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Genetic Diversity Studies in Chickpea (*Cicer arietinum* L.) Germplasm in a Semi-Arid Environment of North Karnataka

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Abstract In the present study, an attempt was made to assess the genetic divergence among the 79 germplasm lines, including indigenous and exotic collections using Mahalanobis D^2 statistic. The experiment was carried out during *rabi* season of 2014. The observations were recorded on plant height (cm), number of branches per plant, number of pods per plant, biomass (g), 100 seed weight (g) and seed yield (kg/ha). Based on D^2 analysis, the 79 germplasm lines were grouped into ten different clusters indicating diverse nature of material studied. Cluster I was the largest with 32 genotypes followed by cluster II (30 genotypes) and cluster IV (10 genotypes), while clusters III, V, VI, VII, VIII, IX and X were solitary indicating the grouping of exotic collections in definite groups. Among the seed yield components, 100 seed weight (80.10%) followed by number of pods per plant (11.59%) and seed yield (4.84%) contributed maximum towards the divergence. Cluster VIII showed the maximum mean value for seed yield. The intra and inter cluster divergence among the genotypes was varying in magnitude. The intra-cluster distance was maximum in cluster II followed by clusters I and IV. The widest inter cluster distance was noted between cluster VI and VIII and both the clusters were solitary giving scope for hybridization program for improvement of chickpea genotypes. The grouping of genotypes was irrespective of desi or kabuli types used in the study.

Keywords Chickpea, D^2 statistics, Genetic variability, Inter cluster distance, Intra cluster distance.

Introduction

Chickpea (*Cicer arietinum* L.) is an integral part of an Indian agriculture since time immemorial, because of its intrinsic value in terms of higher protein content, carbohydrates, minerals, nitrogen fixing ability and indispensability as alternative crop for crop diversification. On the basis of cultivated area, chickpea ranks 19th among the crops and is grown in 34 countries of the world. Area under pulses in India, Pakistan, Nepal, and Bangladesh covers about 90% of the world acreage [1].

Limited or lack of genetic variability is important factor for the limited progress achieved in increasing the productivity of grain legumes including chickpea [1]. When the parents utilized in across are genetically similar, it is quite likely that the different lines derived reveals low diversity. On the contrary, when diverse parents are used in obtaining a segregating population, the derived lines reveal greater diversity despite sharing a common percentage [2].

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Table 1. Estimates of variability parameters for different characters of chickpea. GCV= Genotypic coefficient of variation ; bs = Broad sense ; h^2 = Heritability ; PCV = Phenotypic coefficient of variation ; GA = Genetic advance ; $\sigma^2 g$ = Genotypic variation ; $\sigma^2 p$ = Phenotypic variation ; $\sigma^2 e$ = Environmental variation.

Sl. No.	Name of the character	Range	$\sigma^2 g$	$\sigma^2 p$	GCV (%)	PCV (%)	h^2 (bs) (%)	GA	GA as % of mean
1	Plant height (cm)	13.67 to 40.67	25.5031	135.2187	15.6075	35.9382	18.86	4.5180	13.9630
2	No. branches/plant	1.33 to 3.33	0.1552	2.3484	16.4131	63.8357	06.61	0.2087	8.6933
3	No. of pods/ plant	2.50 to 47.33	85.2395	85.3408	38.8755	38.8985	99.88	19.0077	80.0359
4	Biomass	18.50 to 53.00	17.0368	26.2639	17.7313	22.0153	64.87	6.8482	29.4186
5	100 seed weight (g)	6.50 to 39.00	36.3670	70.7316	28.4373	39.6590	51.42	8.9077	42.0051
6	Seed yield (g)	14.00 to 171.00	1184.2419	1187.5663	44.8594	44.9223	99.72	70.7911	92.2809

Table 2. Distribution of 79 genotypes of chickpea in different clusters.

Cluster No.	No. of genotypes	Genotypic included
I	32	ICCX-070163- F4-P7-BP, ICCX-070163- F4-P8-BP, ICCX-060157-F3(Early) BP-P1-BP, ICCX-060155-F3-BP-P10-BP, ICCX-060156-F3-BP-P12-BP, ICCX-060156-F3-BP-P22-BP, ICCX-060119-F3-BP-P2-BP, ICCX-060119-F3-BP-P6-BP, ICCX-060119-F3-BP-P17-BP, ICCX-060121-F3-BP-P4-BP, ICCX-060150-F3-BP-P13-BP, ICCX-070011-F2-BP-P68-BP-P1-BP-BP, ICCMABCA-12, ICCMABCA-22, ICCMABCA-28, ICCMABCA-42, ICCMABCA-24, ICCX-080058-F4-P2-BP, ICCX-080058-F4-P4-BP, ICCX-080062-F4-P6-BP, ICCX-090021-F4-P7-BP, ICCX-080066-F4-P10-BP, ICCX-090035-F4-P12-BP, ICCX-090038-F4-P15-BP, ICCRIL01-0246ICCRIL01-0250, ICCRIL01-0266, ICCRIL05-0089, ICCV 88202, JG-11, NEC2303, WP2793 C and Shimbera
II	30	ICCX-080026-F4-P3-BP, ICCX-080026- F4-P5-BP, ICCX-070157- F4-P4-BP, ICCX-070157- F4-P6-BP, ICCX-060119-F3-BP-P19-BP, ICCX-060119-F3-BP-P30-BP, ICCX-060122-F3-BP-P13 (Pea type)-BP, ICCX-060152-F3-BP-P11-BP, ICCX-070007-F2-BP-P40-BP-P1-BP-BP, ICCX-070011-F2-BP-P87-BP-P1-BP-BP, ICCMABCA-8, ICCMABCA-23, ICCMABCA-34, ICCX-080058-F4-P1-BP, ICCX-080058-F4-P12-BP, ICCX-080063-F4-P1-BP, ICCX-090040-F4-P6-BP, ICCX-080058-F4-P17-BP, ICCX-080062-F4-P18-BP, ICCX-080062-F4-P19-BP, ICCX-090019-F4-P12-BP, ICCRIL01-0246, ICCRIL01-0306, ICCRIL01-0334, ICCRIL01-0410, ICCRIL-0088, ICCV 96029, ICCV 96030, NEC1153, P1360347 and T 70 B
III	1	ICCV 11603
IV	10	ICCX-070163- F4-P2-BP, ICCX-060119-F3-BP-P4-BP, ICCX-060119- F3-BP-P12-BP, ICCX-070010-F2-BP-P108-BP-P1-BP, ICCX-070011-F2-P120-P2-P1-BP-BP, ICCX-090031-F4-P8-BP, ICCX-090031-F4-P7-BP, ICCX-090039-F4-P1-BP, H 1128 and P3046, PI 450953
V	1	ICCX-080026-F4-P2-BP17
VI	1	ICCX-060119-F3-BP-P7-BP
VII	1	ICCX-090036-F4-P23-BP
VIII	1	F3WF × 16BR
IX	1	ICCX-060119-F3-BP-P19-BP
X	1	ICCX-080026- F4-P9-BP

Table 3. Cluster means for different traits in chickpea.

Cluster	Plant height (cm)	No. of branches/ plant	No. of pods/ plant	Biomass (g)	100 seed weight (g)	Seed yield (g)
I	33.25	2.37	22.97	22.69	89.16	21.73
II	31.83	2.34	21.92	22.47	44.48	20.13
III	29.00	2.67	22.67	21.50	113.00	11.00
IV	34.60	2.60	31.80	25.00	124.15	24.10
V	25.50	2.00	2.50	25.00	70.50	25.00
VI	18.33	2.67	11.67	24.00	14.00	14.00
VII	13.67	2.67	23.00	18.50	24.50	7.00
VIII	39.33	2.00	38.00	26.50	158.50	31.00
IX	29.33	2.67	25.00	20.50	171.00	21.00
X	36.00	2.67	42.67	53.00	80.00	26.00
% contribution	2.08	0.00	11.59	1.40	80.10	4.84

In any program aimed at genetic amelioration of yield, genetic diversity is the basic requirement. Effective hybridization program between genetically diverse parents will lead to considerable amount of heterotic response in F_1 hybrids and broad spectrum of variability in segregating generations. Mahalanobis's D^2 statistics is a powerful tool in quantifying the degree of variability at the genotype level [3]. So, the present experiment was formulated to study the genetic divergence and clustering pattern of the chickpea genotypes for selection of suitable parents for utilizing in hybridization program and to study the genetic parameters attributing to yield.

Materials and Methods

The experimental material comprising seventy nine genotypes of chickpea was grown during *rabi* 2014 in an augmented design at Regional Agricultural Research Station, Vijayapura, University of Agricultural Sciences, Dharwad. Data were recorded on five randomly tagged plants for viz., plant height (cm), number of primary branches / plant, number of pods / plant, biomass (g), 100 seed weight (g) and seed yield (g). The experimental data was analyzed statistically to find out the significance mean difference between varieties different genetic parameters were estimated. Analysis of variance was performed to test the significance of difference among the genotypes for the characters studied Mahalanobis D^2 technique [3] was used to analyze genetic diversity.

Results and Discussion

Seventy nine genotypes of chickpea showed significant differences among all characters under study. The relative contribution of different characters towards divergence showed 100 seed weight (g) con-

Table 4. Intra cluster and inter cluster distances of 10 clusters of chickpea.

	Group 1	Group 2	Group 3	Group 4	Group 5	Group 6	Group 7	Group 8	Group 9	Group 10
Cluster I	**22.52**	50.32	30.81	42.26	33.00	79.41	71.02	73.60	83.48	40.77
Cluster II		**24.26**	71.22	83.58	37.54	39.25	34.68	117.20	127.72	54.42
Cluster III			**0.00**	25.46	49.34	100.26	89.96	53.27	58.91	52.49
Cluster IV				**22.38**	63.61	114.59	104.91	38.94	50.24	55.52
Cluster V					**0.00**	58.74	55.16	96.09	103.24	50.99
Cluster VI						**0.00**	18.43	149.37	158.14	81.33
Cluster VII							**0.00**	139.57	148.03	74.28
Cluster VIII								**0.00**	23.70	83.20
Cluster IX									**0.00**	98.58
Cluster X										**0.00**

Table 5. Means of different characters in chickpea.

Sl. No.	Genotypes	Plant height (cm)	Branches/ plant	No. of pods/ plant	Biomass (g)	100 seed wt (g)	Seed yield (g)
1	ICCX-080026-F4-P2-BP	25.50	2.00	2.50	25.00	25.00	70.50
2	ICCX-080026-F4-P3-BP	30.00	2.33	19.33	21.00	21.50	50.00
3	ICCX-080026-F4-P5-BP	33.33	2.33	33.00	23.50	21.50	43.50
4	ICCX-080026-F4-P9-BP	36.00	2.67	42.67	53.00	26.00	80.00
5	ICCX-070157-F4-P4-BP	33.67	2.33	26.00	23.50	22.50	42.50
6	ICCX-070157-F4-P6-BP	34.00	2.33	19.67	22.50	16.50	50.50
7	ICCX-070163-F4-P2-BP	39.67	3.33	40.67	27.00	21.00	107.00
8	ICCX-070163-F4-P7-BP	40.67	2.33	38.33	24.00	13.00	81.50
9	ICCX-070163-F4-P8-BP	38.67	3.00	28.33	26.50	22.50	98.50
10	ICCX-060157-F3 (Early) BP-P1-BP	26.00	2.00	30.00	20.50	10.00	75.50
11	ICCX-060155-F3-BP-P10-BP	31.33	2.33	29.67	24.50	26.50	68.50
12	ICCX-060156-F3-BP-P12-BP	36.33	2.67	24.00	26.00	39.00	92.00
13	ICCX-060156-F3-BP-P22-BP	34.00	3.00	14.33	21.00	20.50	110.00
14	ICCX-060119-F3-BP-P2-BP	29.00	2.33	22.33	23.50	27.00	83.00
15	ICCX-060119-F3-BP-P4-BP	37.33	2.67	41.00	26.50	24.00	117.50
16	ICCX-060119-F3-BP-P6-BP	34.33	2.33	20.67	24.50	21.00	77.00
17	ICCX-060119-F3-BP-P7-BP	18.33	2.67	11.67	24.00	14.00	14.00
18	ICCX060119-F3-BP-P12-BP	30.00	2.67	35.33	29.50	26.00	126.00
19	ICCX-060119-F3-BP-P17-BP	30.00	2.00	26.33	21.00	15.50	87.50
20	ICCX-060119-F3-BP-P19-BP	29.33	2.67	25.00	20.50	21.00	171.00
21	ICCX-060119-F3-BP-P19-BP	32.00	3.00	10.67	22.00	15.00	25.00
22	ICCX-060119-F3-BP-P30-BP	32.00	2.00	7.33	20.50	10.00	47.00
23	ICCX-060121-F3-BP-P4-BP	30.00	2.33	19.67	22.00	18.50	109.50
24	ICCX-060122-F3-BP-P13 (Pea type)-BP	34.33	3.00	19.33	23.50	19.50	58.00
25	ICCX-060150-F3-BP-P13-BP	36.67	3.00	18.33	23.50	22.00	67.50
26	ICCX-060152-F3-BP-P11-BP	33.00	2.67	26.00	21.00	24.50	46.50
27	ICCX-070007-F2-BP-P40-BP-P1-BP-BP	29.67	2.33	14.67	20.00	19.00	66.50
28	ICCX-070010-F2-BP-P108-BP-P1-BP	35.00	2.67	24.00	21.50	19.50	120.50
29	ICCX-070011-F2-BP-P68-BP-P1-BP-BP	31.00	3.00	44.00	25.50	19.00	84.50
30	ICCX-070011-F2-BP-P87-BP-P1-BP-BP	28.00	2.33	5.00	22.50	24.50	43.50
31	ICCX-070011-F2-P120-P2-P1-BP-BP	34.33	2.67	17.67	23.00	32.00	129.50
32	ICCMABCA-8	27.00	2.67	14.67	21.50	19.50	36.50
33	ICCMABCA-12	36.00	2.33	24.67	23.50	22.50	107.00
34	ICCMABCA-22	31.33	2.33	24.00	22.00	23.50	73.00
35	ICCMABCA-23	37.67	3.33	26.67	25.00	27.50	32.00
36	ICCMABCA-28	35.67	2.67	27.00	22.00	24.00	87.50
37	ICCMABCA-34	39.67	1.33	22.67	22.00	24.50	53.50
38	ICCMABCA-42	36.67	2.33	21.33	22.50	29.00	87.00
39	ICCMABCA-24	33.00	2.00	11.33	19.50	30.00	86.50
40	ICCX-080058-F4-P1-BP	25.33	2.33	12.67	19.50	14.00	30.50
41	ICCX-080058-F4-P2-BP	34.00	2.33	18.00	23.00	24.50	89.50
42	ICCX-080058-F4-P4-BP	32.00	2.33	22.67	23.50	23.00	100.00
43	ICCX-080058-F4-P12-BP	35.67	3.00	23.00	26.00	27.00	63.00
44	ICCX-080062-F4-P6-BP	34.00	2.33	16.67	24.50	24.50	73.00
45	ICCX-080063-F4-P1-BP	32.67	2.33	18.00	21.50	21.00	23.00
46	ICCX-090021-F4-P7-BP	33.00	2.67	22.00	22.50	23.00	108.50
47	ICCX-090031-F4-P8-BP	37.67	2.33	32.33	26.00	27.50	113.00
48	ICCX-090031-F4-P7-BP	22.00	1.67	23.67	23.00	18.50	134.50
49	ICCX-090039-F4-P1-BP	39.33	2.67	47.33	27.50	29.50	122.50
50	ICCX-090040-F4-P6-BP	32.67	2.00	30.33	22.50	23.00	23.00
51	ICCX-080058-F4-P17-BP	29.67	1.67	21.67	20.50	13.50	38.00
52	ICCX-080062-F4-P18-BP	31.33	2.67	40.00	23.00	22.50	61.00
53	ICCX-080062-F4-P19-BP	39.00	2.67	27.67	24.50	29.00	56.00

Table 5. Continued.

Sl. No.	Genotypes	Plant height (cm)	Branches/ plant	No. of pods/ plant	Biomass (g)	100 seed wt (g)	Seed yield (g)
54	ICCX-080066-F4-P10-BP	37.00	2.67	19.67	25.00	23.00	90.00
55	ICCX-090019-F4-P12-BP	29.00	2.00	30.00	21.00	18.50	44.50
56	ICCX-090035-F4-P12-BP	34.33	2.00	21.33	21.50	18.00	97.00
57	ICCX-090036-F4-P23-BP	13.67	2.67	23.00	18.50	7.00	24.50
58	ICCX-090038-F4-P15-BP	25.00	2.00	14.33	20.50	28.50	76.50
59	ICCRIL01-0246	33.67	2.00	22.33	21.50	20.00	48.00
60	ICCRIL01-0246ICCRIL01-0250	33.67	2.33	29.00	22.50	28.00	104.00
61	ICCRIL01-0266	26.33	1.67	7.00	21.50	24.50	100.00
62	ICCRIL01-0306	24.33	2.00	17.33	21.00	29.00	29.00
63	ICCRIL01-0334	25.00	2.67	16.00	20.00	22.80	22.80
64	ICCRIL01-0410	25.67	2.67	22.67	20.00	20.00	41.00
65	ICCRIL05-0088	33.33	2.00	37.33	25.50	21.50	60.00
66	ICCRIL05-0089	25.67	2.33	27.67	21.50	10.50	100.00
67	ICCV 88202	32.00	2.00	18.67	21.00	18.50	86.00
68	ICCV 96029	33.33	2.33	18.33	22.50	16.00	62.50
69	ICCV 96030	33.33	1.67	17.33	21.00	18.00	35.00
70	ICCV 11603	29.00	2.67	22.67	21.50	11.00	113.00
71	JG-11	35.67	2.67	23.00	19.50	6.50	91.50
72	F3WF × 16BR	39.33	2.00	38.00	26.50	31.00	158.50
73	NEC1153, PI360347	38.00	2.33	42.33	30.00	9.50	49.50
74	T 70 B	28.67	2.00	15.67	25.50	12.50	52.50
75	NEC 2303	39.33	2.33	29.33	25.00	21.00	85.50
76	WP 2793 C	35.67	2.33	23.33	21.00	19.50	85.00
77	H 1128	32.33	3.00	27.67	20.00	20.00	129.50
78	Shimbera	35.67	2.00	18.00	21.50	19.00	90.50
79	P 3046, PI 450953	38.33	2.33	28.33	26.00	23.00	141.50
	Mean	32.36	2.40	23.75	23.28	21.21	76.71

tributed maximum towards divergence followed by number of pods / plant (cm), the same characters are positively associated with yield and are the main yield components in chick pea [1].

The parameters of genetic variability revealed high PCV and GCV values for seed yield followed by number of pods per plant and 100 seed weight and number of primary branches per plant respectively (Table 1) indicating that these traits could be used as selection indices for yield improvement, similar findings were reported by [1, 2 and 3]. High heritability (>60%) was observed in number of pods / plant, seed yield (g), biomass (g). The high heritability with high genetic advance was recorded for the character number of pods per plant (99.88%) followed by seed yield plant (99.72%) and biomass (64.87%). The estimates of GA ranged from 0.2087 and 0.7911 with the highest estimate in case of seed yield (g). The highest genetic advance as per cent of mean was observed for seed yield (92.280) followed by number of pods/plant (80.0359), 100 seed weight (42.0051), biomass (29.4186) and plant height (13.9630). It indicates that most likely the heritability is due to additive gene effects and selection for these traits may be rewarding. Similar findings have been reported earlier [1, 3] in chickpea.

The seventy nine genotypes studied were grouped into ten clusters (Table 2) by using Tocher's methods, cluster I with 32 genotypes, cluster II with 30 genotypes, cluster IV with 10 genotypes and clusters III, V, VI, VII, VIII, IX and X were solitary indicating the grouping of exotic collections in definite groups.

The intra-cluster distance was maximum in cluster II (D = 24.26) followed by clusters I (D = 22.52) and

IV (D = 22.38). The widest inter cluster distance was noted between cluster VI and VIII (D = 149.37) indicating wide divergence among the clusters. This also suggests that genetic architecture of the lines in one cluster differs entirely from those included in the other cluster and both the clusters were solitary giving scope for hybridization program for improvement of chickpea genotypes. The distance between clusters VII and VI (18.43) was minimal indicating close relationship between those clusters suggesting that the genotypes in this cluster may be used as parents in hybridization program to obtain desirable recombinants.

Cluster means were found highest for different characters (Table 3) viz., Cluster X showed highest mean performance for No. of primary branches / plant (42.67), No. of pods / plant (2.67) and biomass (g) (53.00). Cluster VIII showed highest mean performance for plant height (39.33) and seed yield (31.00). Cluster IX showed higher mean performance for 100 seed weight (g) (171.00).

Genotypes belonging to clusters separated by high genetic distance may be used in hybridization program to obtain a wide spectrum of variation among the segregates [1] and in the present study similar suggestion had been made. The genotypes included in the diverse clusters namely, III, V, VI, VII, VIII, IX and X hold good promise as parents for obtaining potential hybrids and thereby creating greater variability of these characters to improve the yield.

So from the above result it can be concluded that the genetic diversity was not related to geographic diversity. The cluster combinations were classified into eight divergence classes, following the method suggested earlier [1—3].

Crosses were suggested between clusters in a pair from inter cluster D values, which fall in divergence classes DC1 (32), DC2 (30) and DC3 (only 1). On the basis of divergence classes the potential parent's viz. ICCV 11603, ICCX--080026-F4-P2-BP17, ICCX-060119-F3-BP-P7-BP, ICCX-090036-F4-P23-BP, F3 WF × 16 BR, ICCX-060119-F3-BP-P19-BP and ICCX-080026-F4-P9-BP can be used in the hybridization program for chickpea improvement to obtain better transgressive segregants.

Two characters viz. number of pods / plant and seed yield (g) exhibited high heritability estimates (in broad sense). These characters should be given importance for further improvement of yield and yield components.

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