The Andhra Agric. J 56(2):151-158, 2009

Principal Component and Cluster Analyses in Desi chickpea (*Cicer arietinum* L.)

U Lakshmi Annapurna, S Srimannarayana Murthy, C Panduranga Rao and R Srinivasulu
Dept of Genetics and Plant Breeding, Agricultural College, Bapatla 522 101, Andhra Pradesh.

ABSTRACT

Forty genotypes of *Desi* chickpea were evaluated to study genetic divergence by using principal component analysis and cluster analysis. These genotypes were grouped into 7 clusters. Principal component analysis identified five principal components with eigen values more than one which contributed 92.14 per cent of the cumulative variance. The genotypes selected from the above analysis were K-850, ICC 927, ICC -7425, SAKI 9516, DCP 92-3, and L-550 which appear to be desirable for inclusion in crossing programme aimed for improvement of *Desi* chickpea

Key words : Cluster Analysis, *Desi* Chickpea, Genetic Divergence, Principal Component Analysis.

Chickpea is the third most important grain legume, occupying first position both in area and production among the pulse crops grown in India. Chickpea being an autogamous crop, the generation of variability through natural means is limited. Hence, the chances of selection of desirable parental lines for breeding improved varieties are also limited. The present study was envisaged to measure the genetic diversity among the genotypes of *Desi* chickpea to identify the diverse stocks for their further use in hybridization programme for yield improvement.

MATERIAL AND METHODS

The material for the investigation comprised 40 *Desi* chickpea genotypes (Table 1), collected from different parts of the world. These genotypes of Desi Bengalgram were grown in *rabi* season during 2006-07 in a randomized block design with three replications at Regional Agricultural Research Station, Lam, Guntur. Each entry was planted in a single row of 4 m length with inter- and intra-row spacing of 30 X 10 cm. The observations were recorded on ten randomly selected competitive plants or on plot basis in each entry and in each replication on 11 component characters *i.e.,* days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, 100 seed weight (g), harvest index, biological yield per plant (g), protein content (%) and seed yield per plant (g) and mean values were used for statistical analysis. The data were subjected to principal component analysis (Jackson, 1991) and hierarchical cluster analysis (Anderberg, 1993), using the software 'INDOSTAT'.

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among the 40 *Desi* genotypes of chickpeas indicating that the existence of substantial genetic variability for all the characters under study.

Principal component analysis (PCA) identified five principal components with eigen values more than one which contributed 92.14 per cent of cumulative variance (Table 2). The first principal component (PC_1) contributed maximum towards variability (47.75%) with significant loading of 100 seed weight (-0.887) which was negatively correlated. The second principal component (PC_2) accounted for 18.18 per cent of total variance and it reflected significant loading of days to 50% flowering (0.680) and harvest index (0.206) which were positively correlated, where as number of secondary branches per plant (-0.442) and seed yield per plant (-0.285) were negatively correlated. The third principal component (PC_3) contributed 12.91 per cent of cumulative variance and it was characterized by conspicuously high loading of protein content (-0.715) and days to maturity (-0.553) which were negatively correlated (Table 3). Based on these first three principal components mean genotype scores were computed (Table 4). Principal factor scores for all the 40 genotypes were estimated in all 3 PC's and utilized to construct precise 2D and 3D plot (Fig 1 and 2). All the genotypes were plotted for PC_1, PC_2 and PC_3 which cumulatively explained 78.84 per cent of variability accounted for all the characters (Table 4).

The plot of PC_1, PC_2 and PC_3 showed character differentiation of genotypes according to

Table 1. Source of the 40 *Desi* chickpea (*Cicer arietinum* L.) genotypes/ germplasm lines studied

Sl.No.	Genotype/ germplasm accession No.	Source	Sl.No.	Genotype/ germplasm accession No.	Source
1	GNG 469	ARS, Sriganganagar	21	ICC 5168	PAU, Ludhiana
2	BG 256	IARI, New Delhi	22	ICC 4948	PAU, Ludhiana
3	Pusa 372	IARI, New Delhi	23	ICC 3500	ICRISAT, Hyderabad, (collection by RPIP, Turkey from Ankara)
4	JG 315	JNKVV, Jabalpur	24	ICC 432	ICRISAT, Hyderabad, (collection by RPIP, Pusa, Bihar)
5	L 550	PAU, Ludhiana	25	ICC 12237	ICRISAT, Hyderabad
6	KWR 108	CSAUAT, Kanpur	26	ICC 453	ICRISAT, Hyderabad, (collection by RPIP, Pusa, Bihar)
7	RSG 888	ARS, Durgapura	27	ICC 506	ICRISAT, Hyderabad, (collection by ANGRAU, Rajendranagar)
8	SAKI 9516	JNKVV, Jabalpur	28	ICC 3296	ICRISAT, Hyderabad, (collection from Iran)
9	HC -3	HAU, Hisar	29	ICC 1564	ICRISAT, Hyderabad, (collection from IIPR Kanpur)
10	Avrodhi	GBPUAT, Pantnagar	30	ICC 16644	ICRISAT, Hyderabad, (collected from Pakistan)
11	Pant G 186	GBPUAT, Pantnagar	31	ICC 12373	ICRISAT, Hyderabad, (collected from Maharashtra)
12	C 235	PAU, Ludhiana	32	JG 11	ICRISAT, Hyderabad,
13	BGM 408	IARI, New Delhi	33	ICCV-10	ICRISAT, Hyderabad
14	Radhey	GBPUA &T, Pantnagar	34	ICCC 37	ICRISAT, Hyderabad
15	DCP 92-3	GBPUA &T, Pantnagar	35	ICC 927	ICRISAT, Hyderabad, (collection from IARI, New Delhi)
16	K-850	GBPUA &T, Pantnagar	36	ICC 706	ICRISAT, Hyderabad (collected by IARI from Punjab)
17	Dahood yellow	ARS, Junagadh	37	Jyothi	RARS, Lam
18	ICC 3219	ICRISAT, Hyderabad	38	Vijay	MPKV, Rahuri
19	ICC 92338	ICRISAT, Hyderabad	39	Annegiri	UAS, Dharwad
20	ICC 7425	IIPR, Kanpur	40	ICC 14694	ICRISAT, Hyderabad (collected by JNKVV, Jabalpur)

Table 2.The Eigen values per cent variance, cumulative percent variance for principal components in *Desi* chickpea (*Cicer arietinum* L.).

Character	PC_1	PC_2	PC_3	PC_4	PC_5
Eigen value	32.18	19.86	16.73	14.16	9.37
% of variance	47.75	18.18	12.91	9.24	4.05
Cumulative variance	47.75	65.93	78.84	88.09	92.14

Table 3. Character loading of five principal components forty (40) different genotypes of *Desi* chickpea (*Cicer arietinum* L.).

Character	PC_1	PC_2	PC_3	PC_4	PC_5
Days to 50% flowering	0.144	0.680	0.154	0.349	0.184
Days to maturity	0.131	-0.209	-0.553	0.292	-0.257
Plant height (cm)	-0.026	0.120	0.099	0.196	-0.025
No. of primary branches / plant	-0.013	0.031	-0.042	-0.064	-0.169
No. of secondary branches / plant	0.129	-0.422	0.038	0.104	0.822
No. of pods /plant	-0.125	0.204	0.317	-0.502	0.081
100- seed weight (g)	-0.887	0.091	-0.179	0.318	0.141
Harvest index (%)	0.123	0.206	-0.070	0.001	-0.135
Biological yield / plant (g)	-0.348	-0.164	0.062	-0.422	-0.112
Protein content (%)	0.059	0.313	-0.715	-0.452	0.275
Seed yield / plant (g)	0.023	-0.285	0.053	0.032	-0.244

their cluster membership for each cluster. The mean scores of genotypes were used as input for clustering in order to group the genotypes into various clusters. Hierarchical clustering procedure (Ward's method) was followed to group the genotypes into 7 clusters (Table 5 Fig 3). This reflects that there was no relation between geographical origin and genetic diversity.

The biggest cluster was cluster III consisting of 15 genotypes followed by cluster V and VII comprising 6 genotypes each. The maximum inter-cluster distance was observed between cluster II and IV (840.03) followed by cluster II and III (819.83) and cluster II and VI (734.14) as shown in Table 6. Cluster IV is characterized by high mean value for days to 50% flowering (65.22), plant height (45.07), number of primary branches per plant (2.24). Cluster VI recorded high mean values for number of pods per plant (60.98), harvest index (43.92), biological yield per plant (57.53) and seed yield per plant (12.27). Where as cluster II recorded high mean values for 100 seed weight (g) (31.33) (Table 7). Based on these studies crosses may be effective between the genotypes of these clusters to obtain better and desirable segregants. Utilization of principal component analysis combined with hierarchical cluster analysis in genetic diversity studies was reported by earlier workers Narendra Singh (2002) in Bengal gram and Altaher and Singh (2003) in cotton. Genotypes K-850, ICC- 927, ICC - 7425, SAKI -9516, DCP 92-3, and L-550 appear to be desirable for inclusion in crossing programme aimed for improvement of *Desi* chickpea.

The present study depicted the relative divergence in morphological and yield traits. The clustering pattern could be utilized in identifying the best cross combinations for generating variability with respect to various traits under study. The genotypes clubbed in the different clusters if inter crossed may generate wide variability. Some

Table 4. The PCA scores or genotypic mean scores for 40 *Desi* genotypes of chickpea (*Cicer arietinum* L.).

Genotype	PCA I	PCA II	PCA III
	X Vector	Y Vector	Z Vector
GNG 469	-6.416	29.042	-28.934
BG 256	-8.679	27.570	-25.333
PUSA 372	2.886	24.929	-23.926
JG 315	-2.426	27.590	-28.347
L550	0.242	31.716	-24.945
KWR 108	1.785	23.812	-30.637
RSG888	2.227	23.863	-24.048
SAKI 9516	-0.789	30.240	-24.712
HC 3	-2.184	23.374	-26.781
AVRODHI	2.963	24.680	-26.548
PANT G 186	2.610	23.492	-26.036
C 235	4.256	27.202	-25.958
BGM 408	7.547	22.638	-25.693
RADHEY	-2.059	23.143	-24.677
DCP 92-3	2.866	28.905	-24.546
K 850	-7.819	21.351	-24.011
DAHOOD	-0.376	26.266	-24.305
ICC 3219	0.481	27.325	-23.908
ICC 92338	-1.779	20.923	-25.547
ICC 7425	-14.495	17.936	-23.575
ICC 5168	1.375	28.232	-16.945
ICC 4948	6.368	18.686	-23.249
ICC 3500	-1.172	24.386	-17.674
ICC 432	2.550	25.179	-25.476
ICC 12237	5.631	24.881	-26.248
ICC 453	3.699	21.612	-26.031
ICC 506	0.930	23.909	-21.935
ICC 3296	5.518	24.895	-21.207
ICC 1564	4.743	21.074	-24.881
ICC 16644	-1.984	23.222	-22.676
ICC 12373	-9.858	26.115	-29.252
JG 11	-3.516	25.490	-23.056
ICCV 10	2.262	20.568	-25.524
ICCV 37	-1.364	20.611	-26.929
ICC 927	-10.805	21.238	-24.148
ICC 706	-6.276	21.896	-24.092
JYOTHI	2.054	21.256	-23.406
VIJAY	2.904	25.686	-28.251
ANNEGIRI	2.462	22.727	-26.827
ICC 14694	-9.037	29.045	-21.820

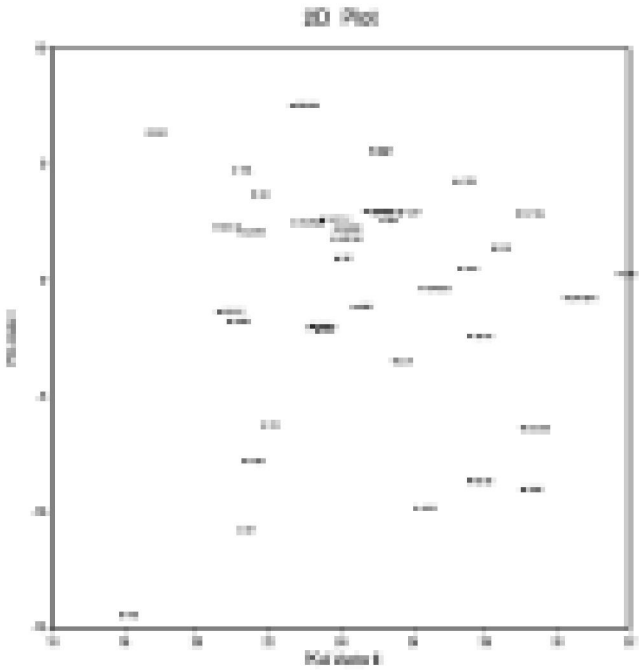

Fig. 1. Two dimensional graph showing relative position of genotypes of Desi chickpea (Cicer aritinum L.) based on PCA scores

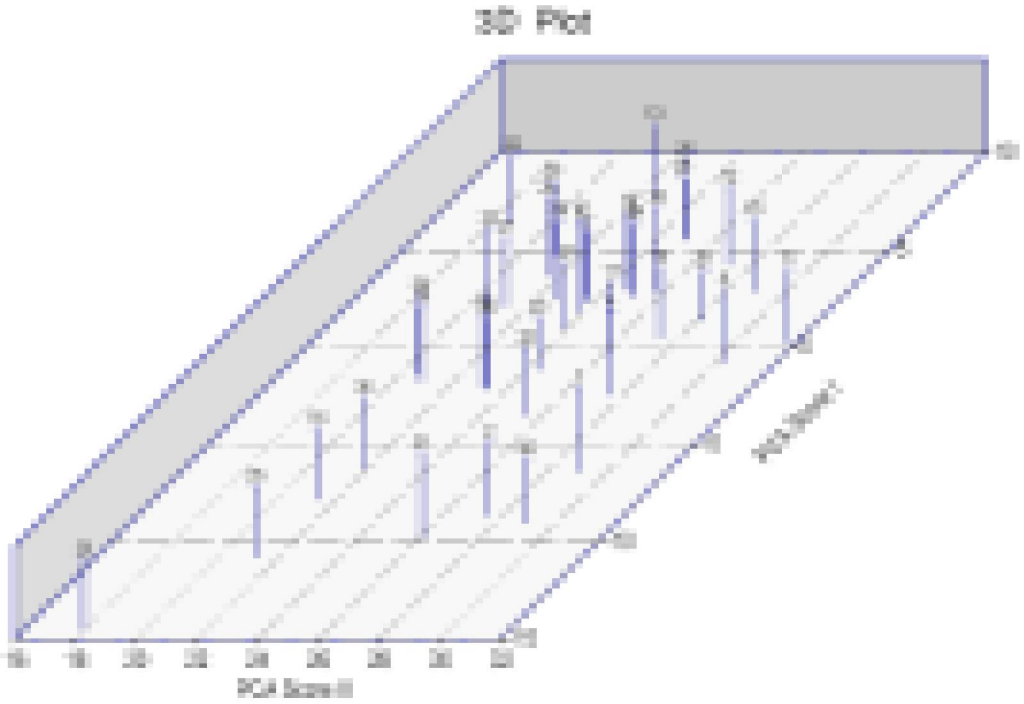

Fig. 2. Three dimensional graph showing relative position of genotypes of *Desi* chickpea (*Cicer aritinum* L*)* based on PCA scores (genotypes number as per Table 1)

Fig. 3. Hierarchical clustering procedure of the *Desi* chickpea (*Cicer arietinum* L.) genotypes using Ward's minimum variance method

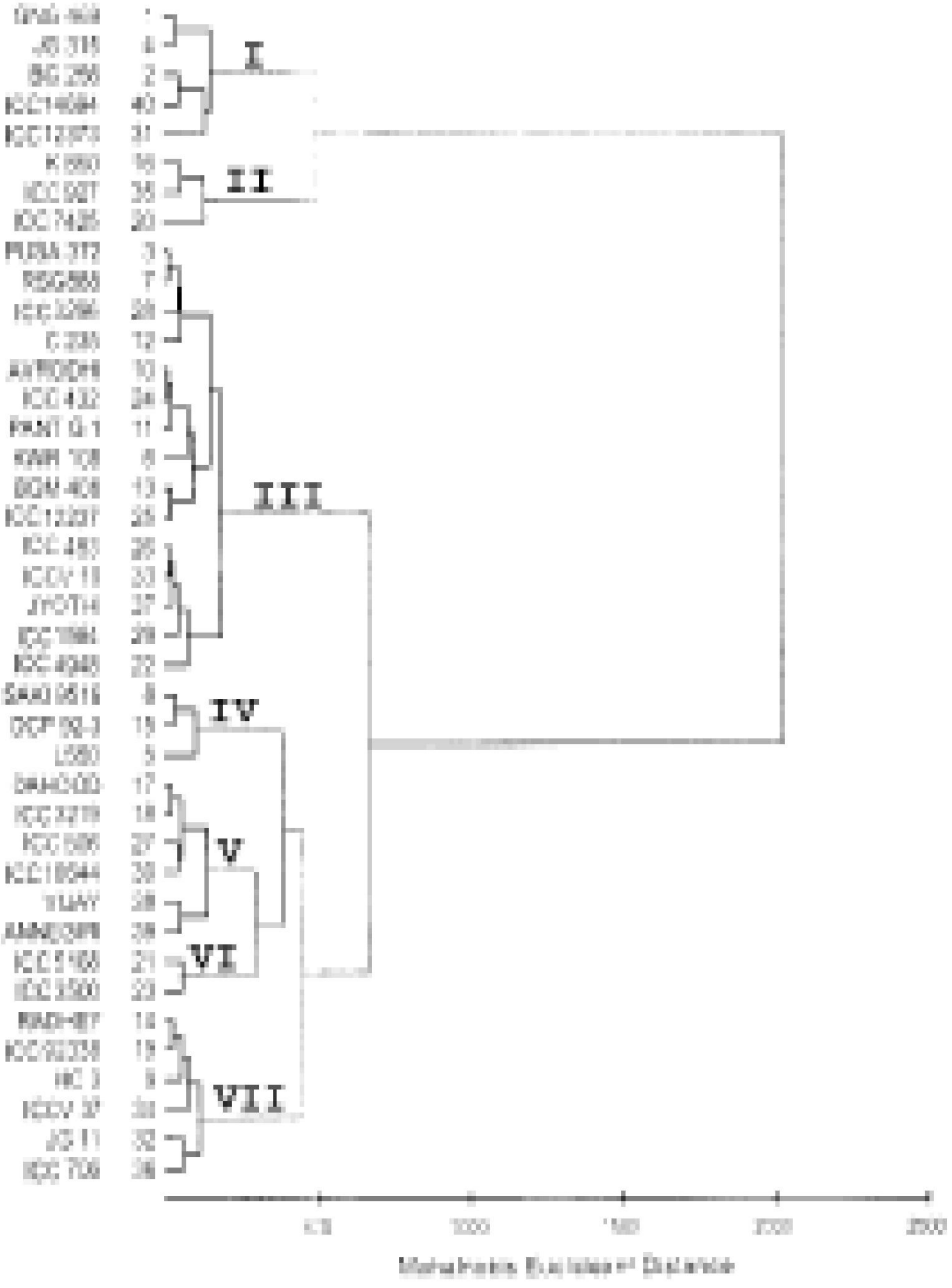

Table 5. Cluster position of forty genotypes of *Desi* chickpea (*Cicer arietinum* L.).based on Ward's minimum variance method.

Cluster	No. Of. Genotypes	Name of genotypes
I	5	GNG 469, JG315, BG 256, ICC 12373
II	3	K-850, ICC-927, ICC-7425
III	15	Pusa-372, RSG 888, ICC-3296, C-235, Avrodhi, ICC-432, Pant G 186, KWR 108, BGM-408, ICC-12237, ICC-453, ICCV-10, Jyothi, ICC-1564, ICC-4948
IV	3	SAKI-9516, DCP 92-3, L-550
V	6	Dahood yellow, ICC-3219, ICC-506, ICC-16644, Vijay, Annegiri
VI	2	ICC-5168, ICC-3500
VII	6	Radhey, ICC-92338, HC-3, ICCV-37, JG-11, ICC-706

Table 6. Mean intra (bold) and inter cluster distance among seven clusters using Ward's minimum variance method in Desi chickpea (Cicer arietinum L.).

Cluster	I	II	III	IV	V	VI	VII
I	**182.43**	395.05	570.33	384.48	396.39	549.26	290.56
II		**183.0**	819.83	840.03	671.45	734.14	340.84
III			**118.69**	304.79	196.85	356.78	250.29
IV				**131.64**	292.86	340.93	331.40
V					**123.97**	277.41	222.57
VI						**113.95**	353.99
VII							**128.84**

Table 7. Mean values of clusters from 40 germplasm accessions of *Desi* chickpea (*Cicer arietinum* L.) for 11 characters

Cluster number	Days of 50% flowering	Days to maturity	Plant height (cm)	No. of. primary branches	No. of. secondary branches / plant	No. of. pods per plant	100 seed weight (g)	Harvest index (%)	Biological yield per plant (g)	Protein content (%)	Seed yield per plant (g)
I	55.53	90.73	41.01	2.42	4.46	39.98	26.56	41.72	23.45	21.68	9.79
II	42.66	85.77	44.11	1.88	9.25	36.44	31.33	40.51	24.27	15.66	9.92
III	52.80	94.75	39.06	2.08	9.34	29.12	14.38	37.56	15.44	18.36	5.97
IV	65.22	90.44	45.07	2.24	6.71	26.85	18.60	40.40	11.93	21.22	4.83
V	49.83	85.66	41.68	1.91	7.98	47.10	16.30	43.46	17.78	21.07	7.79
VI	60.16	80.16	42.10	1.84	8.65	60.98	16.21	43.92	27.86	14.20	12.27
VII	49.50	91.16	41.12	1.88	9.69	32.43	22.43	40.74	18.93	18.12	7.60

combinations may also exhibit high heterosis for seed yield *i.e.,* transgressive segregants for yield and yield components may also be expected.

Clustering pattern indicated no association between geographical distribution of accessions and genetic divergence. There are forces other than geographical separation, which are responsible for diversity such as natural and artificial selection, exchange of breeding material, genetic drift and environmental variations as shown in Table 1 (Murthy and Arunachalam, 1966). Similar results were derived by Sarvaliya and Goyal (1995) and Kumar (1997).

LITERATURE CITED

Altaher A F and Singh R P 2003. Genetic diversity studies in upland cotton (*Gossypium hirrustum* L.) using two methods of clustering. Indian Society of Cotton Improvement, 158-163.

Anderberg M R 1993. Cluster Analysis for Applications New York: Academic Press.

Jackson J E 1991. A Users Guide to Principal Components. John Wiley and Sons, New York.

Kumar N 1997. Genetic diversity among chickpea accessions. Indian Journal of Genetics and Plant Breeding, 57: 87-90.

Murthy B R and Arunachlam V 1966. The nature of genetic divergence in relation to breeding system in crop plants. Indian Journal of Genetics and Plant Breeding, 26: 188-198.

Narendra Singh 2002. Multivariate analysis in *Kabuli* chickpea accessions. India Journal of Pulses Research. 15(1): 70-72.

Sarvaliya V M and Goyal S N 1995. Genetic divergence in chickpea. Gujarat Agricultural University Research Journal, 21: 207-212.

(Received on 31.10.2007 and revised on 28.01.2008)