The Pharma Innovation Journal 2022; 11(12): 1321-1324

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2022; 11(12): 1321-1324

www.thepharmajournal.com
Received: 02-09-2022
Accepted: 06-10-2022

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Assessment of genetic variability and diversity in chickpea (*Cicer arietinum* L.)

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Abstract
The investigation on "Genetic diversity studies in chickpea (*Cicer arietinum* L.)" was conducted on 44 genotypes of chickpea to know the variability, interrelationship among yield and its components, their direct and indirect effects on seed yield and genetic divergence of various chickpea genotypes. A wide range of variability was observed for almost all the characters except number of seeds per pod. The character number of pods per plant showed highest range of variability followed by 100-seed weight, plant height, days to 50 percent flowering, seed yield per plant showed considerable amount of variability. The variability was lowest for number of seeds per pod, number of secondary branches per plant.

Genotypic and phenotypic coefficients of variation were highest for 100-seed weight followed by seed yield per plant, number of pods per plant, number of secondary branches per plant and plant height. High heritability coupled with high genetic advance as percent of mean was observed for the 100-seed weight, number of seeds per plant, number of pods per plant, number of secondary branches per plant, plant height, seed yield per plant suggesting that the selection of these traits would be effective for the desired improvement. The cluster I was the largest cluster comprising of 21 genotypes, cluster VII was 6 genotypes, cluster II with 5 genotypes and cluster VI with 4 genotypes, cluster IV (2) genotypes. The cluster III, V, VIII, IX, X, XI was solitary since they had only one genotype. The highest cluster distance (D=28.40) was found between the clusters VII and XI, followed by the cluster VI and VII (26.63) and cluster IV and VII (24.01). This indicated that hybridization among the genotypes between these clusters would produce successful hybrids and desirable segregants in further generations. The D^2 statistics showed that there was adequate diversity among the genotypes. On the basis of D^2 values 44 genotypes studied were grouped into eleven clusters. On the basis of inter cluster distance and cluster means the genotypes *viz*., BG-4010, Phule Vikram, NDG 18-9, RVSSG-79, GNG-2462, RKG 19-1, BAUG-106 and BRC 9-14 were identified for their use in hybridization programme.

Keywords: Genetic diversity, chickpea and D^2 values, GCV & PCV effects, genetic advance

Introduction
Pulses production in India is characterized by diversity of crops and their regional specificity based on adaption to prevailing agro climatic conditions. This group of crops can utilize limited soil moisture and nutrients more efficiently than cereals. Pulses have a significant role in farming systems as a substitute for fallow in cereal rotations.

Chickpea (*Cicer arietinum* L.) is traditionally grown in many parts of the world since ancient time, both in Asia and Europe. Chickpea (*Cicer arietinum* L.) is an annual, cleistogamous, self-pollinated and diploid (2n=16) grain legume crop grown in a wide range of environments including the Mediterranean, South and West Asia, North America, and North and East Africa. It belongs to genus Cicer and tribe Cicerae Alef and family Fabaceae. Chickpea is known to have nine annual and thirty five perennial species (Van der Maesen *et al*., 2007) [16]. Based on seed protein electrophoresis, Ladizinsky and Adler (1976) [7] considered *Cicer reticulatum* the wild progenitor of cultivated chickpea and South Eastern Turkey as the center of origin for the crop.

Among the pulses, chickpea is important *Rabi* crop of India. Nearly 90 percent of the crop is cultivated under rainfed condition on receding soil moisture and on marginal lands. In India, area under chickpea was 10.17 million ha, production of over 11.35 million tons and the ever highest productivity level of 1116 kg ha^{-1} (Anonymous, 2019-20) [2, 3]. In India, Madhya Pradesh, Uttar Pradesh, Rajasthan, Maharashtra, Andhra Pradesh, Tamilnadu and Telangana are major chickpea producing states contributing more than 88 percent to the total chickpea production. Madhya Pradesh is the single largest producer in the country accounting for over 40 percent of total production followed by Rajasthan, Maharashtra, Uttar Pradesh and

Karnataka Maharashtra grows total pulses on about 43.87 lakh ha area producing 40.27 lakh tons and the productivity of pulses 918 kg ha^{-1} in the year 2019-20. The chickpea area in Maharashtra was about 23.21 lakh ha with production 25.97 lakh tons and the productivity level of 1118 kg ha^{-1} (Anonymous, 2019-20) [2, 3].

Pulses are important constituents of the Indian diet and supply a major part of the protein requirement. Chickpea provides high quality protein, particularly for vegetarians. It is also used as a feed for livestock. Like other pulse crops chickpea has multiple function in the traditional farming systems in many developing countries.

Chickpea seed contain on average 22 percent protein, 4.5 percent fat, 63 percent Carbohydrates, 1-5 percent crude fibre, 2.7 percent ash and 358 calories (Miao *et al.*, 2009) [9]. Being fairly tolerant to soil moisture stress, it occupy important position in different cropping system. Chickpea (*Cicer arietinum* L.) is mainly divided into two types Desi and Kabuli. Desi type is characterized by small, coloured seeds, angular shape with high percentage of fibre and Kabuli type characterized by large, ram-head-shaped, coloured seeds with low percentage of fibre. It is mostly used in the form of dhal. An acrid liquid from the glandular hairs is collected by spreading a cloth over the crop at night, which absorbs the exudation with the dew, it contains malic and oxalic acid and is used medicinally and as vinegar. Due to its high protein content, health benefits and various domestic uses there is wide scope for production of chickpea and develop small scale industries.

The cultivation of chickpea is very wide hence the information about the nature and magnitude of genetic divergence is essential and there is need to critically analyze the formulation of yield in diverse material of chickpea. Indeed this in turn helps in establishing the selection strategy and identification of diverse parents which upon hybridization lead to a wide spectrum of gene combination.

Genetic diversity among the parents, which is heritable is a pre-requisite for any successful breeding programme. The proper choice of parents in the breeding programme is of paramount importance. Genetic divergence among the parents plays a vital role in cultivar improvement because, crosses involving genetically diverse parents is likely to produce high heterotic effects and also more variability in segregating generations, which can be exploited for the improvement. Generally, plant breeders select the parents on the basis of phenotypic divergence, but for effective breeding, the knowledge of genetic diversity among the parents with respect to the characters which are to be improved is must.

The Mahalanobis (1936) [8] D^2 statistic is powerful tool for quantifying the divergence between two populations. Many studies based on this technique also indicated that geographical diversity is not necessarily related to genetic diversity. It, thus, gives better idea about the magnitude of divergence and is independent of size of sample and provides the basis for selection of parental lines for future breeding programme.

Material and Methods

The investigation of 44 genotypes which were obtained from the Principal Scientist, Pulses Improvement Project, M.P.K.V., Rahuri. The experiment was evaluated in a Randomized Block Design (RBD) with three replications each genotype was sown in single row of 4 m length with spacing 30 cm between row and 10 cm within rows. The observations were recorded on five randomly selected plants from each treatment in each replication for eight morphological characters *viz*., Days to maturity, Days to 50% flowering, Plant height, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100-seed weight, seed yield per plant (g).

Analysis of variance commonly applicable to the Randomized Block Design (Panse and Sukhatme, 1995) [12]. The analysis of divergence was carried out by D^2 statistics proposed by Mahalanobis (1936) [8] as described by Rao (1952) [14].

Results and Discussion

The analysis of variance revealed significant genotypic differences for all the eight characters. Mean sum of squares due to treatments were significant for all the characters indicating genotypes differed significantly. Mean and range traits of the genotypes are presented in Table 1. Genotypic coefficient variation (GCV) was highest for 100 seed weight (23.40%) followed by seed yield per plant (22.88%), number of pods per plant (21.65%) and number of secondary branches per plant (19.30%). While, low GCV were observed for days to maturity (2.97%) and days to 50% flowering (8.09%). (Table 1)

The high estimates of PCV were observed for seed yield per plant (24.44%) followed by 100 seed weight (23.57%), number of pods per plant (22.82%), number of secondary branches per plant (20.36%). However, the low PCV were observed for days to fifty 50% flowering (8.17%) and days to maturity (3.05%). Genetic variability is the basis for any heritable improvement in the crop plants (Table 1). The estimates of GCV and PCV for all the characters studied showed little difference the latter being slightly greater than the former, thus indicating that the variability existing in these characters was not only due to genetic factors but also due to environmental factors.

Table 1: Estimates of variability parameters for seed yield and its contributing characters in forty four chickpea genotypes

Sr. No.	Character	Mean	Range	GCV (%)	PCV (%)	Heritability (h^2) (b.s.) (%)	Genetic Advance	Genetic Advance % of Mean
1	Days to 50 percent flowering	52.25	43.00-63.00	8.09	8.17	98.20	8.62	16.51
2	Days to maturity	98.40	92.00-105.00	2.97	3.05	94.50	5.84	5.94
3	Plant height (cm)	45.21	34.90-58.00	13.31	14.05	89.70	11.75	25.96
4	Number of secondary branches/plant	11.58	8.20-19.60	19.30	20.36	89.80	4.36	37.68
5	Number of pods/plant	45.92	23.80-70.00	21.65	22.82	90.00	19.32	42.30
6	Number of seeds/pod	1.13	1.00-1.51	10.21	10.52	94.10	0.23	20.40
7	100 seed weight (g)	24.67	12.53-37.76	23.40	23.57	98.50	11.80	47.85
8	Seed yield /plant (g)	14.11	6.34-22.90	22.88	24.44	87.70	6.30	44.13

The character 100 seed weight and seed yield per plant exhibited highest estimates of genotypic (GCV) and phenotypic coefficients of variation (PCV) indicating good scope for their improvement through selection. The phenotypic coefficients of variation (PCV) were highest for the character 100 seed weight and seed yield per plant. This was in the conformity with the results, Astereki *et al.*, (2015) [4] studied genetic diversity of 25 chickpea genotypes, the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for seed yield, days to flowering, flowering period, canopy height, number of pods per plant, Kishor *et al.*, (2018) [6] lowest GCV and PCV were recorded for days to maturity and days to 50% flowering, high genotypic coefficient of variation and phenotypic coefficient of variation was found for 100 seed weight.

In general, the magnitude of phenotypic coefficient of variation was higher than the genotypic coefficient of variation. The highest magnitudinal difference between GCV and PCV was recorded for seed yield per plant (1.56) followed by number of pods per plant (1.17), number of secondary branches per plant (1.06) and plant height (0.74). While, lowest difference between GCV and PCV was found for days to maturity (0.08), days to 50% flowering (0.08).

Heritability in broad sense is presented in Table 1. The heritability (b.s.) estimate range varied 98.50% to 87.70%. High estimates of heritability (>60%) was observed for almost characters studied. The maximum estimates of heritability exhibited in 100 seed weight (98.50%) followed by days to 50 percent flowering (98.20%), days to maturity (94.50%), number of seeds per pod (94.10%), number of pods per plant (90.00%), number of secondary branches per plant (89.80%), plant height (89.70%) and seed yield per plant (87.70%).

The range of genetic advance (GA) observed from 0.23 to 19.32. The highest estimate of GA for number of pods per plant (19.32) followed by 100 seed weight (11.80), plant height (11.75), days to 50 percent flowering (8.62) and seed yield per plant (6.30).

Table 2: Grouping of forty four genotypes of chickpea into different clusters based on D^2 values

Cluster No.	Number of genotypes in cluster	Name of Genotypes
I	21	PG-237, PG-227, JG-315, GJG-1707, Phule G-0405, IPC 2016-107, DBGC-1, AKG-1506, GL-17020, IPCD 2016-44, GJ-1708, BUC-1, BDNG 2017-44, ADBG-487, RVSSG-81, NDG 18-2, BDNG 2017-49, GCP-101, DC 18-1104, DC 18-1107, RLBG-6
II	5	JG-16, BRC 9-14, RKG 19-2, BG-4010, Phule Vikram
III	1	BG-4011
IV	2	GNG-2477, RSGD-1057
V	1	NDG 18-9
VI	4	RSGD-1071, GL-16063, H-13-36, IPC 2015-12
VII	6	Phule G-171105, NBeG-698, NBeG-690, JG 2019-155-118, Phule G-171103, RVSSG-79
VIII	1	BAUG-106
IX	1	GNG-2462
X	1	RKG 19-1
XI	1	H-12-22

Clustering of forty four genotypes were grouped into eleven clusters. The cluster I was the largest cluster comprising of 21 genotypes, cluster VII was 6 genotypes, cluster II with 5 genotypes and cluster VI with 4 genotypes, cluster IV (2) genotypes. The cluster III, V, VIII, IX, X, XI was solitary since they had only one genotype (Table 2). The results were observed by Jeena et al. (2005) [18] grouped 80 genotypes into 11 clusters out of which in cluster I maximum of 60 genotypes were grouped. Nimbalkar and Harer (2001) [10] grouped 40 chickpea genotypes into 16 clusters; out of that, 10 were solitary. Pandey (2016) [11] conducted experiment in 100 genotypes were grouped into sixteen clusters. The cluster I consisted of maximum 29 genotypes, Brindaban et al. (2020) [5] the diversity analysis revealed grouping of 20 chickpea genotypes in five clusters. The cluster I consisted of maximum 13 genotypes.

Table 3: Average intra and inter cluster D values for eleven clusters in forty four chickpea genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	7.51	11.85	9.60	13.13	10.33	16.16	15.51	13.15	11.42	12.36	16.41
II		8.18	13.66	12.11	18.20	14.31	23.49	10.41	16.34	16.72	10.85
III			0.00	12.20	10.86	11.01	17.52	17.01	8.75	14.22	15.76
IV				4.41	19.42	12.68	24.01	12.97	16.56	18.80	11.20
V					0.00	20.78	9.45	19.63	11.51	11.23	22.57
VI						7.76	26.63	18.85	15.24	21.20	13.65
VII							10.99	23.56	16.23	16.29	28.40
VIII								0.00	19.42	19.98	13.59
IX									0.00	16.40	21.92
X										0.00	19.48
XI											0.00

Diagonal: Intra cluster and above diagonal inter cluster D values

The average intra and inter cluster D values are presented in Table 3. The inter cluster distance (D) varied from 8.75 to 28.40. Maximum inter cluster distance (D=28.40) was found between the clusters VII and XI, followed by the cluster VI and VII (26.63) This indicated that hybridization among the genotypes between these clusters would produce successful

hybrids and desirable segregants in further generations, and cluster IV and VII (24.01). The minimum inter cluster distance (D=8.75) was between clusters III and IX. An examination of intra cluster divergence among the eleven clusters revealed that, cluster VII had highest intra cluster distance (D=10.99) followed by cluster II (8.18), indicating that this clusters are more heterogeneous. As the clusters III, V, VIII, IX, X, XI was solitary; there was no intra cluster divergence.

The estimates of D^2 values ranged from 6.39 to 1150.90. This clearly indicates the presence of adequate diversity between genotypes studied. Nimbalkar and Harer (2001) [10], Sandhu *et al.* (2006) [15], Parhe *et al.* (2014) [13], Ambilwade *et al.* (2018) [1], Brindaban *et al.*(2020) [5] reported wide genetic diversity in chickpea germplasm. The highest D^2 value was between a pair of genotypes viz., IPC-2015-12 and RVSSG-79 (1150.90), while lowest (6.39) was between PG-237 and PG-227.

The usefulness of D^2 analysis was enhanced by its application to estimate the relative contribution of the various plant characters to genetic divergence. The percent contribution of eight characters studied, it was observed that 100 seed weight (57.93%), days to 50% flowering (18.92%) contributed highest for divergence followed by number of seeds per pod (7.93%). Seed yield per plant (0.63%).

Conclusion

Thus it was concluded that, sufficient variability was present among the genotypes studied for all the characters except seeds per pod. The character 100 seed weight and seed yield per plant exhibited highest estimates of genotypic (GCV) and phenotypic coefficients of variation (PCV) indicating good scope for their improvement through selection. High heritability coupled with high genetic advance as percent of mean was observed for 100 seed weight, number of seeds per plant, number of pods per plant, number of secondary branches per plant, plant height, seed yield per plant suggesting that, these traits are under control of additive gene action and potential possibilities exist for the improvement of these characters through simple selection. The D^2 values showed adequate genetic diversity among the genotypes studied. On the basis of D^2 values all the genotypes were grouped into eleven clusters with varying number of genotypes in the clusters. A considerable inter-cluster variation was observed among the cluster means for the characters studied *viz*., number of pods per plant, 100 seed weight and seed yield per plant. The highest cluster mean for 100 seed weight was (34.27) observed in cluster VII and lowest for cluster XI (16.97). Hence, the cluster means for important yield components and inter-cluster distance the various clusters the following parents may be used in further hybridization programme, for yield improvement.

Acknowledgement

The author is very thankful to the Pulses Improvement Project, M.P.K.V., Rahuri, as availability genotypes of chickpea and for providing the all facilities during the present investigation.

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