of the Indian pulse production (Asiwal et al 2023). In 2020-21, Maharashtra's share of chickpea production share was 20.12 per cent to the all India production (Anon 2023).

The area of chickpea grown under late-sown condition is expanding these days because of temperature swings, delayed monsoon and increased cropping intensity. Abiotic stresses like heat and drought harm late-sown crops, which is one of the main issues that must be handled rightly. It also negatively impacts agricultural productivity and production. It is possible to develop early to extra-early maturing cultivars that are appropriate for late sowing to solve this issue. Also due to limited genetic diversity chickpea production and productivity in our country is relatively less.

Genetic diversity is essential to any breeding effort and is crucial for improving crops. It enables breeders to choose genotypes with high yields. Selecting a particular genotype from various genetic populations is made easier with the use of heritability estimation. The likelihood of creating the intended plant species increases with population variability. The concept of

genetic advancement suggests that the new population may be selected to be better than the previous population. Plant breeders can choose parents from a diverse population for intentional hybridization with the assistance of accurate genetic divergence information (Shamsuddin 1985).

The Mahalanobis D^2 statistics serves as the foundation for the genetic divergence study. As per Murthy and Arunachalam (1966), multivariate analysis with Mahalanobis D^2 statistics is a powerful tool to know the clustering pattern for establishing the relationship between genetic and phenotypic divergence and to determine the role of different quantitative characters towards the maximum diversity. Therefore, the present investigations were undertaken to study the genetic diversity in fifty genotypes of chickpea for eleven quantitative characters by using Mahalanobis D^2 statistics during rabi 2022-23 with the objective to study the genetic divergence among different genotypes and group them into suitable clusters.

MATERIAL and METHODS

The experimental material used for present investigations included 50 chickpea genotypes collected from Pulses Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra. The experiment was conducted during rabi 2022-23 at Zonal Agricultural Research Station, Ganeshkhind, Pune, Maharashtra.

The experiment was laid out in randomized block design with three replications. Data were recorded on randomly selected five plants per replication of each genotype for eleven 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, protein content and seed yield per plant. The mean data of these five plants were employed for statistical analysis.

The genetic divergence was computed by using Mahalanobis D^2 (Mahalanobis 1936) statistics among all the fifty genotypes. Based on genetic divergence, the cluster formation was done by using Tocher's method as described by Rao (1952).

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 crop improvement programme. Among the different approaches of selecting parents, selection based on diversity has its own merits.

RESULTS and DISCUSSION

In the present study, diversity among different genotypes was studied which yielded valuable information that could be useful in suggesting potent parents for crossing.

All the fifty genotypes studied under investigations were grouped into eleven clusters. Cluster I with 35 genotypes emerged as the largest cluster followed by cluster V with 6 genotypes. The cluster II, III, IV, VI, VII, VIII, IX, X and XI were monogenotypic containing only one genotype. The distribution of 50 genotypes into different clusters is presented in Table 1.

The results of average intra- and inter-cluster D and D^2 values are presented in Table 2. The D^2 values varied from 28.70 to 585.64. The lowest value was observed between the pair of genotypes Phule G-14481 and Local Awasari-3 and the highest between the genotypes Phule G-1424-4-2 and Vijay.

The maximum inter-cluster distance was found between Clusters IV and X (24.20) followed by Clusters IV and VIII (23.44), Clusters II and XI (23.20), Clusters II and VII and clusters II and X (22.90 each) and Clusters II and VI (21.72) indicating that these clusters were more heterogenous. This also suggests that the genetic architecture of the genotypes in the one cluster differed entirely from those included in the other clusters. The minimum inter-cluster distance was observed between Clusters VI and VII (6.35) indicating proximity with each other.

Cluster I (10.00) had maximum intra-cluster distance followed by Cluster V (9.03) suggesting that genotypes included in the clusters might have genetically different architecture and had originated from different genetic pools. The monogenotypic Clusters II, III, IV, VI, VII, VIII, IX, X and XI 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 eleven clusters suggested the

Table 1. Distribution of 50 genotypes of chickpea among different clusters on the basis of D^2 analysis

Cluster	Number of genotypes included	Genotypes
I	35	C-2263, C-2264, Phule G-1511-29-7, C-2272, C-2261, PDKV Kanak, Phule G-1511-29-1, C-2271, C-2262, Local Kolhapur, RVG-202, Phule G-1521-12-3, C-2269, Phule Vikram, Phule G-1521-12-2, Phule G-211205, C-2270, Phule G-1517-1-8, Local Karvir, Phule G-1511-17-11,Vishal, Local Pahadadara, Phule G-201216, Phule G-1504-8-4, Phule Vikrant, Jaki-9218, Phule G-1424-7-7, Phule G-1511-17-4, Phule G-211103, Phule G-211110, Phule G-1504-5-7, C-2268, Local Awasari-1, Phule G-1511-17-7, C-2267
II	1	Local Gawadevadi
III	1	Local Awasari-3
IV	1	Phule G-1424-4-2
V	6	Local Baramati, Local Awasari-4, Local Gadhinglaj, TRCH-4, Local Awasari-2, TRCH-2
VI	1	Phule G-14481
VII	1	C-2266
VIII	1	C-2265
IX	1	Phule G-1403-18-14
X	1	Vijay
XI	1	Digvijay

Table 2. Average intra- and inter-cluster D and D^2 values in 50 genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	100.00 (10.00)	158.76 (12.60)	215.50 (14.68)	174.24 (13.20)	184.96 (13.60)	217.85 (14.76)	231.04 (15.20)	228.61 (15.12)	177.68 (13.33)	321.12 (17.92)	304.85 (17.46)
II		0.00 (0.00)	377.91 (19.44)	97.61 (9.88)	163.58 (12.79)	471.75 (21.72)	524.41 (22.90)	451.98 (21.26)	311.87 (17.66)	524.41 (22.90)	538.24 (23.20)
III			0.00 (0.00)	435.55 (20.87)	176.89 (13.30)	28.70 (14.35)	115.99 (10.77)	72.93 (8.54)	114.70 (10.71)	99.80 (9.99)	255.68 (15.99)
IV				0.00 (0.00)	356.45 (18.88)	370.56 (19.25)	442.68 (21.04)	549.43 (23.44)	350.06 (18.71)	585.64 (24.20)	479.61 (21.90)
V					81.54 (9.03)	400.00 (20.00)	369.40 (19.22)	207.36 (14.40)	193.48 (13.91)	257.92 (16.06)	438.48 (20.94)
VI						0.00 (0.00)	40.32 (6.35)	153.26 (12.38)	87.23 (9.34)	339.66 (18.43)	171.87 (13.11)
VII							0.00 (0.00)	103.83 (10.19)	111.09 (10.54)	229.21 (15.14)	191.26 (13.83)
VIII								0.00 (0.00)	99 (9.95)	205.63 (14.34)	256.96 (16.03)
IX									0.00	199.65 (14.13)	204.49 (14.30)
X										0.00 (0.00)	309.05 (17.58)
XI											0.00 (0.00)

presence of relatively wide amount of genetic diversity in the material under study.

The data given in Table 2 indicate that the genotypes originating in different geographical areas 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. Mahalanobis (1936) and Jethava et al (1996) revealed from clustering pattern of the genotypes that genetic diversity was not always related to geographical diversity.

The mean performances for cluster values of eleven characters are presented in Table 3. Based on the mean performances of clusters for eleven

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 the cluster was observed among the various clusters for eleven characters studied. Cluster means for various characters indicated that none of the cluster genotypes was with all the desirable traits.

Based on mean performance, genotype in Cluster VIII (55.73) was early for days to 50 per cent flowering followed by Cluster V (60.38), whereas, genotypes in Cluster X (67.07), Cluster IV (64.40) and Cluster VII (63.07) were late for days to 50 per cent flowering. The highest cluster mean for days to maturity was recorded in Cluster IV (109.80) followed by Cluster III (107.47), whereas, the low cluster mean was in Cluster IX (101.40) followed by Cluster VI (102.87).

Cluster VII (47.13 cm) showed maximum plant height followed by Cluster I (44.75 cm) and Cluster VI (44.40 cm), while minimum plant height was recorded in Cluster IX (31.60 cm) followed by Cluster II (34.33 cm). Cluster VI (30.27 cm) showed minimum plant spread, whereas, maximum plant spread was recorded in Cluster X (51.00 cm) followed by Cluster XI (41.40 cm) and Cluster IV (40.53 cm).

The highest cluster mean for number of primary branches per plant was recorded in Cluster XI (3.80) followed by Cluster VII (3.53), whereas, the lowest cluster mean was observed in Cluster II (2.93). The highest cluster mean for number of secondary branches per plant was recorded in Cluster XI (10.33) followed by Cluster VII (10.20), whereas, the lowest cluster mean was observed in Cluster III (9.07).

The highest cluster mean for number of pods per plant was recorded by Cluster X (77.13) followed by Cluster XI (68.60) and the Cluster VIII (40.27) recorded lowest cluster mean followed by Cluster III (42.13). The highest cluster mean for number of seeds per pod was recorded in Cluster XI (1.20) followed by Cluster X (1.11), whereas, the lowest was observed in Cluster III (1.00). The highest cluster mean for 100-seed weight was recorded by Cluster VI (28.87) followed by Clusters XI (27.63) and VII (26.50) and the lowest in Cluster V (15.27) followed by Cluster II (17.87).

The highest cluster mean for protein content was recorded in Cluster X (23.91%) followed by Clusters III (23.66%) and VIII (23.35%) and the least in Cluster IV (20.51%). Cluster V (8.00) exhibited minimum seed yield per plant. Maximum seed yield per plant was recorded in Cluster XI (22.72 g) followed by Clusters X (16.76 g) and VI (14.82 g) and minimum in Cluster V (8.00 g).

Singh et al (2012) studied the nature and magnitude of genetic divergence among 64 genotypes of chickpea using Mahalanobis D^2 statistics. The 64 genotypes were grouped into 9 clusters. Cluster II was the largest with 14 genotypes. Highest inter-cluster distance was recorded between Clusters VI and IX while highest intra-cluster distance was found among the genotypes of Cluster VIII. Characters like biological yield per plot, seed yield per plot and days to 50 per cent flowering contributed maximum towards the

Table 3. Cluster mean values for 11 characters in 50 genotypes of chickpea

Cluster	Number of days to 50% flowering	Number of days to maturity	Plant height (cm)	Plant spread (cm)	Number of primary branches/ plant	Number of secondary branches/ plant	Number of pods/plant	Number of seeds/pod	100-seed weight (g)	Protein content (%)	Seed yield/ plant (g)
I	61.66	106.21	44.75	38.47	3.40	9.62	52.16	1.07	21.07	21.64	11.78
II	61.67	107.27	34.33	35.67	2.93	9.93	45.20	1.01	17.87	20.67	8.18
III	62.27	107.47	37.60	39.27	3.07	9.07	42.13	1.00	20.27	23.66	8.54
IV	64.40	109.80	38.53	40.53	3.33	9.53	49.40	1.01	24.23	20.51	12.14
V	60.38	105.02	34.60	36.23	3.18	9.99	49.13	1.06	15.27	22.25	8.00
VI	60.40	102.87	44.40	30.27	3.07	10.00	49.93	1.03	28.87	22.41	14.82
VII	63.07	104.60	47.13	35.93	3.53	10.20	44.53	1.07	26.50	23.16	12.62
VIII	55.73	103.07	43.33	35.60	3.40	9.33	40.27	1.08	20.40	23.35	8.89
IX	60.87	101.40	31.60	37.27	3.00	9.73	51.33	1.01	23.90	22.42	12.44
X	67.07	106.87	35.87	51.00	3.13	9.93	77.13	1.11	19.67	23.91	16.76
XI	62.07	104.67	38.73	41.40	3.80	10.33	68.60	1.20	27.63	22.86	22.72

genetic diversity. The genotypes GL29009, GL29012, GL29013, GL29017, GL29019, GL29034, GL29042, GL29046, GL29069, GL29072 and GL29078 were identified as genetically diverse parents.

Parashi et al (2013) grouped sixty chickpea genotypes into 13 clusters. Cluster I was the largest cluster with 33 genotypes. Highest inter-cluster distance was observed between Clusters VII and XIII (D^2 =194.04) followed by Clusters XI and XIII (D^2 = 156.50), Clusters VI and XIII (D^2 = 130.64) and Clusters IV and XI (D^2 = 119.46). Three characters viz yield per plant (34.29%), stomatal conductance (27.97%) and number of pods per plant (16.33%) contributed maximum genetic diversity. The genotypes Virat, Digvijay, Rajas, IC-269643, IC-268978, IC269257 and Vijay were identified as genetically diverse parents.

Temesgen et al (2015) tested forty nine Kabuli chickpea genotypes in 7 x 7 simple lattice design to estimate genetic divergence among the genotypes and clustering them into genetically divergent class. Cluster analysis revealed that the 49 Kabuli chickpea genotypes were grouped into eight clusters. Distances between these clusters were significantly different for all the cluster combinations except between Clusters I and IV. Crosses involving Cluster III with Cluster VII and Cluster V with Cluster VII were suggested to exhibit high heterosis and could result in segregants with higher seed yield. Principal component analysis indicated that four principal components explained about 79.92 per cent of the total variation. Differentiation of the genotypes into different clusters was because of a cumulative effect of a number of characters, mainly phenological traits: days to 50 per cent flowering, days to maturity, number of primary branches per plant and number of seeds per pod.

Gupta et al (2016) studied the genetic variation, genetic divergence, correlations and path analysis of six important quantitative traits among 25 chickpea genotypes to ascertain their potential to grow in new agro-climatic zone of northwestern Himalayas. The chickpea genotypes exhibited sufficient variability for all the traits. Path analysis revealed that number of pods per plant had highest direct effect followed by plant height on plant yield. Genotypes were grouped into seven clusters and cluster I was the largest among them. They recommended that based on highest inter-cluster distance, genotypes from Cluster III (ICC 4984 and RIL 115) and Cluster IV (ICCL 81316) and from Cluster III and Cluster VI (Vijay and Annigeri) could be selected as parents in hybridization programme. Two genotypes, ICCC 37 and ICCL 87314 were rated superior based on damage ratings in sustaining *Helicoverpa armigera* infestation. ICCV 10 followed by ICC 4984 and RIL 27 had highest seed yield per plant.

Genetic diversity in chickpea with 132 genotypes revealed significant differences among the genotypes for yield and its component characters (Durga et al 2005). The genotypes were grouped into nine clusters. Cluster I was the largest, comprising 20 genotypes followed by Clusters V and VII with 16 and 15 genotypes respectively. Maximum intra-cluster distance (1.806) was observed in Cluster VI followed by Cluster IV (1.799), Cluster I (1.705) and Cluster IX (1.642). Maximum inter-cluster distance was noticed between Clusters I and VIII (5.114).

Prakash and Shekhawat (2012) evaluated thirty genotypes of chickpea to know the genetic divergence for grain yield and yield contributing traits. Significant differences among the genotypes were observed for all the characters studied. Genotypes were grouped into nine clusters based on D^2 values. Clusters III and IX were more divergent. Genotype GNG 2000 formed mono-genotypic cluster with earliest flowering and maturity. Pods per plant contributed most in genetic divergence followed by 100-seed weight and days to 50 per cent flowering. The diverse genotypes such as GNG 2000, GNG 1581, GNG 469, CSG 8962, GNG 1999, GNG 2004 and GNG 2010 were recommended to be used in breeding programme to generate the spectrum of variability.

Naveed et al (2015) searched newly developed sixty chickpea genotypes for the desirable recombinants possessing wilt resistance along with other yield components. Significant diversity among the genotypes was revealed. High to moderate estimates of heritability and genetic advance were recorded for fusarium wilt incidence, days to 50 per cent flowering, total branches per plant, pods per plant, 100-seed weight, grain yield and harvest index. Significant relationship of grain yield with these characters was further established by means of principal component analysis. Days to 50 per cent flowering, 100-seed weight and grain yield contributed highest weight on PC1 that explained 31.80 per cent of total variation. PC2 described 21.60 per cent of digression and was mainly related to pods per plant, plant height and canopy

temperature. Cluster analysis classified the genotypes into 3 clusters with maximum 33 genotypes in Cluster II. Cluster I comprised drought tolerant accessions based on canopy temperature while Cluster III consisted of bold seeded genotypes regarding 100-seed weight. Cluster II incorporated wilt resistant, early flowering yet late maturing genotypes having highest pods per plant, grain yield and harvest index. D^2 statistics further confirmed the versatility of Cluster II genotypes over Clusters I and III for most of the studied characters.

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 protein content, number of pods per plant, seed yield per plant, 100-seed weight, days to maturity and plant height in selecting parents for hybridization programme.

CONCLUSION

This study successfully assessed the genetic diversity among 50 chickpea genotypes using Mahalanobis D^2 statistics, grouping them into 11 distinct clusters. The analysis revealed significant genetic divergence, with Clusters IV and X showing the maximum inter-cluster distance, indicating high heterogeneity and potential for breeding programmes. Cluster I, containing the majority of genotypes, also displayed substantial intra-cluster diversity.

The study highlighted that genetic diversity was not necessarily linked to geographical origin, emphasizing the importance of genetic analysis in selecting diverse parents for hybridization. Cluster mean performances for various agronomic traits showcased a wide range of variability, suggesting that no single cluster possessed all desirable traits. Cluster XI exhibited high seed yield, number of secondary branches and 100-seed weight, while Cluster X was notable for high protein content, number of pods and plant spread. Cluster VIII was early maturing and Cluster VI had the highest 100-seed weight.

The findings underscore the importance of selecting parents based on maximum genetic divergence and considering key traits like protein content, seed yield, 100-seed weight, days to maturity and plant height. Based on per se performance and intra- and inter-cluster distances, genotypes Jaki-9218, Phule Vikram, Vishal, TRCH-4, Local Gawadevadi, Local Awasari-3, Phule G-1424-4-2, Phule G-14481, C-2266, C-2265, Phule G-1403-18-14, Vijay and Digvijay were found promising for cultivation and could be used as potential parents in future crop improvements programmes with enhanced yield, nutritional quality and adaptability to late-sown conditions.

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