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Genetic Divergence Estimation by Different Methods in *Desi* Chickpea (*Cicer arietinum* L.)

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ABSTRACT

Thirty genotypes of *desi* chickpea were evaluated for genetic diversity using Mahalanobis' D^2 statistic, cluster analysis and principal component analysis (PCA). By using Mahalanobis' D^2 statistic and cluster analyses 5 and 6 clusters were obtained, respectively. Divergence studies indicated that geographical diversity not necessarily associated with genetic diversity. 100-seed weight and days to maturity contributed maximum towards divergence in D^2 analysis and PCA. Principal component analysis identified four principal components with eigen values more than one which contributed 90.661 per cent of cumulative variance. The genotypes selected from above analyses were ICC 16036, CSJ 313, ICC 12960, ICC 14334, ICC 188, 1CC 14194, ICC 8927, BG 2070, Phule G 01103, JSC 39, JG 2003-01101 and IPC 00-59. Utilizations of these genotypes as parents in hybridization programme may result in good recombinants.

Key words : Chickpea, Cluster Analysis, D^2 Statistic, Principal Component Analysis

Chickpea is the world's most widely cultivated pulse crop. It provides protein of high biological value to vegetarian diets for overcoming malnutrition. Genetic diversity is the basic requirement for any successful breeding programme. It has been well known that genetically diverse parents are likely to yield desirable gene recombinants to produce high heterotic effect. Hence, the present investigation was undertaken to assess the nature and the magnitude of genetic diversity in chickpea genotypes through different methods *i.e.,* D^2 statistic, cluster and principal component analyses (PCA).

MATERIAL AND METHODS

The present investigation was carried out with 30 genotypes of *desi* chickpea collected from different sources (Table 1), grown in a randomized block design with three replications during *rabi* 2007-08 season at Regional Agricutlural Research Station (RARS) Lam, Guntur. Each genotype was sown in a single row of 4 meter length with inter and intra-row spacing of 30 x 10 cm. Ten competitive plants of each genotype in each replication were randomly tagged to record observations on plant height, number of primary branches plant^{-1}, number of pods plant^{-1}, harvest index, biological yield and seed yield plant^{-1} and mean values were used for statistical analysis.

Days to 50 % flowering, days to maturity, 100-seed weight, harvest index, biological yield plant^{-1} and protein content were recorded on plot basis.

D^2 analysis (Mahalanobis,1928), principal component analysis (Jackson, 1991) and hierarchical cluster analysis (Anderberg, 1993) were carried using SPSS computer programme.

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among the genotypes for all the eleven characters studied. On the basis of D^2 analysis the 30 genotypes were grouped into 5 clusters (Table 2). Cluster II was largest with 13 genotypes followed by cluster I (7), cluster III (6), cluster IV (3) and cluster V which had only one genotype. No geographical demarcation was visible in the pattern of distribution of genotypes into various clusters, as also reported by Jeena *et al.* (2005).

Mean intra-cluster and inter-cluster D^2 values are presented in Table 3. The intra-cluster D^2 values ranged from 0.0 to 33.1, maximum intra-cluster distance was found in cluster III (33.1) and it was lowest (0.0) in cluster V. The lowest inter-cluster value was observed between cluster II and III and highest inter-cluster value was observed between cluster I and V. Among the five clusters, cluster I and cluster V were the most divergent to other clusters and could be used as donors in hybridization

Table 1. Source of the 30 chickpea (*Cicer arietinum* L.) genotypes/ germplasm lines studied.

Sl.No	Genotype/ germplasm accession No.	Source
1	ICC 14334	ICRISAT, Hyderabad
2	ICC 14194	ICRISAT, Hyderabad (collected from Mexico)
3	ICC 3496	ICRISAT, Hyderabad (collected by RPIP, Iran)
4	ICC 12960	ICRISAT, Hyderabad
5	ICC 188	ICRISAT, Hyderabad (collected by RPIP, India)
6	ICC 16036	ICRISAT, Hyderabad
7	ICC 16460	ICRISAT, Hyderabad
8	ICC 10629	ICRISAT, Hyderabad (collected by TNAU, Tamilnadu)
9	ICC 8927	ICRISAT, Hyderabad
10	ICC 12430	ICRISAT, Hyderabad
11	ICC 11322	ICRISAT, Hyderabad
12	GL 22044	PAU, Ludhiana
13	IPC 00-59	IIPR, Kanpur
14	GJG 0107	GAU, Junagadh
15	GNG 0315	GAU, Junagadh
16	JSC 38	Sehore
17	BGM 558	IARI, New Delhi
18	GL 22007	PAU, Ludhiana
19	JG 2003-01101	JNKVV, Jabalpur
20	H-02-113	CCS HAU, Hisar
21	GNG 1744	ARS, Sriganganagar
22	H 02 -125	CCS HAU, Hisar
23	IPC 2004-52	IIPR, Kanpur
24	GNG 1685	ARS, Sriganganagar
25	Phule G 01103	MPKV, Rahuri
26	CSJ 313	ARS, Durgapur
27	BG 2070	IARI, New Delhi
28	JSC 39	Sehore
29	JG 2000-7	JNKVV, Jabalpur
30	LBeG 21	RARS, Lam

Table 2. Distribution of 30 chickpea *(Cicer arietinum L.)* genotypes in different clusters by Tocher's method.

Cluster	No.of genotypes	Genotypes
I	7	ICC 16036, CSJ 313, ICC 12960, ICC 14334, ICC 188, ICC 14194, ICC 8927
II	13	Phule G 01103, JSC 39, JG 2003-01101, JG 2000-7,GJG 0107, IPC 00-59, GL 22007, GNG 0315, GNG 1744,BGM 558, H02 -125, GL 22044, H02-113
III	6	IPC 2004-52, GNG 1685, ICC 12430, ICC 10629, LBeG 21, ICC 3496
IV	3	ICC 16460, JSC 38, ICC 11322
V	1	BG 2070

Table 3. Intra-(bold) and inter-cluster average divergence (D^2) values of 5 clusters from 30 germplasm accessions of chickpea (*Cicer arietinum* L.).

Cluster	I	II	III	IV	V
I	**24.1**	87.1	85.9	57.0	185.4
II		**32.3**	54.7	69.1	65.6
III			**33.1**	111.8	96.9
IV				**17.5**	146.3
V					0.0

Table 4. Contribution of each character to the diversity in chickpea (*Cicer arietinum* L.)

Character	Times Ranked first	Contribution in percentage
Days to 50 % flowering	69	15.86
Days to maturity	139	31.95
Plant height (cm)	3	0.69
No. of primary branches plant^{-1}	11	2.53
No. of secondary branches plant^{-1}	1	0.23
No. of pods plant^{-1}	25	5.75
100-seed weight (g)	150	34.48
Harvest index (%)	0	0.00
Biological yield plant^{-1} (g)	16	3.68
Protein content (%)	21	4.83
Seed yield plant^{-1} (g)	0	0.00

Table 5. Mean values of clusters based on D^2 analysis from 30 germplasm accessions of chickpea (*Cicer arietinum* L.) for 11 characters

Cluster Number	Days to 50 % flowering	Days to maturity	Plant height (cm)	No .of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No .of pods plant^{-1}	100-seed weight (g)	Harvest index (%)	Biological yield plant^{-1} (g)	Protein content (%)	Seed yield plant^{-1} (g)
I	44.429	83.714	39.376	2.062	10.233	46.600	15.156	46.221	18.521	16.419	8.814
II	48.462	89.564	45.905	2.300	10.259	45.126	22.012	45.049	22.978	18.283	10.687
III	52.722	93.556	42.378	2.011	9.094	41.178	14.837	39.487	19.137	18.957	7.424
IV	44.000	82.556	39.944	2.400	12.533	52.300	24.743	43.520	30.658	19.019	13.093
V	47.333	91.333	48.533	2.733	14.200	62.433	26.996	47.373	34.998	17.492	16.978

Table 6. The eigen values, per cent variability, cumulative per cent variability for 4 principal components in chickpea (*Cicer arietinum* L.).

	PC_1	PC_2	PC_3	PC_4
Eigen value	454.848	210.684	120.585	74.281
% of variance	47.928	22.200	12.706	7.827
Cumulative variance	47.928	70.128	82.834	90.661

Table 7. Character loading of 4 principal components of 30 different genotypes of chickpea (*Cicer arietinum* L).

Character	PC_1	PC_2	PC_3	PC_4
Days to 50 % flowering	0.281	0.399	0.479	0.359
Days to maturity	0.648	0.266	-0.385	-0.264
Plant height (cm)	0.123	-0.007	-0.034	0.137
No. of primary branches plant^{-1}	0.332	0.051	-0.118	-0.152
No. of secondary branches plant^{-1}	-0.168	-0.219	-0.164	0.256
No. of pods plant^{-1}	-0.132	-0.124	-0.582	0.345
100-seed weight (g)	0.414	-0.798	0.085	-0.017
Harvest index (%)	0.181	0.031	-0.116	-0.147
Biological yield plant^{-1} (g)	0.161	0.181	-0.352	0.575
Protein content (%)	0.305	-0.179	0.312	0.463
Seed yield plant^{-1} (g)	0.083	-0.038	0.011	-0.091

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

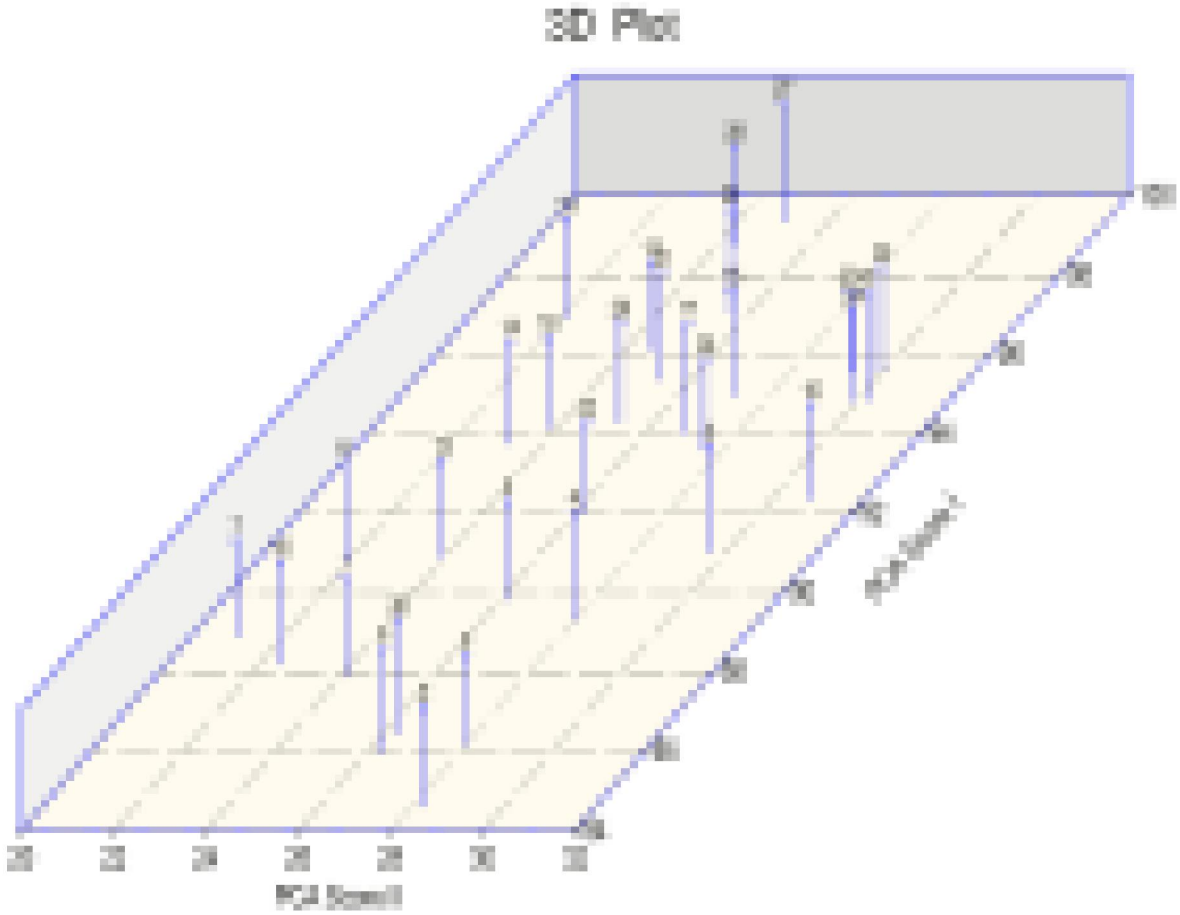

Table 8. Cluster composition of 30 genotypes of chickpea (*Cicer arietinum* L.). genotypes by Ward's minimum variance method.

Cluster	No.of genotypes	Genotypes
I	7	ICC 14334, ICC 188, ICC 16036, CSJ 313, ICC 12960, ICC 14194, ICC 8927
II	3	ICC 16460, JSC 38, ICC 11322
III	7	ICC 10629, LBeG 21, ICC 3496, ICC 12430, H02-113, IPC 2004-52, GNG 1685
IV	5	GL 22044, H02-125, GL 22007, GJG 0107, JG 2000-7
V	4	Phule G 01103, JSC 39, JG 2003-01101, IPC 00-59
VI	4	BGM 558, GNG 1744, GNG 0315, BG 2070

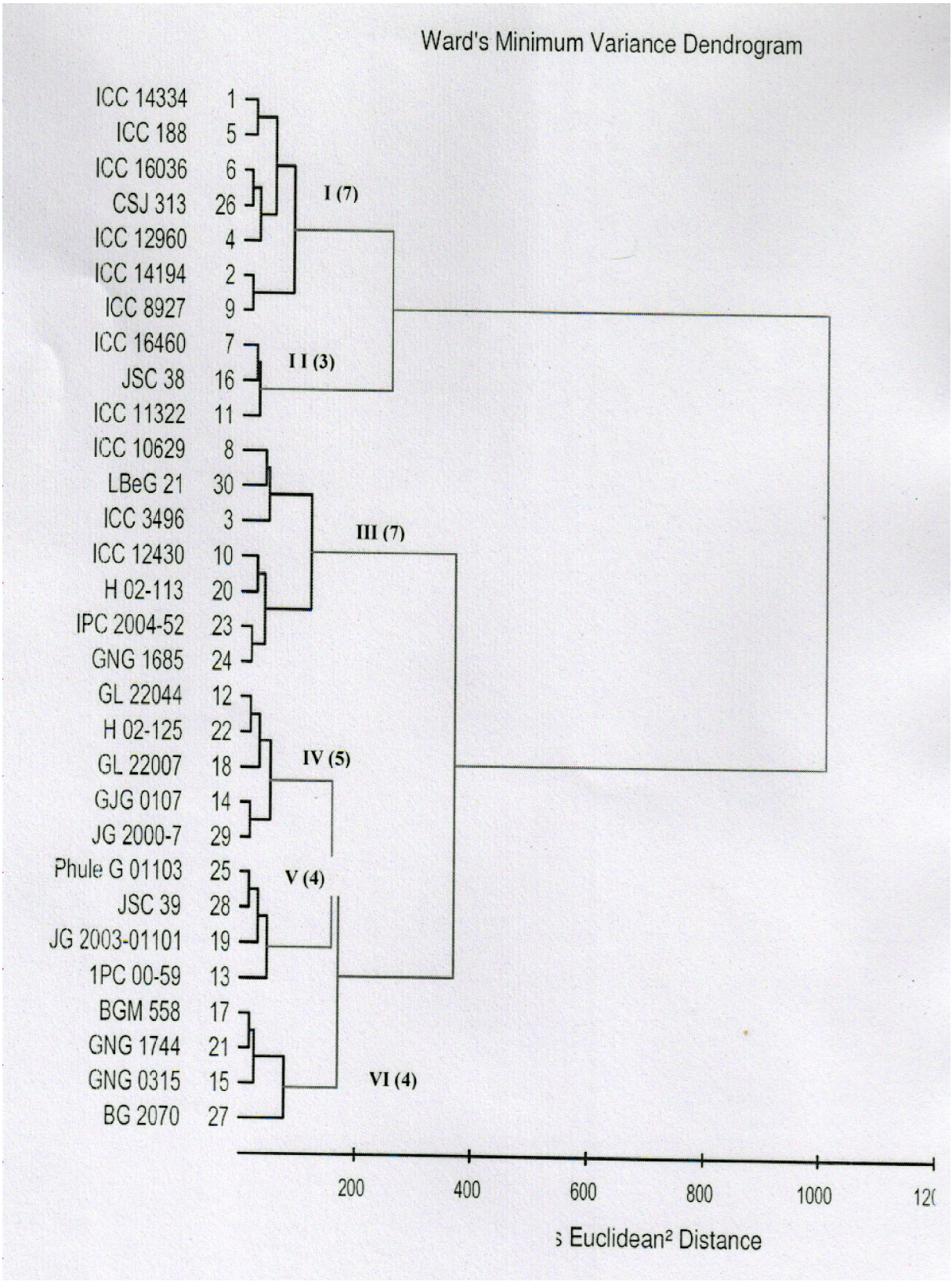

Fig 2. Diagram illustrating the clustering pattern by Ward's minimum variance method in chickpea genotypes

Table 9. Mean intra (bold) and inter cluster distance among 6 clusters using Ward's minimum variance method in chickpea (*Cicer arietinum* L.).

Cluster	I	II	III	IV	V	VI
I	**72.4**	171.0	251.8	182.9	386.5	319.4
II		**52.6**	317.0	130.8	295.4	272.6
III			**95.9**	154.0	207.6	160.1
IV				**57.2**	116.7	129.0
V					**61.0**	134.4
VI						**79.4**

programme for obtaining a wide spectrum of variation among the segregants. Kanaka Durga *et al.* (2005) reported similar results.

100-seed weight (34.48 %) contributed maximum towards divergence followed by days to maturity (31.95 %), days to 50 % flowering (15.86 %), number of pods plant^{-1} (5.75 %), protein content (4.83) and biological yield $^{-1}$(3.68 %) (Table 4).

Cluster V (BG 2070) had highest mean value for maximum of eight characters viz., plant height, number of primary branches, number of secondary branches, number of pods plant^{-1}, 100-seed weight, harvest index and biological yield plant^{-1} (Table 5).

Principal component analysis (PCA) identified four principal components (Table 6) with eigen value more than one which contributed 90.661 per cent of cumulative variance. The first principal component (PC_1) contributed maximum towards variability (47.928) with significant loading of days to maturity (0.648), 100-seed weight (0.414), number of primary branches plant^{-1} (0.332) and protein content (0.305).

The second principal component (PC_2) described 22.20 per cent of the total variance and it reflected significant loading of 100-seed weight (0.798) and number of secondary branches plant^{-1} (-0.219). The third principal component (PC_3) recorded high loading of number of pods plant^{-1} (-0.582), days to 50 % flowering (0.479), days to maturity (-0.385), biological yield plant^{-1} (-0.352) and protein content (0.312). The fourth principal component (PC_4) showed high loading of biological yield plant^{-1} (0.575), protein content (0.463), days to 50 % flowering (0.359) and number of pods plant^{-1} (0.345) (Table 7).

The three PCA scores were plotted in graph to get the 3D (Fig 1) scattered diagram. This 3D plot clearly indicated clustering of genotypes BG 2070 (27), JSC 39 (28),Phule G 01103 (25) and JG 2003-01101 (19) towards positive side of PC_1 axis. The genotypes ICC 12430 (10), ICC 10629 (8), LBeG 21 (30) and GNG 1685 (24) clustered towards positive portion of PC_2 axis. while the genotypes IPC 2004-52 (23), IPC 00-59 (13) and H 02-113 (20) stood towards positive side of PC_3 axis. The genotypes BG 2070 (27), JSC 39 (28),Phule G 01103 (25) and JG 2003-01101 (19) found desirable when PC_1, PC_2 and PC_3 were considered simultaneously. Genotypes belonging to common cluster have fallen nearer to each other and *vice versa*. The mean scores of genotypes were used as input for clustering in order to group the genotypes into various clusters. Genotypes 2 (ICC 14194) and 27 (BG 2070) were falling far apart and are widely divergent. Hierarchial clustering procedure (*i.e.,* Ward's method) was followed to group the 30 genotypes into 6 clusters (Table 8 and Fig 2).

The distribution of genotypes into various clusters was random, indicating lack of parallelism between genetic and geographic diversities as in case of D^2 analysis. Cluster I and III were largest comprising of 7 genotypes each followed by cluster IV (5) and cluster V and VI with 4 genotypes each and cluster II with 3 genotypes. The average intra-and-inter cluster distances are presented in Table 9.

Cluster III had maximum intra-cluster distance (95.9) followed by cluster VI (79.4) and maximum inter-cluster distance was observed between I and V (386.5) followed by I and VI (319.4). Crosses can be effective between the genotypes of these clusters to obtain better and desirable segregants.

Utilization of principal component analysis combined with hierarchical cluster analyses in genetic diversity studies was reported by Bhattacharya and Vijayalaxmi (2005) and Supriya *et al.* (2006) in greengram.

Above two methods of classifying genotypes into different groups are equally useful. Hierarchical cluster analysis had an additional advantage of creating sub-groups with in a cluster. So, relative position of the genotypes within the cluster can be determined by seeing the dendrogram distance.

Hence, genotypes ICC 16036, CSJ 313, ICC 12960, ICC 14334, ICC 188, ICC 14194, ICC 8927, BG 2070, Phule G 01103, JSC 39, JG 2003-01101 and IPC 00-59 appear to be desirable for inclusion in crossing programme aimed for improvement of yield in chickpea.

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