Journal of Pharmacognosy and Phytochemistry

Available online at www.phytojournal.com

E-ISSN: 2278-4136
P-ISSN: 2349-8234
www.phytojournal.com
JPP 2020; 9(4): 3307-3310
Received: 20-05-2020
Accepted: 22-06-2020

Rahul V Chahande
Department of Agricultural Botany, Post Graduate Institute, Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra, India

Pawan L Kulwal
Department of Agricultural Botany, Post Graduate Institute, Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra, India

Laxman B Mhase
Department of Agricultural Botany, Post Graduate Institute, Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra, India

Corresponding Author:
Rahul V Chahande
Department of Agricultural Botany, Post Graduate Institute, Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra, India

Genetic diversity analysis in chickpea (*Cicer arietinum* L.) genotypes grown under drought stress condition

Rahul V Chahande, Pawan L Kulwal and Laxman B Mhase

DOI: https://doi.org/10.22271/phyto.2020.v9.i4ag.12128

Abstract
Genetic diversity study was conducted in 32 chickpea (*Cicer arietinum* L.) genotypes using Mahalanobis D^2 Statistics. Based on D^2 values, 32 genotypes were grouped into eight clusters. The cluster III consisted of maximum 9 genotypes, followed by Cluster II, cluster I and cluster IV, which had 8, 7 and 4 genotypes, respectively. Inter cluster values varied from 3.27 to 11.60. The maximum inter cluster distance was recorded between cluster IV and VI (11.60). Characters 100 seed weight (58.67%), days to maturity (13.91%) and days to 50% flowering (13.10) contributed maximum towards diversity. On the basis of cluster mean values, cluster IV was superior for 100 seed weight and seed yield per plant. The genotypes belonging to the clusters separated by high genetic distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregants.

Keywords: Chickpea, D^2Statistics

Introduction
Chickpea (*Cicer arietinum* L.) is an important Rabi season legume having extensive geographical distribution. Chickpea is a diploid species with a chromosome number 2n=2x = 16. It is a self-pollinated crop and it belongs to family Leguminosae. Chickpea is the third most important pulse crop in the world after beans and peas. Chickpea is an important source of protein, minerals, fibres and vitamins in the diets of millions of people in Asia and Africa. Chickpea seed contains 29% protein, 59% carbohydrate, 3% fibre, 5% oil and 4% ash. Chickpea protein is rich in lysine and arginine but most deficient in sulphur-containing amino acids methionine and cystine (Iqbal *et al*., 2006) [2].

A healthy crop of chickpea can fix up to 141 kg nitrogen per hectare. India is the largest producer, with about 8 million tons, accounting of about 70% of total world production. In Maharashtra, production of 1058 thousand tonnes were recorded with productivity of 844 kg/ha on area of 1314 thousand hectares. Maharashtra is the second largest producing state in the country after Madhya Pradesh with share of 14% (www.mahaagri.gov.in, 2015).Chickpea production is adversely affected by various biotic and abiotic stresses. Among the various major concerns caused by different abiotic stresses in rain-fed ecosystem globally, terminal drought is the major constraint for chickpea production (Kashiwagi *et al*., 2006) [3]. Terminal drought causes yield losses of around 3.7 Mt that amounts to 40 to 50% of the average loss (Varshney *et al*., 2009) [9]. The more diverse the parents within reasonable limits, the more are the chances of obtaining heterotic broader spectrum of variability in the segregating populations. The present study was, therefore, conducted with a view to identify divergent parents for future hybridization programmes for yield improvement of chickpea under drought stress condition.

Materials and methods
The experiment consisted of 32 chickpea genotypes of diverse origin developed by various research institutes/stations (Table 1) within the country. The trial was laid out following Randomized Block Design with two replications at Agricultural Botany Farm, Mahatma Phule Krishi Vidyapeeth, Rahuri during Rabi 2017-18. Each entry was grown in a two rows of 3.0 m length (30 plants/genotype) with inter and intra-row spacing of 30 × 10 cm. Irrigation was given at the time of sowing for germination of seeds. Further irrigations were not given to crop as we wanted to create drought stress condition. Data were recorded on five randomly tagged plants for plant height after one month of sowing, plant height after second month of sowing, plant height at maturity, days to 50% flowering, primary branches per plant, pods per plant, seeds per five pods, days to maturity, 100 seed weight and yield per plant.

The data recorded were subjected to D^2 statistics to know the genetic diversity among the germplasm as suggested by Mahalanobis (1936) [5]. Grouping of genotype into different clusters was done as per the method describe by Rao (1952) [6].

Table 1: Details of chickpea genotypes used in the investigation

S. No.	Genotypes	Pedigree	Source
1	H-12-01	GL-94022 × ICC-4958	Hissar
2	GNG-2300	HC-5 × GNG-663	Shriganganagar
3	JG-35	JG-130 × ICC-11551	Jabalpur
4	CSJ-859	RSG-143-1 × JG-315	Durgapura
5	GNG-2294	HC-5× GNG-1581	Shriganganagar
6	RVSSG-35	BG-362 × JG-16	Sehore
7	H-12-80	C-235 × HOO-216	Hissar
8	BG-3066	BG-391×BG-240	IARI, New Delhi
9	NDG-14-11	Avrodhi × NDG-30	Faizabad
10	IPC-2011-141	KWR-108 × EC-56270	IIPR, Kanpur
11	IPC-2012-31	Katila × ICCV-10	IIPR, Kanpur
12	Phule G-13107	ICCV-03112 × JAKI-9218	Rahuri
13	Digvijay	Phule G-91028 × Bhima	Rahuri
14	NBeG-806	(ICCV-10 ×ICC-4958) × ICCV-10	Nandyal
15	NBeG-807	(ICCV -10 X ICC-4958) × ICCV-10	Nandyal
16	Phule G-12113	ICCV- 03112 × JG-130	Rahuri
17	JG-74315-2	(JG-74×WR-315) × JG 74-2010-1-3-5-11-15-10-2	Jabalpur
18	H-12-26	HSC-5 × CSJ-8962	Hissar
19	GCP-101	GCP-2× ICCV-2	Junagad
20	PBC-508	ICC-5717 × ICC-96149-F_3-BP-BP67P-BP	Bhanswara
21	RVSSG-32	BG-0-112 × JSC-37	Sehore
22	NBeG-738	(ICCV-93954 × ICC-4958) ×ICCV-93954	Nandyal
23	RVSSG-33	JG-130 × KAK 2	Sehore
24	JG-315	Self from Kanpur germplasm	Jabalpur
25	ICC-4958	Germplasm collection	Jabalpur
26	PG-160	ICCV 89445 × ICCV 88502	Pantnagar
27	BG-3064	BG-1088/ FLIP	IARI, New Delhi
28	JG-16	ICCV-42 × ICCV-10	Jabalpur
29	Vijay	P-1270×Annigeri	Rahuri
30	Vishal	K850 × ICCL 80074	Rahuri
31	PBC-507	ICCV-04112 × JAKI-9218	Bhanswara
32	Phule G-0616	Phule G-00109 × GCP-101	Rahuri

Results and discussion

Based on the D^2 values the 32 genotypes were grouped into eight clusters (Table 2; Figure 1) which revealed that the genotypes varied significantly for all the characters studied indicating considerable variation in the germplasm. Tomar *et al*., (2011) [8] grouped 45 chickpea genotypes in eight clusters. Thirty diverse genotypes of chickpea were grouped into eight different clusters by Koinain *et al*., (2015) [4]. Cluster III consist of maximum 9 genotypes, followed by cluster II, I and IV which had 8, 7 and 4 genotypes, respectively. Cluster III consisted of maximum 9 genotypes indicating that the genotypes had narrow genetic divergence among them. The similarity in the base population, from which they had been evolved, might be the cause of genetic uniformity. Clusters V, VI, VII and VIII were solitary cluster with single genotype. The monogenotypic cluster indicated that genotypes belonging to these clusters had wide diversity from the rest as well as from each other. Thus, these genotypes have entirely different genetic make-up from the others.

In present investigation chickpea genotype ICC-4958 was also included. ICC-4958 was drought resistant accession available from the ICRISAT germplasm collection. It is used as a drought resistant donor parent that produces high yields in terminal drought prone environments. It is known for its prolific root system. Cluster IV consisted of 4 genotypes including chickpea genotype ICC-4958 (Table 2). In our study we evaluated chickpea genotypes under drought stress condition. Other 3 genotypes in cluster IV *viz*; IPC-2011-141, NBeG-807 and NBeG-738 might have some drought tolerant related traits due to which all these genotypes belongs to same cluster IV in which genotype ICC-4958 also belongs.

Intra cluster and inter cluster D^2 values were computed for the eight clusters (Table 3). The maximum genetic distance was found between the clusters IV and VI (11.60) followed by cluster I and IV (9.14) and cluster VI and VIII (8.58). It has been well established fact that more the genetically diverse parents used in hybridization programme, the greater will be the chances of obtaining high heterotic hybrids and broad spectrum variability in segregating generations (Arunachalam, 1981) [1]. The results of present investigation indicated that the genotypes grouped in these clusters were highly divergent from each other. Assessment of chickpea germplasm and its utilization in selection of diverse genotype from above clusters would produce a range of genetic variability for quantitative traits studies which might enable further selection and improvement.

The per cent contribution of ten characters studied, towards total divergence is presented in Table 4. It was observed that, 100 seed weight (58.67%) contributed highest for divergence. It was followed by days to maturity (13.91%) and days to 50% flowering (13.10%). The maximum contribution towards divergence was observed by Shedge *et al*., (2019) [7] in 100 seed weight (30.90%) and days to maturity (19.38%). Under drought stress condition these characters were responsible for expressing maximum diversity between the clusters and therefore, should be given due weightage during selection. Remaining characters exhibited very low or negligible contribution towards divergence.

The cluster mean values for 10 characters are presented in Table 5. Wide ranges of mean values among the clusters were recorded for different traits. The cluster mean for plant height after one month of sowing varied from 16.60 cm (VI) to 24.32 cm (II). The cluster mean for plant height after second month of sowing varied from 37.34 cm (VI) to 43.54 cm (VII). The highest cluster mean for plant height at maturity was 53.25 cm, which was observed in cluster (VIII) and lowest for (VI) 44.45 cm. The cluster mean for days to 50% flowering ranged from 53.88 days (II) to 67.00 days (VIII). The highest cluster mean for primary branches per plant was 2.43 (III) and lowest was 2.10 (VII). The highest cluster mean for pods per plant was 49.94 (I) and lowest was 17. 60 (VII). The genotypes in cluster V were found mature earlier (94.50 days) than genotypes in other clusters. Genotypes in cluster VII took maximum days to attain maturity (119.00 days). The highest cluster mean for 100 seed weight and yield per plant was found in cluster IV. Under drought stress condition genotypes in cluster IV performed better for traits 100 seed weight as well as for yield per plant. It is important to mention here that drought tolerant genotype ICC-4958 also belongs to the same cluster. Hence, these genotypes (IPC-2011-141, NBeG-807 and NBeG-738) can be used as drought tolerant parent in hybridization programme.

Yucel *et al*., (2006) [10] concluded that the yield and yield components are multigenic traits and are strongly influenced by the environment. Under drought stress condition traits 100 seed weight, days to maturity and days to 50% flowering contributed maximum towards divergence. Therefore, the emphasis should be given to these characters for improvement of chickpea yield under drought stress condition. Narrow genetic base of the material is the major limiting factors for initiating the breeding programme aimed at increasing the yield potential of any crop. It is generally observed that the genetically diverse parents show maximum heterosis and provide scope for the selection of the transgressive segregants. The hybridization between the genotypes of the same cluster thus, may not provide good segregants. Therefore, in the present investigation, based on large inter-cluster distances, it is advisable to attempt crossing of the genotypes from clusters IV and VI, which may lead to broad spectrum of favourable genetic variability for yield improvement in chickpea.

Table 2: Grouping of 32 chickpea genotypes into 8 clusters by Tocher's method

Cluster No.	Number of Genotypes	Genotypes
I	7	PBC-508, Phule G-0616, JG-315, H-12-26, BG-3064, JG-34315-2, Vijay
II	8	Phule G-13107, Digvijay, RVSSG-33, NBeG-806, Phule G-12113, PBC-507, JG-35, Vishal,
III	9	GCP-101, RVSSG-32, H-12-80, GNG-2294, RVSSG-35, BG-3066, IPC-2012-31, GNG-2300, NDG-14-11
IV	4	IPC-2011-141, NBeG-807, ICC-4958, NBeG-738
V	1	CSJ-859
VI	1	JG-16
VII	1	H-12-01
VIII	1	PG-160

Table 3: Average intra and inter cluster distance D^2 values

Clusters	I	II	III	IV	V	VI	VII	VIII
I	3.38	6.14	4.99	9.14	4.97	3.95	6.29	7.05
II		3.35	5.97	5.08	4.47	8.33	4.89	6.79
III			4.37	7.88	5.04	5.92	5.59	5.81
IV				3.27	7.59	11.60	5.62	7.71
V					0.00	6.04	6.51	7.57
VI						0.00	8.15	8.58
VII							0.00	4.80
VIII								0.00

Table 4: Percent contribution of 10 characters for diversity in chickpea

S. No	Characters	Times ranked 1st	Contribution (%)
1	Plant height after one month of sowing	30	6.05
2	Plant height after second month of sowing	1	0.20
3	Plant height at maturity	5	1.01
4	Days to 50% flowering	65	13.10
5	Primary branches per plant	2	0.40
6	Pods per plant	6	1.21
7	Seeds per five pods	2	0.40
8	Days to maturity	69	13.91
9	100 seed weight	291	58.67
10	Yield per plant	25	5.04
	Total	496	100

Table 5: Cluster means performance for 10 characters of 32 chickpea genotypes

Clusters	PH1	PH2	PM	DF	PB	PP	SP	DM	SW	YP
I	19.73	39.73	46.37	54.00	2.24	49.94	5.86	105.43	18.36	52.21
II	24.32	41.93	50.28	53.88	2.30	39.31	7.00	103.69	24.81	60.00
III	17.59	41.48	49.77	61.28	2.43	38.46	6.00	105.50	20.67	48.00
IV	21.68	42.61	51.04	57.38	2.30	41.20	6.38	106.13	28.76	69.63

V	24.30	37.95	44.60	57.00	2.20	31.20	7.50	97.50	22.42	50.00
VI	16.60	37.34	44.45	54.00	2.40	32.60	6.00	103.00	15.72	33.00
VII	17.30	43.54	48.65	57.00	2.10	17.60	5.50	111.50	24.04	30.50
VIII	17.17	41.53	53.25	67.00	2.20	34.80	8.00	119.00	20.40	32.00

PH1- Plant height after one month of sowing, PH2-Plant height after second month of sowing, PM-Plant height at maturity, DF-Days to 50% flowering, PB-Primary branches per plant, PP-Pods per plant, SP-Seeds per five pods,
DM-Days to maturity, SW-100 seed weight, YP-Yield per plant

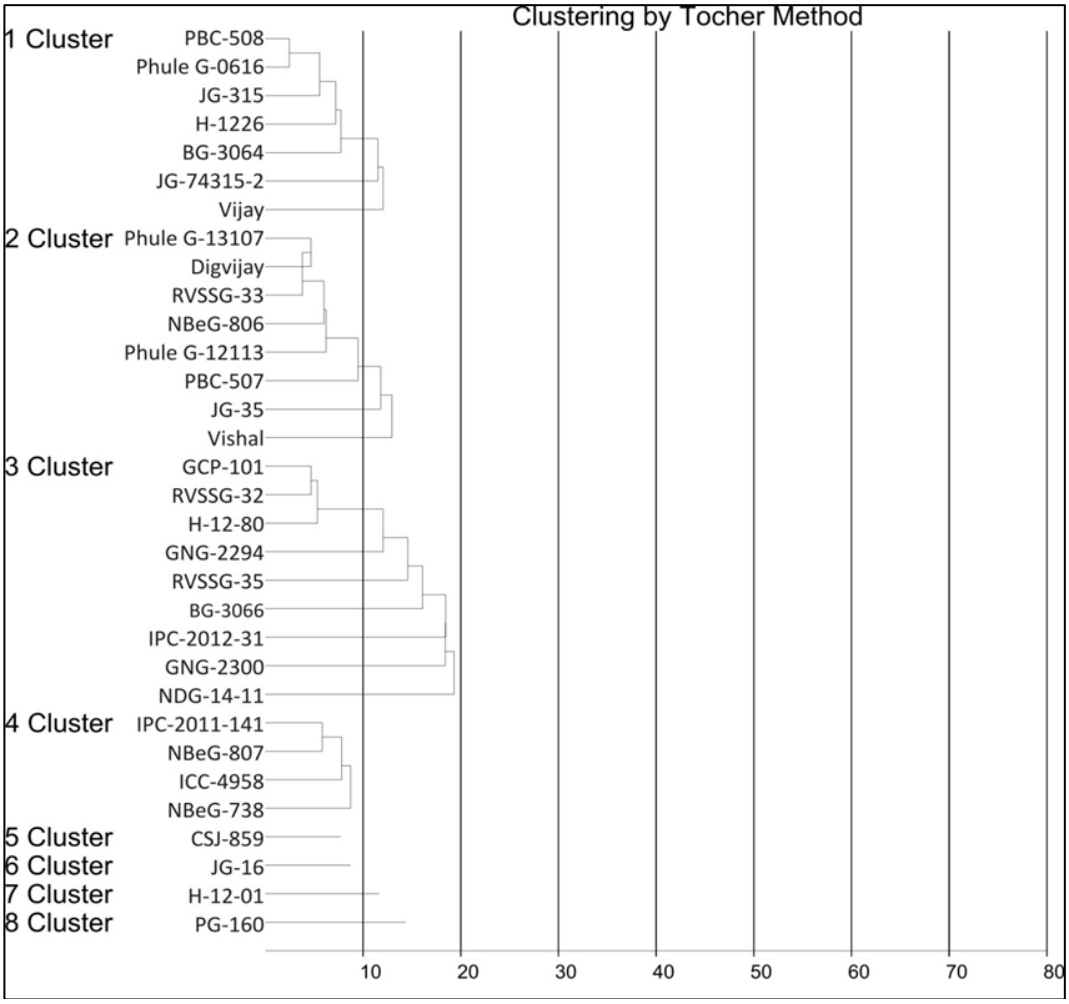

Fig 1: Grouping of 32 chickpea genotypes into 8 clusters by Tocher's method

Acknowledgment
The author is highly thankful for the financial support in the form of UGC-Maulana Azad National Fellowship during the entire Ph.D. programme at Department of Agricultural Botany, Post Graduate Institute, Mahatma Phule Krishi Vidyapeeth, Rahuri-413722, Maharashtra, India.

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