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Genetic Diversity for Yield and Its Component Traits in Chickpea (*Cicer arietinum* L.)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The present experiment was carried out to study the 40 chickpea genotypes to evaluate the Genetic diversity among the chickpea genotypes for yield and yield contributing traits and to identify genetically divergent parents for future hybridization. The present experiment was carried out during rabi 2019-2020 in Randomized complete block design with three replications at Sam Higginbottom university of agriculture technology and sciences, Prayagraj, Allahabad, U.P. The data was analyzed for 13 quantitative traits to study genetic variability, heritability, genetic advance, genetic advance as percent of the mean. The magnitude of genotypic coefficient of variation and phenotypic co-efficient recorded highest for a number of seeds for plant (33.31 and 34.24), high heritability associated with high genetic advance was recorded for a number of secondary branches for plant (97.11 and 59.98) suggesting that there was greater role of additive gene action in inheritance. The distribution of 40 genotypes into six clusters was by Tocher's method at a random with the Maximum number of genotypes were grouped into cluster I which includes 29 genotypes. The highest intra-cluster distance was observed for cluster I (59.53) which comprised of 29 genotypes. The highest inter-cluster distance (407.97) was found between clusters II and VI. Genotypes (IPC-71, IPC 04-52, JG-31416, L-550, IPCK 09-165, ICC-244263, IPC 94-94 and IPC 06-11 to these clusters may be used as parents to create transgressive segregants. Cluster VI

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recorded maximum mean values for the number of primary branches per plant (3.67), number of secondary branches per plant (6.47), number of pods per plant (117.13), number of seeds per plant (155.53), and seed yield per plant (g) (25.94).

Keywords: Chickpea; genetic parameters; cluster analysis; intra-cluster distance; inter-cluster distance; cluster means; Mahalanobis D^2*.*

1. INTRODUCTION

Chickpea (*Cicer arietinum* L.) is a crucial winter-season food legume having extensive geographical distribution. Its nutritional value and ecological adaptability make it an important crop globally. A chickpea seed contains 17-24% proteins, 41-50.8% carbohydrates, a high percentage of other mineral nutrients, and unsaturated linoleic and oleic acid and is one of the most important crops for human consumption [1]. Chickpea makes up for the deficiency of cereal diets. In India, the area under chickpea was grown 9.539 million hectares with a production of 90.75 million tons while the productivity was 951kg/ha. In Uttar Pradesh, it is grown on a 5.89 lakh hectares area with a total production of 5.967 lakh tons and average productivity of 1013 kg/ha during 2018-19. It occupies 61 percent of the total area under pulses producing about 65 percent of total production in Uttar Pradesh. However; its productivity is less than that in other countries due to the cultivation of chickpea on marginal lands. Lack or limited genetic variability is the crucial factor for the limited progress achieved in increasing the productivity of grain legumes including chickpeas [2]. Genetic diversity is the basis for the survival of plants in nature and for crop improvement. Genetic divergence among the oldsters plays an important role in cultivar improvement thanks to more variability in segregating generations, which may be exploited for improvement [3].

The insertion of diverse parents in hybridization helps to isolate the superior recombinants. Mahalanobis's D2 statistics could also be a strong tool in quantifying the degree of variability at the genotype level. The utility of the statistical method has been emphasized [4]. Several scientists studied the genetic diversity, clustering pattern, relative contribution of various characters towards divergence, and effectiveness of selection [5,6,7]. The genetic distance had a specific role to play in the efficient choice of parents for hybridization programs [8]. The present study aims to find out the genetic diversity among the 40 chickpea genotypes. The present investigation was carried out to identify the genetically divergent parents for the future hybridization program and to obtain more yielding varieties.

2. MATERIALS AND METHODS

The Experimental material was obtained from the ICAR-Indian Institute of pulses research, Kanpur, Uttar Pradesh. The experimental materials comprising of 40 genotypes including one check variety was grown during rabi 2019-2020 under Randomized Block Design (RBD) with three replications. The experimental field was divided into 3 blocks of equal size and each line contained a single genotype. Data were recorded on five randomly selected plants for traits, days to 50% flowering, days to 50% pod setting, plant height (cm), number of primary branches per plant, number of secondary branches per plant, days to maturity, number of pods per plant, number of seeds per pod, number of seeds per plant, biological yield per plant (g), 100 seed weight (g), harvest index (%) and seed yield per plant (g). The data analysed for 13 characters in forty chickpea genotypes were discussed under the Variability, heritability, and genetic advance as percent of the mean, Genetic divergence. Analysis of variance was performed to test the significance of differences among the genotypes for the characters studied. Mahalanobis D^2 technique [9] was used to analyse genetic diversity.

3. RESULTS AND DISCUSSION

40 genotypes of chickpea showed a significant difference among all characters studied. Analysis of variance showing there is a significant difference among the genotypes for thirteen characters used under the study at 5% and 1% level of significance (Table 1). This indicates that there is ample scope for the selection of genotypes for yield and its components. Variability is measured by estimation of Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), heritability (h^2) in the broad sense, genetic advance and genetic advance as percent of the

mean. (Table 2) Wide range of differences for GCV were observed which varied from 2.066 for days to maturity to 33.31% (Number of seeds per plant). indicating considerable amount of variability present among the genotypes. Comparison of coefficient of variance indicated that the phenotypic coefficient of variance was higher than the genotypic coefficient of variance for all the characters which indicated effect of environment on the characters expression. Similar results are reported by Mushtaq et al. [10] and Kuldeep et al. [11]. Among all the characters, (Table 2), high GCV and PCV were observed for the number of seeds per plant (33.31 & 34.24), Number of pods per plant (31.85 & 33.69), number of secondary branches per plant (29.54 & 29.98), biological yield per plant (g) (29.35 & 30.67 g), Seed yield per plant (g) (25.47 &28.29), Number of primary branches per plant (24.41 & 26.02) and100 Seed weight (g) (22.33 & 23.64). Selection for these characters would be effective because the response to selection is directly proportional to the variability present within the experimental material. Similar results are reported by Saleem et al. [12], Mushtaq et al. [10], and Kuldeep et al. [11], Kumar et al. [13]. Burton [14] suggested the genetic variation alongside heritability estimates would provide a better idea about the expected efficiency of selection thus a personality possessing high GCV along the high heritability is going to be valuable within the selection program. High heritability (broad sense) (>60%) was recorded for character Number of secondary branches per plant (97.1%), Number of primary branches per plant (95.6%), Number of seeds per plant (94.6%), Biological yield per plant (g) (91.6%), Number of pods per plant (89.4%),100 Seed weight (g) (89.2%), Seed yield per plant (g) (81%) and Plant height (cm) (80.5%).

In the present investigation, high heritability along with high GCV was recorded for the number of seeds per plant (94.64 & 33.31), Number of pods per plant (89.35 & 31.85), number of secondary branches per plant (97.11 & 29.54), biological yield per plant (g) (91.55 & 29.35), Seed yield per plant (g) (81.01 & 25.47), Number of primary branches per plant (88.03 & 24.41) and100 seed weight (g) (89.21 &22.33). This indicates the closeness of respective σ2p and σ2g values thereby low environmental effect on the expression of these characters. Thus phenotypic selection could also be effective for these characters. Similar results are reported by Saleem et al. [12], Mushtaq et al. [10], and Kuldeep et al. [11], Kumar et al. [13]. The estimation of genetic advance helps to understand the type of gene action involved within the expression of various traits varied from 0.21 to 54.55. Low to high genetic advance was recorded for the characters under study. The high value of genetic advance indicates the additive gene action whereas the low value indicates the non-additive gene action.

Table 1. Analysis of variance for 13 quantitative characters in chickpea genotypes (*Cicer arietinum* L.)

S. No.	Characters	Mean sum of squares		
		Replication (df=2)	Treatments (df=39)	Error (df=78)
1	Days to 50% flowering	12.16	17.15**	8.57
2	Days to 50% pod setting	9.37	13.53**	6.74
3	Plant height (cm)	45.74	272.10**	20.39
4	Number of primary branches per plant	0.13	1.63**	0.07
5	Number of secondary branches per plant	0.01	3.89**	0.03
6	Days to maturity	1.16	9.43**	4.72
7	Number of pods per plant	198.24*	1329.62**	50.76
8	Number of seeds per pod	0.01	0.07**	0.01
9	Number of seeds per plant	197.28*	2265.31**	41.94
10	Biological yield per plant (g)	47.18**	324.40**	9.64
11	100 Seed weight (g)	0.17	76.16**	2.95
12	Harvest index (%)	87.28	174.93**	43.09
13	Seed yield per plant (g)	0.01	58.90**	4.26

, significant at 5 and 1% level, respectively*

Table 2. Genetic parameters for 13 quantitative characters of 40chickpea genotypes

Characters	GCV	PCV	h^2 (Broad Sense)	GA 5%	GAM 5%
Days to 50% flowering	2.06	4.13	25.02	1.74	2.12
Days to 50% pod setting	1.47	2.93	25.13	1.55	1.52
Plant height (cm)	13.04	14.54	80.45	16.92	24.10
Number of primary branches per plant	24.41	26.02	88.03	1.39	47.18
Number of secondary branches per plant	29.54	29.98	97.11	2.30	59.98
Days to maturity	1.01	2.03	24.95	1.29	1.04
Number of pods per plant	31.85	33.69	89.35	40.20	62.03
Number of seeds per pod	9.39	12.67	55.01	0.21	14.35
Number of seeds per plant	33.31	34.24	94.64	54.55	66.75
Biological yield per plant (g)	29.35	30.67	91.58	20.19	57.86
100 Seed weight (g)	22.33	23.64	89.21	9.61	43.46
Harvest index (%)	13.46	18.95	50.49	9.70	19.71
Seed yield per plant (g)	25.47	28.29	81.01	7.91	47.22

GCV: Genotypic Co-efficient of Variation; PCV: Phenotypic Co-efficient of Variation
h^2: Heritability; GA: Genetic Advance; GAM: Genetic Advance as percent of Mean

Table 3. Distribution of 40 chickpea genotypes into different clusters based on D^2 statistic

Cluster	No. of genotypes	Genotypes
I	29	IPC-10-134, Pusa-209, HC-5, ICC-5439, IPCK-11-201, CSJ-515, ICC-4968, ICCV-16303, IPC-97-29, BG-1053, JGM-7, IPC05-66, IPCK-97-67, IPC-05-59, ILC-3279, ICC-4958, IPC-04-01, Phule-G-5, IPC-1185, IPC-08-103, BGD-72, BG-212, ICC-1202, ILC-6335K, NEC-799, IPC-2000-33, ICC-3070, JG-130, Uday (check)
II	7	IPC-71, IPC-04-52, JG-31416, L-550, IPCK-09-165, ICC-244263 and IPC 94-94,
III	1	JG-24
IV	1	ICCV-16306
V	1	IPCK-02-29
VI	1	IPC 06-11

Table 4. Intra and inter cluster distances in chickpea (*Cicer arietinum* L.)

	Cluster Distances					
	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	59.53	114.70	97.83	83.96	173.05	174.18
Cluster 2		57.02	219.85	195.78	376.34	407.97
Cluster 3			0.00	45.40	105.79	89.45
Cluster 4				0.00	72.91	142.11
Cluster 5					0.00	85.61
Cluster 6						0.00

Johnson et al. [15] and Gandhi et al. [16] suggested that high heritability along with high genetic gain showed the most effective condition of selection. In the present study genetic advance as % of mean varied from 1.047 to 66.75%. High genetic advance as % mean (>20%) was recorded for the number of seeds per plant (66.757), Number of pods per plant (62.032), Number of secondary branches per plant (59.985), Biological yield per plant (g) (57.867), Number of primary branches per plant (49.907), Seed yield per plant (g) (47.226), 100 Seed weight (g) (43.461) and Plant height (cm) (24.102).

High genetic advance as % mean along with high heritability and high GCV (>20%) was recorded for a number of primary branches per plant (47.18 & 88.03), number of secondary branches per plant (59.58 & 97.11), number of pods per plant (62.03 & 89.35), Number of seeds per plant (66.75 & 94.64), 100 seed weight (g) (43.46 & 89.21), Biological yield per plant (g) (57.86 &91.55) and Seed yield per plant (g) (47.22 & 81.01). Such values could also be attributed to the additive gene effects and direct selection for these traits would be fruitful. Similar results are reported by Saleem et al. [12], and Mushtaq et al. [10], and, and Kuldeep et al. [11], and Kumar et al. [13].

The data collected on thirteen yield and yield contributing traits for 40 genotypes of chickpea were subjected to a statistical procedure and genetic divergence by using Mahalanobis' D^2 statistic. The distribution of 40 genotypes into six clusters was by Tocher's method (Table 3 & Fig. 1) at a random with a maximum number of genotypes (29) for cluster I and minimum genotypes (One) for clusters III, IV, V & VI. The distribution of genotypes indicated that the geographical diversity and genetic diversity were not related and there are forces other than geographical separation which are responsible for diversity like natural and artificial selection, exchange of breeding material, genetic drift, and environmental variation.

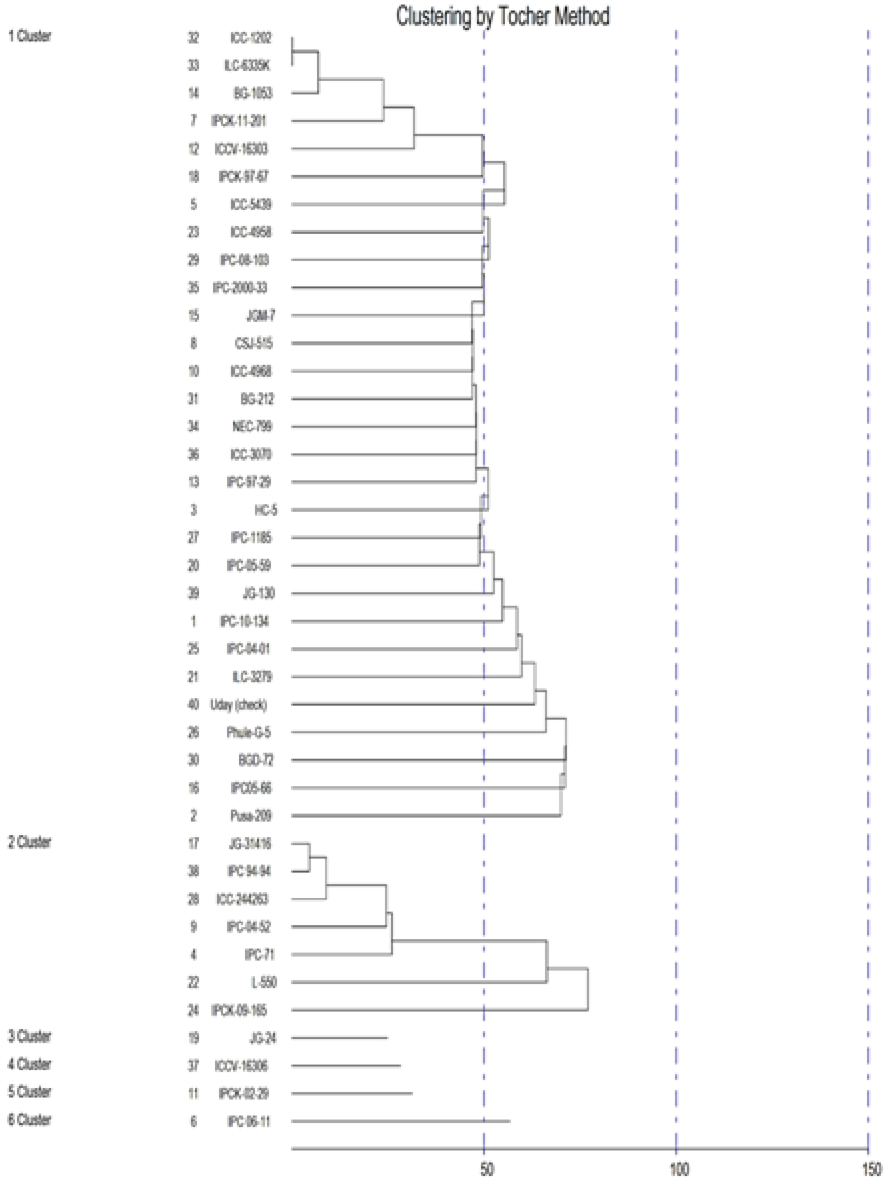

Fig. 1. Clustering by using Tocher's method

Table 5. Cluster mean values for 13 quantitative characters in Chickpea genotypes

Cluster	Days to 50% Flowering	Days to 50% pod setting	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Days to maturity	Number of pods per plant	Number of seeds per pod	Number of seeds per plant	Biological yield per plant (g)	100 Seed weight (g)	Harvest index (%)	Seed yield per plant (g)
Cluster 1	83.25	105.30	69.33	3.00	3.96	123.71	68.38	1.52	86.89	34.61	21.74	50.55	17.11
Cluster 2	80.62	102.67	69.03	2.91	2.22	121.67	36.86	1.48	44.77	25.01	22.71	45.73	10.82
Cluster 3	81.00	103.00	93.79	3.40	5.40	123.00	81.60	1.36	92.40	55.67	30.07	44.67	24.87
Cluster 4	85.33	107.33	57.92	2.20	5.32	126.67	64.07	1.26	67.40	45.40	24.61	49.86	22.27
Cluster 5	81.00	103.00	73.51	1.46	5.93	123.00	88.67	1.63	120.47	58.87	20.63	43.32	25.27
Cluster 6	82.33	104.33	89.92	3.67	6.47	124.33	117.13	1.61	155.53	57.07	19.76	45.46	25.94
% Contribution	0.13	2	1.67	2	8	10	3.97	0.2	12.82	13.21	11	14	21

The highest intracluster distance was observed for cluster I (59.53) which comprised of 29 genotypes. A hybridization program involving genetically diverse parents belonging to different distant clusters would offer a chance for bringing together gene constellations of diverse nature, promising hybrid derivatives resulted probably due to the complementary interaction of divergent genes in parents [17].

In the present study, (Table 4) the highest inter-cluster distance (407.97) was found between clusters II and VI followed by clusters II and V (376.34), cluster II and cluster III (219.85), cluster II and cluster IV (195.78), cluster I and cluster VI (174.18). The genotypes (IPC-71, IPC 04-52, JG-31416, L-550, IPCK 09-165, ICC-244263, IPC 94-94 and IPC 06-11) of the foremost distant clusters II and VI were quite contrasting in performance with reference to days to 50% flowering, days to 50% pod setting, Number of primary branches per plant, number of secondary branches per plant, number of pods per plant, Number of seeds per plant and seed yield per plant (g). The smallest inter-cluster distance (45.40) was observed between cluster III and cluster IV. The smallest inter-cluster distance indicates less diversity between the genotypes contained in these clusters. It indicates a close relationship and similarity of the genotypes for most of the characters. However, these genotypes can be undertaken for hybridization in order to exploit variation for the specific characters for which the genotypes of the two clusters shown the marked differences. For a successful breeding program, the selection of genetically diverse parents is an important prerequisite to obtain better and desirable recombinants. Cluster VI include genotypes (BG-1053, BG-212, Pusa-209, Phule-G-5, JGM-7, IPC-97-29, IPC05-66, IPC-04-01, IPC 06-11, and HC-5) recorded maximum mean values (Table 5) for the number of primary branches per plant (3.67), number of secondary branches per plant (6.47), number of pods per plant (117.13), number of seeds per plant (155.53), and seed yield per plant (g) (25.94).

(Table 5) The percent contribution of individual characters towards genetic divergence was recorded for Seed yield per plant (g) (21%), Harvest index (%) (14%), Biological yield per plant (g) (13.21%), Number of seeds per plant (12.82%),100 Seed weight (g) (11%), Days to maturity (10%), Number of secondary branches per plant (8%), Number of pods per plant (3.97%), Number of primary branches per plant (2%), Days to 50% pod setting (2%), Plant height (cm) (1.67%), Number of seeds per pod (0.2%) and Days to 50% flowering (0.13%) in the chickpea genotypes under the study.

4. CONCLUSION

On the basis of analysis of variance significant difference was recorded for all the seed yield and its components indicating presence of large variability in the genotypes. The magnitude of GCV and PCV recorded highest (33.31 & 34.24) for number of seeds for plant. High heritability associated with high genetic advance was observed for number of secondary branches per plant (97.11 & 59.98) suggesting that there was greater role of additive gene action in inheritance. Maximum number of genotypes were grouped into cluster I which include 29 genotypes. The highest intercluster distance (407.97) was found between clusters II and VI. Genotypes to these clusters may be used as parents to produce transgressive segregants.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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