Website : www.asthafoundation.in
Progressive Research : An International Journal
Vol 17 (1) : 30-33 (January-2022), Print ISSN : 0973-6417, Online ISSN : 2454-6003
Society for Scientific Development in Agriculture and Technology, Meerut (U.P.) India

Genetic Diversity Studies in Desi Chickpea (*Cicer arietinum* L.) Genotypes Suitable for Machine Harvest

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Abstract

The experiment was conducted to assess genetic diversity and suitability to machine harvest in *desi* chickpea (*Cicer arietinum* L.) genotypes during Rabi 2019-20grown in a Randomized Block Design with three replications. The data were recorded on 11 quantitative traits with two morphological traits. Genetic diversity study grouped 44 genotypes into eight distinct clusters. Reproductive phase duration contributed maximum (73.68%) towards genetic divergence, followed by number of pods per plant (10.36%), 100-seed weight (7.19%) and seed yield per plant (3.38%). Based on inter cluster distance, Cluster VIII had high mean value for plant height, number of branches per plant, number of pods per plant, stem thickness, seed yield per plant and 100-seed weight. Cluster VII and cluster III was desirable for early days to 50% flowering; days to maturity and short reproductive phase duration, respectively. Whereas, cluster I and cluster VI had high mean value for height of the first fruiting node and number of seeds per pod, respectively. Based on yield and traits related to machine harvest, genotype F6-2018-08, ICCV 181607, BG 3062 and CSJ 515 were identified for mechanical harvesting. These superior genotypes can be utilized in further breeding programme.

Key words : *Chickpea, genetic diversity and mechanical harvesting.*

Introduction

Chickpea [*Cicer arietinum* (L.) 2n=2x=16] popularly known as Gram, Bengal gram, Chhola and Garbanzo bean is one of the first seed legumes to be domesticated by humans in old world (1). The genus *Cicer* belongs to the sub-family *Papilionaceae* of the family *Leguminoceae* (2) now popularly known as *Fabaceae*. It is an annual, self-pollinating, diploid pulse crop. The origin of the crop is considered to be western Asia from which it has spread to India and elsewhere in the world (3). In India, the area under chickpea was 95.5 lakh hectares with a production of 99.4 lakh tonnes and productivity of 1041 kg/ha during 2018-19. In Gujarat, an area under chickpea was 1.73 lakh hectares with a total production of 2.35 lakh tonnes and productivity of 1358 kg/ha during 2018-19. (4). Over 90% of the chickpea area is in developing countries, such as India, Pakistan, Iran, Myanmar, Ethiopia, Tanzania and Malawi, where chickpeas are largely harvested manually. However, in developed countries like Australia, Canada, the United States and Spain, chickpeas are harvested by machine. The traits required for the suitability to machine harvesting include tall and erect to semi-erect growth habit and lodging tolerance. Manual harvesting of chickpeas is becoming more and more costly due to higher labour costs and labour shortages at peak times of need. Delays in harvests result in substantial losses of grain and grain quality. Knowledge of genetic diversity is necessary to successfully implement breeding programmes. To further enhance the crops with the desired trait combinations, it is necessary to use various parents for the hybridization program in order to achieve superior segregation. So, the present experiment was formulated to study the genetic divergence for selection of suitable parents for utilizing in hybridization programme aimed at combining characters related to machine harvest and yield and yield attributes.

Materials and Methods

Investigation was carried out with 44 chickpea genotypes were sown in a Randomized Block Design (RBD) with three replications during *Rabi* 2019-20 at Pulses Research Station, J.A.U., Junagadh. Each population was accommodated in two 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% 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, 100-seed weight (g), and seed yield per plant. The replication wise

Received : December-2021; Revised : December-2021; Accepted : January-2022

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

Cluster no.	No. of genotypes	Name of genotypes
I	5	GJG 1914, GJG 1916, ICCV 181601, ICCV 181603, ICCV 181605
II	6	ICCV 181609, ICCV 181674, JG 16, NBeG 47, PG 01808, ICCP 2
III	11	GJG 1902, ICCV 181608, ICCV 181610,ICCV 181611, ICCV 181612, ICCV 181664, ICCV 181102, ICCV 181106, ICCV 181107, ICCV 181108, KDG2013-2
IV	1	H 14-14
V	11	GJG 1607, GJG 1918, ICCV 181604, ICCV 181668, ICCV 181101, JG 24, AKG 1303, H 15-27, PBC 546-18, DBGV 221, BG 4003
VI	8	GJG 1917, F6-2018-08, ICCV 181607, ICCV 181613, ICCV 181111, RG 2015-08, IPC 14-39, CSJ 515
VII	1	ICCV 181606
VIII	1	BG 3062

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

Sr. No.	Character	Times Ranked 1st	Contribution towards divergence %
1.	Days to 50% flowering	8	0.85%
2.	Days to maturity	1	0.11%
3.	Reproductive phase duration	697	73.68%
4.	Height of first fruiting node (cm)	4	0.42%
5.	Plant height (cm)	9	0.95%
6.	Number of branches per plant	12	1.27%
7.	Number of pods per plant	98	10.36%
8.	Number of seeds per pod	13	1.37%
9.	Stem thickness (mm)	4	0.42%
10.	100-seed weight (g)	68	7.19%
11.	Seed yield per plant (g)	32	3.38%

mean values of randomly selected plants were used for statistical analysis for different characters. (5) D^2 statistics was used for assessing the genetic divergence among 44 genotypes. On the basis of magnitude of D^2 value the genotypes were grouped into number of clusters as suggested by Tocher's method as described by Rao (6). 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

All the 44 genotypes were grouped into 8 clusters exhibiting significant variability for selecting genotypes for further breeding programmes. Cluster III and V were the largest among all the clusters consisting of 11 genotypeseach**.** It was followed by cluster VI consist of 8 genotypes, cluster II consist of 6 genotypes and Cluster I consist of 5 genotypes, while cluster IV, VII and VIII had only 1 genotype each (Table-1).

The characters which showed more contribution (%) towards the divergence should be considered prime during selection. The percentage contribution towards genetic divergence by 11 quantitative characters (Table-2) revealed that, reproductive phase duration (73.68%) contributed most towards genetic divergence, followed by number of pods per plant (10.36%), 100-seed weight (7.19%) and seed yield per plant (3.38%), number of seeds per pod (1.37%) and number of branches per plant (1.27%). These characters were responsible for expressing of maximum diversity between the clusters, whereas days to 50% flowering (0.85%), days to maturity (0.11%), height of first fruiting (0.41%), plant height (0.95%) and stem thickness (0.42%) did show very negligible contribution towards genetic divergence. This results are in similar with (7, 8, 9) for number of pods per plant, seed yield per plant and 100-seed weight. Similar result for plant height contributing negligible towards genetic divergence was observed by (8) and similar result for days to 50% flowering and days to maturity was observed by (10).

The cluster mean for different characters are presented in Table-3. The observations obtained from overall cluster means indicated that, Cluster VIII had high mean value for plant height (61.02 cm), number of branches per plant (3.13), number of pods per plant (75.94), stem thickness (8.99 mm), seed yield per plant (27.41) and 100-seed weight (26.56). Cluster VII was desirable for early days to 50% flowering (39.67 days).

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

Cluster	DF	DM	RPD	HFF (cm)	PH (cm)	NBP	NPP	SPP	ST (mm)	SYP (g)	100-S W (g)
Cluster I	48.13	113.13	65.00	33.85	57.09	1.68	30.35	1.36	5.79	7.67	22.88
Cluster II	45.94	112.00	66.06	29.16	50.66	1.84	31.73	1.43	5.26	7.95	24.46
Cluster III	45.85	108.39	62.55	31.69	55.75	2.29	38.20	1.41	5.60	9.66	25.15
Cluster IV	46.00	109.67	63.67	30.51	46.41	1.33	21.69	1.12	5.14	4.93	12.05
Cluster V	46.52	114.45	67.94	33.26	56.89	2.45	50.13	1.43	6.55	11.86	24.99
Cluster VI	44.33	114.21	69.88	31.46	56.09	2.68	47.67	1.47	6.08	11.71	25.95
Cluster VII	39.67	117.33	77.67	27.79	49.06	1.53	25.83	1.22	5.27	9.21	22.62
Cluster VIII	49.00	125.00	76.00	30.09	61.02	3.13	75.94	1.36	8.39	27.41	26.56

Table-4 : Inter and intra cluster D^2 values for different clusters.

Cluster	I	II	III	IV	V	VI	VII	VIII
I	9.79	29.21	57.47	58.96	30.43	14.20	14.19	34.87
II		11.55	31.51	33.45	15.82	31.46	37.79	23.57
III			12.07	16.49	32.85	58.50	66.70	36.25
IV				0.00	37.30	61.71	67.05	41.10
V					12.76	29.95	40.27	17.26
VI						11.87	19.72	33.74
VII							0.00	43.68
VIII								0.00

Cluster III was desirable for early days to maturity (108.39 days) and short reproductive phase duration (62.55 days). Whereas, cluster I had high mean value for height of the first fruiting node (33.85 cm). Cluster VI had high mean value for number of seeds per pod (1.47).

The experimental result showed that cluster V showed highest intra cluster value (12.76), followed by cluster III (12.07), cluster VI (11.87), cluster II (11.25) and cluster I (9.79), whereas cluster IV, VII, VIII showed zero value for Intra cluster distance. The highest inter cluster divergence was observed between genotypes of cluster IV and cluster VII (67.05), followed by cluster III and cluster VII (66.70), cluster IV and cluster VI (61.71), cluster I and cluster IV (58.96), cluster III and cluster VI (58.50), cluster I and cluster III (57.47), cluster VII and cluster VII (43.68), cluster IV and cluster VIII (41.10), cluster V and VII (40.27). Inter cluster distance was lowest between cluster I and cluster VII (14.19).This sequence is in descending order of magnitude, indicating 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 would give high heterosis / heterotic segregants. The value of inter cluster and intra cluster distances are presented in Table-4.

On the basis of these characters superior genotypes are selected from two clusters having wide inter cluster distance to create maximum variability in segregating generation. Heterosis is generally attributed to genetic divergence among the parental lines involved in the crosses. These findings confirm in earlier studies of (11, 12).

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

Based on the maximum genetic distance, it is advisable to attempt crossing of the genotypes from cluster IV with the genotypes of cluster VII and genotypes of cluster III with genotypes of cluster VII, which may lead to the generation of broad spectrum of favorable 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. On the basis of plant growth habit, height of first node, plant height, resistant to lodging, and seed yield per plant the genotypes *viz.*, F6-2018-08, ICCV 181607, BG 3062 and CSJ 515 were realized as promising for mechanical harvesting.

Table-5 : Genotypes identified for the traits suitable for mechanical harvesting.

S. No.	Characters	No. of genotypes	Name of the genotypes
1.	Erect growth habit	36	GJG 1902, GJG 1914, GJG 1916, GJG 1917, GJG 1918, F6-2018-08, ICCV 181601, ICCV 181603, ICCV 181604, ICCV 181605, ICCV 181606, ICCV 181607, ICCV 181608, ICCV 181610, ICCV 181611, ICCV 181612, ICCV 181613, ICCV 181664, ICCV 181668, ICCV 181102, ICCV 181106. ICCV 181107, ICCV 181108, ICCV 181111, JG 24, NBeG 47, ICCP 2, KDG 2013-2, RG 2015-08, AKG 1303, IPC 14-39, H 14-14, H 15-27, BG 3062, DBGV 221, CSJ 515
2.	Plant height (>50 cm)	35	GJG 1607, GJG 1902, GJG 1914, GJG 1916, GJG 1917, GJG 1918, F6-2018-08, ICCV 181601, ICCV 181603, ICCV 181604, ICCV 181605, ICCV 181607,ICCV 181609, ICCV 181610, ICCV 181611, ICCV 181612, ICCV 181613, ICCV 181664, ICCV 181668, ICCV 181674, ICCV 181101, ICCV 181102, ICCV 181106. ICCV 181107, ICCV 181108, ICCV 181111, JG 24, NBeG 47, AKG 1303, IPC 14-39, H 15-27, PBC 546-18, BG 3062, CSJ 515, BG 4003
3.	Height of the first fruiting node (>25 cm)	42	GJG 1607, GJG 1902, GJG 1914, GJG 1916, GJG 1917, GJG 1918, F6-2018-08, ICCV 181601, ICCV 181603, ICCV 181604, ICCV 181605, ICCV 181606, ICCV 181607, ICCV 181608, ICCV 181609, ICCV 181610, ICCV 181611, ICCV 181612, ICCV 181613, ICCV 181664, ICCV 181668, ICCV 181674, ICCV 181101, ICCV 181102, ICCV 181106. ICCV 181107, ICCV 181108, ICCV 181111, JG 16, JG 24, NBeG 47, ICCP 2, KDG 2013-2, RG 2015-08, AKG 1303, IPC 14-39, H 14-14, H 15-27, PBC 546-18, BG 3062, CSJ 515, BG 4003
4.	Seed yield per plant (>15 g)	6	F6-2018-08, ICCV 181607, BG 3062, DBGV 221, CSJ 515, BG 4003
5.	Lodging resistance (Scale 1)	27	GJG 1607, GJG 1914, GJG 1916, GJG 1918, F6-2018-08, ICCV 181604, ICCV 181607, ICCV 181608, ICCV 181609, ICCV 181610, ICCV 181668, ICCV 181101, ICCV 181102, ICCV 181106, ICCV 181107, ICCV 181108, ICCV 181111, JG 24, NBeG 47, PG 08108, ICCP 2, AKG 1303, IPC 14-39, H 14-14, PBC 546-18, BG 3062, CSJ 515

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