

RESEARCH ARTICLE

Assessment of genetic diversity through morphological characterization in chickpea (*Cicer arietinum* L.)

■ Kadiyala Naga Suresh and Gabriyal M. Lal

SUMMARY

The experiment was conducted at Field Experimentation Centre, Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture Technology and Sciences, Prayagraj during *Rabi* 2019-2020 in Randomized Block Design with three replications. The investigation was prevailed to examine the 40 genotypes along with one check (PUSA 362) to study the genetic variability, genetic advance, heritability and Genetic diversity. Analysis of variance exhibited significant differences among the genotypes for all the characters indicating presence of good amount of variability among the genotypes for all the characters used in study. High GCV and PCV were observed for biological yield (31.5 and 39.47). High heritability (>80%) was recorded for character Days to 50% flowering (89%) followed by days to maturity (87%), days to 50% flowering (86%), seed weight (82%). Higher genetic advance was observed for no. of seeds per plant (39.64) followed by no. of pods per plant (31.77), biological yield (21.07), days to 50% maturity (11.41) and plant height (11.03). D² values showed adequate genetic diversity among the genotypes studied. On the basis of D² values all the genotypes were grouped into five clusters with varying number of genotypes in the clusters. The maximum genetic distance (D) of 54.46 was found between the clusters IV and II. Greater the divergence between the 2 clusters, wider is that the genetic diversity within the genotypes. The cluster mean for days to 50 per cent flowering varied from 84.00(V) to 108 (III). The cluster mean for days to 50 per cent pod setting varied from 86.67 (IV) to 120.67 (II). The cluster mean for 100 seed weight was maximum in (cluster II) 24.33 and minimum in (cluster IV) 20. The cluster mean for harvest index was maximum in (cluster II) 56.71 and minimum in (cluster V) 38.56. The cluster mean for biological yield was maximum in (cluster III) 53.13 and minimum in (cluster II) 36.2. The cluster mean for seed yield was maximum in (cluster III) 20.93 and minimum in (cluster V) 13.2. Therefore, the genotypes present in these clusters can be used for future hybridization.

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Chickpea (*Cicer arietinum* L.) is the most important rabi season crop. It is self-pollinated pulse crop (autogamous crop) and Diploid ($2n=16$). It is the third most important crop in the world, after beans and field pea. It belongs to Family-Fabaceae, Sub-family Papilionaceae, Scientific name – *Cicer arietinum* L. The Latin words “*Cicer*” and “*arietinum*” were derived from Greek words “*Kikus*” meaning ‘force of strength’ and “*Krios*” referring to ram, respectively, because of the similarity between seed shape and head of ram (Aries) (Van der Masen 1987). It is originated from Afghanistan / Persia, South West Asia.

Two types of chickpeas are recognized, the white-seeded “Kabuli” and the brown coloured “desi” types. Desi chickpeas are widely cultivated under dry lands and mainly cultivated in India and Bangladesh. Kabuli type chickpea is mainly cultivated in Africa, Europe, Afghanistan, Pakistan, and Chile. Kabuli type chickpea is relatively bigger in size having a thinner seed coat.

Variability studies in chickpea have gained importance as the crop has high variation for different quality and quantity traits including ideal plant type (tall type), shape and colour of grain, flower colour, podding, colour of seed coat, earliness, resistance to diseases and pests, which helps breeders to release improved and advanced lines and varieties.

Genetic diversity is may be a powerful tool for determination for genetic discrimination among the genotypes which is employed to pick appropriate plant genotype(s) for hybridization to develop high yielding potential variety (Bhatt, 1970). Genetic diversity are often evaluated with morphological traits seed protein, isozymes, and DNA markers. Divergence analysis is a useful tool in quantifying the degree of divergence between the biological population at the genotypic level and to assess the relative contribution of different components to the entire divergence both at intra and inter cluster levels (Murty and Arunachalam, 1996 and Ram and Pawar, 1970). It also permits to pick the genetically diverged parents which may produce new recombinants with desirable traits once they are crossed together. Joshi and Dhawan (1996) reported that genetic diversity was a really important factor for any hybridization program aiming at genetic improvement of yield, especially in self-pollinated crops. They also inferred that Mahalanobis’s D^2 statistics was a robust tool for choosing parents for hybridization aiming at hybrid improvement.

MATERIAL AND METHODS

The experiment was conducted in *Rabi* 2019-2020 at the Field Experimental Centre, Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, U.P. The Experimental Farm is situated on the left side of Prayagraj-Rewa. National Highway, about 5km away from Prayagraj City. All types of facilities and laborers were provided from the Department of Genetics and Plant Breeding, Naini Agriculture Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, U.P.

RESULTS AND DISCUSSION

40 genotypes of chickpea (*Cicer arietinum* L.) were grown under Randomized Block Design with three replications and were evaluated for 13 characters, viz., days to 50% flowering, days to 50% pod setting, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, No. of seeds per plant, 100 seed weight (g), biological yield (g), harvest index (%) and seed yield per plant (g) during *Rabi*, 2019-2020 at field experimentation center, Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, U.P. The data collected from 40 genotypes of chickpea were used to assess mean performances, analysis of variance, genetic parameters, and genetic diversity.

The genetic improvement in plant species is inevitable and continuous process to meet the future challenges. It is necessary to have the knowledge of genetic diversity, genetic variability present in the genetic material. Analysis of variance showed significant difference among the genotypes for thirteen characters under study (Table 1). This indicated that the ample scope for selection of genotypes for yield and its components.

Wide range of differences for GCV were observed which varied from 4.5 for harvest index to 31.5% (Biological Yield) indicating considerable amount of variability present among the genotypes. Comparison of co-efficient of variance indicated that the phenotypic co-efficient of variance was above the genotypic co-efficient of variance for all the characters which indicated effect of environment on the characters expression.

Among all the characters, high GCV and PCV were

Table 1: Analysis of variance for 13 quantitative characters in 40 Chickpea genotypes

Characters	Mean sum of squares		
	Replication (df=2)	Treatments (df=39)	Error (df=78)
Days to 50% flowering	16.63	94.08***	13.38
Days to 50% pod setting	11.72	158.52***	16.57
Days to maturity	22.43	122.69***	16.38
Plant heights (cms)	31.44	173.89***	51.63
Number of primary branches	0.09	0.20***	0.08
Number of secondary branches	5.67	8.52***	2.40
Number of pods per plant	2548.28*	1615.18***	541.64
Number of seeds per pod	0.46*	0.29***	0.08
Number of seeds per plant	6104.04*	2684.98***	957.93
Seed weight (grams)	11.00	71.27***	12.68
Biological yield (grams)	690.08*	773.84***	281.02
Harvest index (%)	59.51*	157.00***	169.49
Seed yield (grams)	145.83*	141.32***	34.98

* and ** indicate significance of values at P=0.05 and 0.01, respectively

Table 2: Genetic parameters for 13 quantitative characters of 40 genotypes during Rabi 2019

	Genotypic co-efficient variance	Phenotypic co-efficient variance	h ² (Broad sense) (%)	Genetic advancement 5%	Gen. adv as % of mean 5%
Days to 50% flowering	5.82	6.28	85.80	9.89	11.10
Days to 50% pod setting	6.18	6.53	89.50	13.40	12.04
Days to maturity	4.74	5.09	86.60	11.41	9.09
Plant height (cm)	9.71	11.58	70.30	11.03	16.78
Number of primary branches per plant	10.69	14.03	58.00	0.31	16.77
Number of secondary branches per plant	23.93	28.24	71.80	2.49	41.79
Number of pods per plant	28.72	35.22	66.50	31.77	48.23
Number of seeds per pod	17.32	20.57	70.90	0.45	30.02
Number of seeds per plant	27.51	34.29	64.30	39.64	45.44
Seed weight (g)	21.78	24.02	82.20	8.25	40.67
Biological yield per plant	31.50	39.47	63.70	21.07	51.79
Harvest index (%)	4.50	15.96	08.00	1.18	2.61
Seed yield per plant	35.07	40.43	75.20	10.64	62.66

Table 3: Composition of forty chickpea genotypes into different clusters by Tocher's method

Cluster No.	No. of genotypes	Genotypes included in the cluster
		RSG-931, ICC-1205,
I	36	JG-130, IPC-04-01, ICC-244263, PHULE-G-5, IPC-1185, ICC-49-58, ILC-195, EC-556270, IPC-05-62, ICC-495, IPC-2000-33, IPC-94-94, RVG-202, GNG-1958 DCP-92-3, CSJ-512, IPC-2K-2000-25, CSQ-89-62, NEC-799, IPC-08-103, FLIP-09-162C, ICCV-16317, IPC-10-134, BGD-72, ICC-3070, KPG-59, IPC-06-77, JG-14 GNG-2226, BGD-9971, IPC-05-62, JG-37, NBEG-49, NBEG-3
II	1	PG-96006
III	1	BG-212
IV	1	IPC-57-21
V	1	PUSA 362 (CHECK)

observed for biological yield (31.5 and 39.47) indicated in Table 2. In comparison to other characters indicating the presence of high amount of genetic variability for these characters. Selection for these characters would be effective because the response to selection is directly proportional to the variability present within the experimental material. High heritability (broad sense) (>80%) was recorded for character Days to 50% flowering (89.5%) followed by days to maturity (86.6%), days to 50% flowering (85.8%), seed weight (82.2%).

D² values showed adequate genetic diversity among the genotypes studied. On the basis of D² values all the genotypes were grouped into five clusters with varying number of genotypes in the clusters mentioned in Table

3. The clustering pattern indicated that cluster I is the largest cluster comprising 36 genotypes out of 40 genotypes, cluster II, III, IV, V comprised of one genotype each. The pattern of constellation proved the existence of significant amount of variation.

Intra and inter cluster distance:

Intra and inter cluster D² and D values were worked out using D² values from diversity analysis. These are presented in Table 4 and Table 5. The minimum Intra cluster distance was found in cluster I (12.88). The monogenetic clusters II, III, IV and V shows Intra cluster values 0.

The maximum Intra cluster distance was observed

Table 4: Average intra and inter cluster distance (D) values in chickpea during Rabi 2019

Clusters	I	II	III	IV	V
I	12.88	25.19	24.38	33.74	32.63
II	25.19	0	44.44	54.46	30.95
III	24.38	44.44	0	26.05	50.30
IV	33.74	54.46	26.05	0	44.72
V	32.63	30.95	50.30	44.72	0

Table 5: Average Intra and Inter cluster D² values in chickpea during Rabi 2019

Clusters	I	II	III	IV	V
I	165.89	634.54	594.38	1138.39	1064.72
II	634.54	0	1974.91	2965.89	957.90
III	594.38	1974.91	0	678.60	2530.09
IV	1138.39	2965.89	678.60	0	1999.88
V	1064.72	957.90	2530.09	1999.88	0
Clusters	I	II	III	IV	V
I	165.89	634.54	594.38	1138.39	1064.72
II	634.54	0	1974.91	2965.89	957.90
III	594.38	1974.91	0	678.60	2530.09
IV	1138.39	2965.89	678.60	0	1999.88
V	1064.72	957.90	2530.09	1999.88	0

Table 6: Cluster mean of different characters to genetic diversity in chickpea during Rabi 2019

	Days to 50% flowering	Days to 50% pod setting	Days to maturity	Plant height	No. of primary branches	No. of secondary branches	No. of pods per plant	No. of seeds per pod	No. of seeds per plant	Seed weight (g)	Biological yield	Harvest index (%)	Seed yield (g)
I	88.74	111.3	124.6	64.92	1.85	5.94	66.40	1.47	87.26	20.09	40.50	45.03	16.96
II	91.33	129	137.67	74.33	1.93	4.40	51.40	2.00	102.67	24.33	36.20	56.71	19.13
III	108	120.67	128.00	68.8	1.20	8.33	86.80	1.47	95.07	21.33	53.13	41.73	20.93
IV	86.67	86.67	120.00	77.13	2.13	6.20	56.47	1.8	73.33	20.00	36.53	54.99	15.27
V	84	110	150.00	71.47	2.00	5.93	49.67	1.6	76.73	22.67	43.47	38.56	13.20

between cluster IV and II (54.46). Maximum Inter cluster distance was followed by 50.3 (cluster V and III), 44.72 (cluster V and IV), 44.44 (cluster III and II), 33.74 (cluster IV and I), 32.63 (cluster V and I), 30.95 (cluster V and II), 26.05 (cluster IV and III), 25.19 (cluster II and I). The minimum Inter cluster distance was observed between cluster III and I (24.38) indicating proximity with each other.

Cluster I was more distance from cluster IV (33.74) followed by cluster V (32.63), cluster II (25.19), cluster III (24.38). While cluster II showed highest distance from cluster IV (54.46) followed by cluster III (44.44), cluster V (30.95). Cluster III showed maximum distance from cluster V (50.3) followed by cluster IV (26.05).

Cluster mean:

Greater the divergence between the 2 clusters, wider is that the genetic diversity within the genotypes. The cluster means for all thirteen characters are mentioned in Table 6. The cluster mean for days to 50 per cent flowering varied from 84.00(V) to 108 (III). The cluster mean for days to 50 percent pod setting varied from 86.67 (IV) to 120.67(II). The cluster mean for days to maturity ranged between 120 (IV) to 150(V). The height cluster mean for plant height 77.13 cm which was observed in cluster IV and lowest 64.92 cm in cluster II. The cluster mean for the number of primary branches ranges from 1.2 (III) to 2.13 (IV). The cluster mean for the number of secondary branches ranges from 4.4 (II) to 8.33 (III).

The cluster mean for number of pods per plant

was maximum in (cluster III) 86.8 and it was minimum in (cluster V) 49.67. The cluster mean for number of seeds per pod was maximum in (cluster II) 2 and it was minimum in (cluster III) 1.47. The cluster mean for number of seeds per plant was maximum in (cluster II) 102.67 and it was minimum in (cluster IV) 73.33. The cluster mean for 100 seed weight was maximum in (cluster II) 24.33 and minimum in (cluster IV) 20. The cluster mean for harvest index was maximum in (cluster II) 56.71 and minimum in (cluster V) 38.56. The cluster mean for biological yield was maximum in (cluster III) 53.13 and minimum in (cluster II) 36.2. The cluster mean for seed yield was maximum in (cluster III) 20.93 and minimum in (cluster V) 13.2.

Per cent contribution of various characters for diversity:

All the 40 genotypes of chickpea studied for thirteen characters and the data collected was used to determine genetic diversity. Per cent contribution of various characters for diversity mentioned in Table 7. Out of thirteen characters studied, the character days to 50 percent pod setting (54.87%) contributed highest for diversity followed by days to maturity (30.90%), seed weight (4.23%), number of seeds per pod (1.79%), seed yield, days to 50 per cent flowering, number of secondary branches per plant (1.54%), harvest index (1.15%). However, the contribution of biological yield (0.13) was lowest followed by number of primary branches per plant (0.38%), number of pods per plant (0.51%), number of seeds per plant (0.64%) and plant height (0.77%).

Table 7: Per cent contribution of different characters of genetic diversity in chickpea during *Rabi* 2019

Sr. No.	Characters	Contribution %	Times ranked 1st
1.	Days to 50% flowering	1.54	12
2.	Days to 50% pod setting	54.87	428
3.	Days to maturity	30.90	241
4.	Plant height	0.77	6
5.	Number of primary branches per plant	0.38	3
6.	Number of secondary branches per plant	1.54	12
7.	Number of pods per plant	0.51	4
8.	Number of seeds per pod	1.79	14
9.	Number of seeds per plant	0.64	5
10.	Seed weight	4.23	33
11.	Biological yield per plant	0.13	1
12.	Harvest index	1.15	9
13.	Seed yield per plant	1.54	12
	Total	100	

Conclusion:

It is concluded that based on the mean performance of 40 genotypes of chickpea, Phule-G-5 was found superior in terms of seed yield per plant (g) followed by ICC-244263, RVG-202 and NEC-799. Analysis of variance showed significant variation among different genotypes for all the characters. No. of primary branches and No. of pods per plant exhibited high estimates of GCV and PCV. High Heritability was observed in No. of primary branches and No. of seeds per plant, high genetic advance and genetic advance as percentage mean was observed in harvest index. D² values showed adequate genetic diversity among the genotypes studied. Maximum number of genotypes were grouped into cluster 1st cluster which included 36 genotypes. Days to 50 per cent pod setting contributed highest (54.87) to divergence. The cluster II and IV and cluster III and V were found more diverse to each other. Therefore, the genotypes present in these clusters can be used for future hybridization.

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★ ★ ★ ★ ★ of Excellence ★ ★ ★ ★ ★