Legume Res., 28 (4) : 250 - 255, 2005

GENETIC DIVERGENCE IN CHICKPEA {*CICER ARIETINUM* (L.)}

K. Kanaka Durga, Y. Koteswara Rao and M.V. Reddy

Regional Agricultural Research Station,
Lam, Guntur - 522 034, India

ABSTRACT

Genetic diversity in chickpea with 132 genotypes revealed significant differences among the genotypes for yield and its component characters. The genotypes were grouped into nine clusters. Cluster I was the largest, comprising of 20 genotypes, followed by clusters V and VII with 16 and 15 genotypes, respectively. Maximum intra - cluster distance (1.806) was observed in cluster VI followed by cluster IV (1.799), cluster I (1.705) and cluster IX (1.642). Maximum inter cluster distance was noticed between clusters I and VIII (5.114). Crossing the genotypes between the clusters I and VIII may lead to maximum diversity in the segregating populations and development of high yielding varieties.

INTRODUCTION

Chickpea is an important pulse crop of Andhra Pradesh and is gaining momentum in the recent years particularly in areas of Guntur and Prakasam district as an alternative to commercial crops. However, the variability available in the crop is very meager. Narrow genetic base of the available material is the major limiting factor for increasing the chickpea yields. It is usually observed that the genetically diverse parents show maximum heterosis and provide scope for the selection of the transgressive segregants. Multivariate analysis by means of Mahalanobis D^2 (1928) statistics is an useful tool in quantifying the degree of divergence between populations and also aids in the choice of genetically diverse parents to obtain recombinants in the segregating generations (Jatasra *et al.*, 1978). Hence, an attempt has been made to group the genotypes of chickpea into different clusters.

MATERIAL AND METHODS

One hundred and twenty six (126) recombinant inbred lines, (derived from crossing two diverse parents ICCV 2 x JG 62), received from ICRISAT, Patancheru, Hyderabad were evaluated against six checks in a randomized complete block design during *rabi* 2000-01 at RARS, Lam, Guntur in three replications. The genotypes were sown in 4 rows of 4 m length each with a spacing of 30 x 10 cm. Thus the gross plot size was 4.8 m^2. The pedigree of different genotypes is presented in Table 4. The recommended package of practices was followed to raise a healthy crop. Observations were recorded on days to 50 per cent flowering, days to maturity, plant height (cm), branches per plant (no.), pods per plant (no.), seed yield (kg ha^{-1}) and test weight (g). The divergence analysis was carried out using Mahalanobis D^2 (1928) and the genotypes were grouped into different clusters according to Tochers method as described by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for the characters under study. The simultaneous test of equality using 'V' statistic (4689.34 at 917 d.f.) which utilized Wilkins criterion confirmed significant differences between the genotypes for all the characters.

On the basis of relative magnitude of the distance, D^2 statistics grouped 132 genotypes into nine clusters (Table 1). Cluster I comprised of 20 genotypes, followed by clusters V and VII with 16 and 15 genotypes, respectively. Clusters IV, VI and IX comprised of 14 genotypes each, while clusters II, III and VIII of 13 genotypes each. The clustering pattern indicated that all the genotypes within a cluster might have some degree of ancestral relationship. The grouping pattern further

Table 1. Clustering pattern of 132 genotypes in chickpea

Cluster	No. of genotypes	D^2 values	Genotypes included in each cluster (Code Numbers)
I	20	58.14 (7.62)	9, 24, 26, 31, 32, 45, 47, 52, 58, 74, 75, 78, 81, 84, 88, 99, 103, 113, 122, 131
II	13	30.38 (5.51)	3, 14, 15, 23, 33, 36, 42, 59, 86, 97, 104, 107, 123
III	13	33.04 (5.75)	2, 4, 5, 20, 25, 35, 73, 87, 95, 98, 114, 116, 128
IV	14	45.30 (6.73)	10, 16, 21, 28, 61, 69, 71, 77, 91, 94, 100, 110, 111, 121
V	16	32.36 (5.69)	7, 12, 22, 29, 34, 49, 50, 51, 76, 79, 101, 112, 118, 119, 120, 127
VI	14	45.68 (6.76)	13, 18, 19, 38, 43, 63, 82, 85, 90, 109, 115, 126, 129, 132
VII	15	30.74 (5.54)	8, 40, 41, 46, 48, 55, 56, 64, 67, 68, 83, 105, 106, 108, 117
VIII	13	33.06 (5.75)	11, 17, 27, 30, 37, 44, 53, 57, 62, 65, 66, 72, 92
IX	14	37.76 (6.14)	1, 6, 39, 54, 60, 70, 80, 89, 93, 96, 102, 124, 125, 130

Values in parentheses show D values.

indicated that many derivatives appeared in different clusters despite the common parentage (Kumar *et al.*, 1993). It is generally expected that the lines derived from the same cross exhibit minimum diversity. However, when diverse parents are involved, the selected lines may reveal greater diversity. Similar observations were earlier reported by Kumar *et al.*, 1993 and Katiyar, 1978. This could be due to some degree of heterogeneity either through balanced polymorphic system, directional selection for some agronomic characters under domestication and use of genetically diverse parents or genetic drift and selection forces under diverse environmental conditions (Katiyar, 1978). Mohanty *et al.*, 2001 also suggested that progenies from genetically diverse parents manifest heterosis and exhibit a broad spectrum of variability, providing a better scope for selection of desirable segregants for crop improvement program.

The intra - and inter - cluster distance values (Table 2) revealed that the average intra - cluster distance values did not exceed the average inter - cluster distance values, indicating considerable amount of genetic diversity among the genotypes studied (Katiyar, 1978). Maximum intra - cluster distance was observed in cluster VI (1.806) followed by cluster IV (1.799), cluster I (1.705) and cluster IX (1.642). This indicated that cluster VI was more heterogeneous and appreciable genetic diversity existed within the clusters. On the other hand, the minimum intra - cluster distance was noticed in cluster V (1.422), followed by cluster VII (1.432) and cluster II (1.529). Thus utilizing the genotypes included in cluster VI and V or VII, desirable transgressive segregants could be expected. Maximum inter cluster distance was noticed between clusters I and VIII (5.114) and these two clusters appear to be most divergent clusters. These observed distances reflect the genetic diversity among the lines and their linkage with respect to one another (Singh, 2002). The distance between the clusters II and VIII (4.675), I and VI (4.188) and VI and VII (4.012) were also relatively high, while minimum between the clusters V and VII (1.928), followed by clusters III and VII (1.932),

Table 2. Average intra - and inter - cluster distances in chickpea

	I	II	III	IV	V	VI	VII	VIII	IX
I	**1.705**	2.095	2.197	3.537	2.920	4.188	2.351	5.114	3.269
II		**1.529**	2.098	3.595	2.679	2.979	3.123	4.675	2.774
III			**1.594**	2.743	2.386	2.660	1.932	3.469	2.500
IV				**1.799**	2.843	3.624	2.696	2.494	2.642
V					**1.422**	3.113	1.928	3.137	3.069
VI						**1.806**	4.012	3.280	2.112
VII							**1.432**	3.563	3.650
VIII								**1.595**	3.525
IX									**1.642**

Values in bold are intra - cluster distances.

Table 3. Cluster means for seven characters in chickpea

Cluster number	Days to 50 % flowering	Days to maturity	Plant height	No. of branches/ plant	No. of pods/ plant	Test weight	Seed yield (g/plot)	Seed yield (kg/ha)
I	37.57	81.93	32.00	3.72	36.73	18.93	395.17	1647
II	43.33	83.54	37.37	4.15	53.55	18.64	397.95	1658
III	46.85	87.77	37.96	3.20	37.29	19.68	477.44	1989
IV	54.95	93.48	36.37	4.40	28.31	22.44	300.24	1251
V	43.31	85.08	41.04	4.43	37.72	27.08	393.33	1639
VI	53.71	91.55	41.99	5.60	50.01	21.41	549.29	2289
VII	41.60	86.84	36.74	2.60	28.41	25.05	401.11	1671
VIII	59.03	96.28	45.94	1.37	27.41	26.35	411.03	1713
IX	54.95	88.55	36.88	6.32	38.05	18.79	451.67	1882
C.V. (%)	2.78	3.33	9.14	19.30	15.28	4.08	14.03	

I and II (2.095) and II and III (2.098). This indicated that the genotypes of these two clusters were not genetically much diversed. Thus the clustering pattern indicated the presence of sufficient genetic diversity among the progenies of ICCV 2 and JG 62.

The data on cluster means (Table 3) indicated the existence of appreciable variation for various yield components. These differences were more conspicuous for branches per plant, pods per plant and seed yield, contributing substantially to genetic diversity as reflected by their coefficient of variation. These findings are in conformity with the findings of Sarma *et al.*, 1994 in pigeonpea. Cluster I was characterized by early genotypes and dwarf plants; while cluster VIII, followed by clusters IV, VI and IX were characterized by late genotypes. Regarding plant height, cluster VIII comprised of tall genotypes, followed by clusters VI and V. Potential genetic donors for seed yield were grouped in cluster VI, while, cluster IV with late genotypes with low yield and minimum pods per plant. However, branches per plant was found to be moderate. Thus the genotypes included in a particular group exhibited more or less similar characteristics but differed from those included in other groups. Therefore, selection of genotypes from different groups and using them in the hybridization would prove fruitful in crop improvement program (Singh, 2002).

Genetic diversity as well as *per se* performance of the parents contributed towards the high performance of the hybrids and the segregants in subsequent generations (Sandhu *et al.*, 1991). A breeding program should aim on the mean performance, genetic distance and clustering pattern. Crossing between divergent parents is expected to produce a

Table 4. Pedigree of chickpea genotypes

Code No.	Pedigree
1	ICCX-930111-1-1-1-1-1SP-1-1-1-1BP
2	ICCX-930111-2-1-1-1-1SP-1-1-1-1BP
3	ICCX-930111-1-1-1-1-2DP-1-1-1-1BP
4	ICCX-930111-3-1-1-1-1SP-1-1-1-1BP
5	ICCX-930111-4-1-1-1-1DP-1-1-1-1BP
6	ICCX-930111-5-1-1-1-1DP-1-1-1-1BP
7	ICCX-930111-6-1-1-1-1SP-1-1-1-1BP
8	ICCX-930111-7-1-1-1-1SP-1-1-1-1BP
9	ICCX-930111-8-1-1-1-1SP-1-1-1-1BP
10	ICCX-930111-9-1-1-1-1SP-1-1-1-1BP
11	ICCX-930111-10-1-1-1-1DP-1-1-1-1BP
12	ICCX-930111-11-1-1-1-1SP-1-1-1-1BP
13	ICCX-930111-12-1-1-1-1DP-1-1-1-1BP
14	ICCX-930111-13-1-1-1-1SP-1-1-1-1BP
15	ICCX-930111-13-1-1-1-2DP-1-1-1-1BP
16	ICCX-930111-14-1-1-1-1SP-1-1-1-1BP
17	ICCX-930111-15-1-1-1-1DP-1-1-1-1BP
18	ICCX-930111-16-1-1-1-1DP-1-1-1-1BP
19	ICCX-930111-17-1-1-1-1SP-1-1-1-1BP
20	ICCX-930111-17-1-1-1-2DP-1-1-1-1BP
21	ICCX-930111-18-1-1-1-1SP-1-1-1-1BP
22	ICCX-930111-19-1-1-1-1SP-1-1-1-1BP
23	ICCX-930111-20-1-1-1-1SP-1-1-1-1BP
24	ICCX-930111-21-1-1-1-1SP-1-1-1-1BP
25	ICCX-930111-22-1-1-1-1SP-1-1-1-1BP
26	ICCX-930111-22-1-1-1-2DP-1-1-1-1BP
27	ICCX-930111-23-1-1-1-1SP-1-1-1-1BP
28	ICCX-930111-24-1-1-1-1DP-1-1-1-1BP
29	ICCX-930111-25-1-1-1-1SP-1-1-1-1BP
30	ICCX-930111-25-1-1-1-2DP-1-1-1-1BP
31	ICCX-930111-26-1-1-1-1SP-1-1-1-1BP
32	ICCX-930111-27-1-1-1-1SP-1-1-1-1BP
33	ICCX-930111-27-1-1-1-2DP-1-1-1-1BP
34	ICCX-930111-28-1-1-1-1SP-1-1-1-1BP
35	ICCX-930111-29-1-1-1-1SP-1-1-1-1BP
36	ICCX-930111-30-1-1-1-1DP-1-1-1-1BP
37	ICCX-930111-31-1-1-1-1SP-1-1-1-1BP
38	ICCX-930111-32-1-1-1-1DP-1-1-1-1BP
39	ICCX-930111-33-1-1-1-1DP-1-1-1-1BP
40	ICCX-930111-34-1-1-1-1SP-1-1-1-1BP
41	ICCX-930111-34-1-1-1-2DP-1-1-1-1BP
42	ICCX-930111-35-1-1-1-1SP-1-1-1-1BP
43	ICCX-930111-36-1-1-1-1DP-1-1-1-1BP
44	ICCX-930111-37-1-1-1-1SP-1-1-1-1BP
45	ICCX-930111-38-1-1-1-1SP-1-1-1-1BP
46	ICCX-930111-39-1-1-1-1SP-1-1-1-1BP
47	ICCX-930111-40-1-1-1-1SP-1-1-1-1BP
48	ICCX-930111-41-1-1-1-1SP-1-1-1-1BP
49	ICCX-930111-41-1-1-1-2DP-1-1-1-1BP
50	ICCX-930111-42-1-1-1-1SP-1-1-1-1BP
51	ICCX-930111-43-1-1-1-1SP-1-1-1-1BP
52	ICCX-930111-44-1-1-1-1SP-1-1-1-1BP

(Contd.

Code No.	Pedigree
53	ICCX-930111-45-1-1-1-1SP-1-1-1-1BP
54	ICCX-930111-46-1-1-1-1SP-1-1-1-1BP
55	ICCX-930111-47-1-1-1-1SP-1-1-1-1BP
56	ICCX-930111-47-1-1-1-2DP-1-1-1-1BP
57	ICCX-930111-48-1-1-1-1SP-1-1-1-1BP
58	ICCX-930111-49-1-1-1-1SP-1-1-1-1BP
59	ICCX-930111-50-1-1-1-1SP-1-1-1-1BP
60	ICCX-930111-51-1-1-1-1SP-1-1-1-1BP
61	ICCX-930111-52-1-1-1-1SP-1-1-1-1BP
62	ICCX-930111-53-1-1-1-1SP-1-1-1-1BP
63	ICCX-930111-53-1-1-1-2DP-1-1-1-1BP
64	ICCX-930111-54-1-1-1-1SP-1-1-1-1BP
65	ICCX-930111-55-1-1-1-1SP-1-1-1-1BP
66	ICCX-930111-56-1-1-1-1SP-1-1-1-1BP
67	ICCX-930111-57-1-1-1-1SP-1-1-1-1BP
68	ICCX-930111-58-1-1-1-1DP-1-1-1-1BP
69	ICCX-930111-59-1-1-1-1SP-1-1-1-1BP
70	ICCX-930111-60-1-1-1-1SP-1-1-1-1BP
71	ICCX-930111-61-1-1-1-1SP-1-1-1-1BP
72	ICCX-930111-62-1-1-1-1SP-1-1-1-1BP
73	ICCX-930111-63-1-1-1-1DP-1-1-1-1BP
74	ICCX-930111-64-1-1-1-1SP-1-1-1-1BP
75	ICCX-930111-65-1-1-1-1SP-1-1-1-1BP
76	ICCX-930111-66-1-1-1-1SP-1-1-1-1BP
77	ICCX-930111-101-1-1-1-1-1-BP
78	ICCX-930111-102-1-1-1-1-1-BP
79	ICCX-930111-103-1-1-1-1-1-BP
80	ICCX-930111-104-1-1-1-1-1-BP
81	ICCX-930111-105-1-1-1-1-1-BP
82	ICCX-930111-106-1-1-1-1-1-BP
83	ICCX-930111-107-1-1-1-1-1-BP
84	ICCX-930111-108-1-1-1-1-1-BP
85	ICCX-930111-109-1-1-1-1-1-BP
86	ICCX-930111-110-1-1-1-1-1-BP
87	ICCX-930111-111-1-1-1-1-1-BP
88	ICCX-930111-112-1-1-1-1-1-BP
89	ICCX-930111-113-1-1-1-1-1-BP
90	ICCX-930111-114-1-1-1-1-1-BP
91	ICCX-930111-115-1-1-1-1-1-BP
92	ICCX-930111-116-1-1-1-1-1-BP
93	ICCX-930111-117-1-1-1-1-1-BP
94	ICCX-930111-118-1-1-1-1-1-BP
95	ICCX-930111-119-1-1-1-1-1-BP
96	ICCX-930111-120-1-1-1-1-1-BP
97	ICCX-930111-121-1-1-1-1-1-BP
98	ICCX-930111-122-1-1-1-1-1-BP
99	ICCX-930111-123-1-1-1-1-1-BP
100	ICCX-930111-124-1-1-1-1-1-BP
101	ICCX-930111-125-1-1-1-1-1-BP
102	ICCX-930111-126-1-1-1-1-1-BP
103	ICCX-930111-127-1-1-1-1-1-BP
104	ICCX-930111-128-1-1-1-1-1-BP
105	ICCX-930111-129-1-1-1-1-1-BP

(Contd.

Code No.	Pedigree
106	ICCX-930111-130-1-1-1-1-BP
107	ICCX-930111-131-1-1-1-1-BP
108	ICCX-930111-132-1-1-1-1-BP
109	ICCX-930111-133-1-1-1-1-BP
110	ICCX-930111-134-1-1-1-1-BP
111	ICCX-930111-135-1-1-1-1-BP
112	ICCX-930111-136-1-1-1-1-BP
113	ICCX-930111-137-1-1-1-1-BP
114	ICCX-930111-138-1-1-1-1-BP
115	ICCX-930111-139-1-1-1-1-BP
116	ICCX-930111-140-1-1-1-1-BP
117	ICCX-930111-141-1-1-1-1-BP
118	ICCX-930111-142-1-1-1-1-BP
119	ICCX-930111-143-1-1-1-1-BP
120	ICCX-930111-144-1-1-1-1-BP
121	ICCX-930111-145-1-1-1-1-BP
122	ICCX-930111-146-1-1-1-1-BP
123	ICCX-930111-147-1-1-1-1-BP
124	ICCX-930111-148-1-1-1-1-BP
125	ICCX-930111-149-1-1-1-1-BP
126	ICCX-930111-150-1-1-1-1-BP
127	ICCV 2
128	JG 62
129	Annigeri
130	ICCV 10
131	ICCV 96029
132	ICCC 37

broad spectrum of variability in segregating generations leading to development of useful genetic stock and varieties. Clusters I and VIII separated by the largest statistical distance showed maximum divergence. It is not always possible to predict high heterosis or transgressive segregants by crossing the genetically diverse parents. Peter *et al.* (1978) obtained maximum heterosis in tomato where parents were moderately diverse. In our experiment, cluster VI for seed yield, cluster II for pods per plant, cluster V for test weight and cluster I for early and dwarf genotypes were found superior. A multiple crossing program involving genotypes from these clusters may lead to the isolation of superior segregants in advanced generations with high genetic yield potential.

REFERENCES

Jatasra, D.S. *et al.* (1978). *Cereal Res. Commun.*, **6**: 307-317.

Katiyar, R.P. (1978). *Indian J. Agric. Sci.*, **48**: 451-454.

Kumar, T.V. *et al.* (1993). *Indian J. Genet.*, **53**: 223-237.

Mahalanobis, P.C. (1928). *J. Asiatic Soc. Bengal*, **25**: 301-77.

Mohanty, B.K. *et al.* (2001). *Agric. Sci. Digest*, **21**: 17-20.

Peter, K.V. *et al.* (1978). *Indian J. Genet.*, **38**: 173-178.

Rao, C.R. (1952). Advanced Statistical Methods in Biometrical Research. John Wiley and Sons, Inc., New York. PP 224-252.

Sandhu, T.S. *et al.* (1991). *Int. Chickpea Newsl.*, **24**: 18-19.

Sarma, R.N. *et al.* (1994). *Indian J. Genet.*, **54**: 184-187.

Singh, N. (2002). *Indian J. Pulses Res.*, **15**: 70-72.