Website : www.asthafoundation.in
Frontiers in Crop Improvement
Vol 11 (2) : 128-131 (July-2023) Print ISSN : 2393-8234 Online ISSN : 2454-6011
Astha Foundation, Meerut (U.P.) India

Genetic Diversity in Chickpea (*Cicer arietinum* L.) Genotypes Amenable to Mechanical Harvesting

K. Durga Prasad[1], R.M. Javia[1], L.K. Sharma[1] and S.P. Singh[2]
[1]Pulses Research Station, Junagadh Agriculture University, Junagadh-362001, Gujarat
[2]CSAUAT-Agriculture Research Station, Kalai, Aligarh, U.P.
Email : dprasadrr@gmail.com

Abstract

Genetic diversity of 52 chickpea genotypes was studied through Mahalanobis D^2 statistics. The genotypes under study fall into 12 clusters. Cluster I was the largest among all the clusters comprising 21 genotypes each, followed by cluster V consist of 9 genotypes, cluster II had 8 genotypes, cluster IV consist of 6 genotypes, whereas cluster III, VI, VII, VIII, IX, X, XI and XII comprising 1 genotype in each. The percent contribution of individual characters toward the total divergence was found high for seed yield per plant (27.38 per cent) followed by days to 50 per cent flowering (20.59 per cent) and number of pods per plant (15.46 per cent). Other characters viz., Height of first fruiting node (11.31 per cent), 100-seed weight (9.05 per cent), number of branches per plant (7.84 per cent), stem thickness (3.62 per cent), number of seeds per pod (2.64 per cent) and plant height (1.58 per cent) showed low percentage of contribution. Intra-cluster distance ranged from 0.00 to 7.96. Cluster V showed highest intra-cluster value (7.96). The highest inter-cluster divergence was observed between genotypes of cluster III and cluster X (17.99), followed by cluster VI and cluster X (16.18). Inter-cluster distance was lowest between cluster III and cluster VI (4.74).

Key words : *Chickpea, D^2 statistics, Genetic divergence, Intra and inter-cluster distance.*

Introduction

Chickpea commonly known as Chana, Gram or Bengal gram. It belongs to the sub-family *Papilionaceae* of family *Fabaceae*, is an important and unique food legume. It is an important pulse crop of the world occupying third position amongst pulses. Chickpea is a self-pollinated crop. Cross pollination is rare; only 0-1 per cent is reported. It is generally grown on heavy or red soils of pH 5.5 - 8.6. Frost, hailstones and excessive rains damage the crop. It is one of the most important *Rabi* pulse crop in Asia.In India, the area under chickpea was 96.8 lakh hectares with a production of 110.8 lakh tonnes and productivity of 1142 kg ha^{-1} during 2020-21. In Gujarat, an area under chickpea was 7.8 lakh hectares with a total production of 13.0 lakh tonnes and productivity of 1662 kg ha^{-1} during 2020-21 (1, 2).

Currently chickpea farming is partially mechanized – the crop is cut manually and then fed into a threshing machine. The total mechanization of harvesting is cost effective and quicker, reducing the risk of the ripened crop's exposure to untimely rain or other extreme weather conditions. Chickpea is harvested manually as the existing cultivars possess inadequate height, semi-spreading growth habit and height of first pods from the ground is about 15-20 cm, thus these cultivars are not suitable for mechanical harvesting. Delay in harvesting due to unfavourable conditions at the time of harvesting may lead to pod drop and shattering. Expensive labour further burdens the manual harvesting process and adds to the cost of cultivation. Availability of cultivars suitable for mechanical harvesting in crops like pigeon pea, wheat and rice have witnessed the tremendous advantage in terms of time and reduced cost per unit production. However non-availability of chickpea cultivar suitable for mechanization has stagnated low levels of production and productivity. In developing countries, lack of chickpea cultivars suitable to mechanizations in contrast to fully mechanized cereal crop cultivation is a major constraint in expansion of the chickpea growing area across the globe. The increased productivity of chickpea in developed countries like Australia, Canada and USA is mainly attributed to the mechanised harvesting. Hence there is an increasing demand for developing chickpea cultivar suitable for mechanisation. Therefore, development of cultivars suitable for machine harvesting is in current need of the chickpea breeding programme.

The knowledge about the source of genetic diversity for the different characters is of considerable importance, since the prime aim of the plant breeding is to improve the yield and the quality by evolving superior varieties. An investigation into the nature and the degree of divergences useful for an understanding of the course of evolution and for classification population into groups on the basic of diversity, particularly, when they are overlapping for one or more characters.

Received : May-2023; Revised : June-2023; Accepted : July-2023

Table-1 : Distribution of chickpea genotypes in different cluster.

Cluster no.	No. of genotypes	Name of genotypes
I	21	RVSSG 97, H 13-03, ICCV 201116, ICCV 201102, H 07-120, ICCV 201118, BG 3062, GL 17020, PG 0405, PBC 574, ICCV 201113, ICCV 191608, PG 191616, ICCV 201101, RKGM 20-2, ICCV 201109, ICCV 201108, RVG 204, RLBGMH 4, PG 252, RLBGMH 3
II	8	ICCV 201106, ICCV 201111, ICCV 201110, IPC 2017-253, ICCV 201105, ICCV 201115, ICCV 201103, IPC 2017-141
III	1	ICCV 201117
IV	6	RSGD 834, JG 2020-5, PG 251, RVSSG 96, IPCB 2015-132, GL 15003
V	9	PBC 582, RKGM 20-1, ICCV 201112, ICCV 201104, GJG 1916, IG 2020-2, ICCV 201107, PHULE VIKRAM, GJG 1913
VI	1	ICCV 191612
VII	1	NBeG 1267
VIII	1	PG 191618
IX	1	IG 2020-1
X	1	ICCV 201114
XI	1	BG 4027
XII	1	BG 4028

Table-2 : Contribution of different characters towards clustering in chickpea genotypes.

Sr. No.	Character	Times Ranked 1st	Contribution towards divergence %
1.	Days to 50 per cent flowering	273	20.59%
2.	Days to maturity	7	0.53%
3.	Reproductive phase duration	0	0.00%
4.	Height of first fruiting node (cm)	150	11.31%
5.	Plant height (cm)	21	1.58%
6.	Number of branches per plant	104	7.84%
7.	Number of pods per plant	205	15.46%
8.	Number of seeds per pod	35	2.64%
9.	Stem thickness (mm)	48	3.62%
10.	Seed yield per plant (g)	363	27.38%
11.	100-seed weight (g)	120	9.05%

Materials and Methods

Investigation was carried out with 52 chickpea genotypes were sown in a Randomized Block Design (RBD) with three replications during *Rabi* 2021-22 at Pulses Research Station, JAU, Junagadh. Each population was accommodated in one row of 4 m length with a spacing of 45 cm. The recommended agronomical and plant protection practices were followed for the successful raising of the crop. The observations were recorded on five randomly selected and tagged plants from each entry and average values were used for the statistical analysis. The data were recorded on quantitative traits such as days to 50 per cent flowering, days to maturity, reproductive phase duration, height of first fruiting node (cm), plant height (cm), number of branches per plant, number of pods per plant, number of seeds per pod, stem thickness, seed yield per plant and 100-seed weight (g). The replication wise mean values of randomly selected plants were used for statistical analysis for different characters.D^2 statistics was used for assessing the genetic divergence among 52 genotypes. On the basis of magnitude of D^2 value the genotypes were grouped into number of clusters as suggested by Tocher's method. The traits considered for evolution for machine harvest were erect, tall, height of the first fruiting node, resistant to lodging and high yielding. Therefore, the genotypes identified for their per se performance which were erect, tall (>50 cm), height of first fruiting node (>25 cm), resistant to lodging and high yielding.

Results and Discussion

Fifty-two genotypes of chickpea were grouped into 12 clusters based on divergence analysis. Distributions of genotypes into different clusters were presented in Table-1. Cluster I was the largest among all the clusters comprising 21 genotypes each, followed by cluster V consist of 9 genotypes, cluster II had 8 genotypes, cluster IV consist of 6 genotypes, whereas cluster III, VI, VII, VIII, IX, X, XI and XII comprising 1 genotype in each.

The characters which showed more contribution (per cent) towards the divergence should be considered prime during selection. The percentage contribution towards

Table-3 : Cluster mean for yield and its component traits of chickpea genotypes : Toucher's method.

Cluster	DF	DM	RPD	HFN (cm)	PH (cm)	NBP	NPP	NSP	ST (mm)	SYP (g)	100-SW (g)
Cluster I	57.68	103.06	45.38	29.86	56.13	6.90	40.12	1.15	7.38	11.45	20.67
Cluster II	63.46	104.13	40.79	35.10	63.79	6.61	34.73	1.17	7.30	8.92	20.94
Cluster III	57.33	106.33	49.00	30.73	54.33	3.93	20.53	1.08	7.49	6.63	23.35
Cluster IV	59.44	104.44	44.89	24.86	47.94	7.94	56.70	1.18	6.98	9.66	18.25
Cluster V	60.33	103.33	42.89	25.27	53.48	7.47	54.43	1.22	7.10	16.70	20.93
Cluster VI	51.33	101.00	49.67	27.53	49.47	4.67	20.33	1.12	5.96	6.50	19.69
Cluster VII	50.00	100.67	50.67	22.20	48.87	6.53	33.73	1.44	6.09	8.40	18.54
Cluster VIII	65.33	104.67	39.33	39.27	69.27	6.67	36.73	1.11	8.94	16.17	18.89
Cluster IX	54.33	100.00	49.00	32.33	61.60	7.63	33.47	1.23	8.95	8.50	22.39
Cluster X	56.67	102.33	45.67	31.20	60.13	8.67	78.00	1.15	7.03	20.93	18.25
Cluster XI	45.00	99.67	54.67	29.53	59.53	5.40	51.57	1.15	7.63	12.47	19.35
Cluster XII	47.00	101.00	54.00	27.00	62.13	9.87	46.00	1.14	8.11	11.03	19.65

Table-4 : Inter and intra cluster D_2 values for different clusters.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	5.41	7.04	8.42	7.66	8.40	7.36	7.44	8.36	6.78	11.59	8.10	8.67
II		6.28	7.89	9.58	10.79	8.29	9.10	8.31	7.36	14.53	11.06	11.49
III			0.00	11.26	12.98	4.74	8.64	11.69	8.73	17.99	11.38	13.34
IV				6.70	9.36	9.86	8.36	12.00	9.55	11.91	10.23	9.27
V					7.96	11.92	10.61	10.03	11.17	9.26	10.41	11.01
VI						0.00	5.73	11.84	8.11	16.18	8.95	10.90
VII							0.00	12.58	8.00	14.56	8.58	9.21
VIII								0.00	9.48	11.35	10.84	12.58
IX									0.00	14.11	8.42	7.67
X										0.00	10.48	11.26
XI											0.00	7.57
XII												0.00

Note : DF= Days to 50 per cent flowering, DM=Days to maturity, RPD= Reproductive phase duration, HFN= Height of first fruiting node (cm), PH= Plant height, NBP= Number of branches per plant, NPP= Number of pods per plant, NSP= Number of seeds per pod, ST= Stem thickness, SYP= Seed yield per plant,100-SW= 100-Seed weight.

genetic divergence by 11 quantitative characters (Table-2) revealed that, seed yield per plant contributed most towards genetic divergence, followed by days to 50 per cent flowering, number of pods per plant, height of first fruiting node, 100-seed weight, number of branches per plant, stem thickness, number of seeds per pod and plant height. These characters were responsible for expressing of maximum diversity between the clusters, whereas days to maturity and reproductive phase duration did show very negligible contribution towards genetic divergence. These results are in agreement with (3) for number of pods per plant, seed yield per plant and days to 50 per cent flowering. Similar result for days to maturity contributing negligible towards genetic divergence was observed by (4) and similar results for days to 50 per cent flowering and number of pods per plant were observed by (5, 6). This results are in similar with (7, 8, 9) for seed yield per plant and number of pods per plant. Similar result for days to 50 per cent flowering was reported by (10).

The cluster mean for different characters are presented in Table-3. The observations obtained from overall cluster means indicated that, Cluster X had high mean value for number of pods per plant and seed yield per plant. Cluster XI was desirable for early days to 50 per cent flowering and days to maturity. Cluster VIII was desirable for short reproductive phase duration and high mean value for height of the first fruiting node and plant height. Whereas, cluster XII had high mean value for number of branches per plant. Cluster VII had high mean value for number of seeds per pod. Cluster IX had high mean value for stem thickness. Cluster X had high mean value for 100-seed weight.

Cluster V showed highest intra-cluster value followed by cluster IV, cluster II and cluster I, whereas III, VI, VII, VIII, IX, X, XI and XII cluster showed zero value for intra cluster distance. The highest inter-cluster divergence was observed between genotypes of cluster III and cluster X followed by cluster VI and cluster X, cluster VII and cluster X, cluster II and cluster X, cluster IX and cluster X, cluster III and cluster XII, cluster III and cluster V, cluster VII and cluster VIII and cluster IV and VIII. Inter-cluster distance was lowest between cluster III and cluster VI.This sequence is in descending order of magnitude, indicating the existence of closer proximity between these clusters. This pattern suggesting the presence of high variability in genetic makeup of genotypes included in these clusters. High heterotic combinations will obtain when genotypes of these distinctly placed clusters were crossed. The value of inter-cluster and intra- cluster distances are presented in Table-4.

Traits considered for genotypes harvest with machine are erect growth habit, plant height (>50 cm), height of the first fruiting node (>25 cm), seed yield per plant (>15 g) and lodging resistant (scale 1) Table-5. Genotypes identified for mechanical harvesting were F6-2018-08, ICCV 181607, BG 3062 and CSJ 515. These superior genotypes can be utilized in further breeding programme.

Conclusions

The genetic diversity analysis revealed the formation of 12 clusters suggested the presence of considerable genetic diversity among the 52 genotypes studied. The analysis of per cent contribution of various characters towards the expression of total genetic divergence indicated that seed yield per plant contributed most towards genetic divergence followed by days to 50 per cent flowering and number of pods per plant. Based on the maximum genetic distance, it is advisable to attempt crossing of the genotypes from cluster III with the genotypes of cluster X and genotypes of cluster VI with genotypes of cluster X, which may lead to the generation of broad spectrum of favourable genetic variability for yield improvement also can be utilized for hybridization and superior recombinants can be obtained from these clusters, which can be exploited in further breeding programmes. Genotypes *viz.,* GJG 1916, ICCV 201107, ICCV 201112, ICCV 201114, IG 2020-2 and PG 191618 were found most suitable and promising for mechanical harvesting.

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