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Principal Component and Cluster Analyses in *Kabuli* Chickpea (*Cicer arietinum* L.)

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ABSTRACT

Thirty genotypes of *Kabuli* chickpea were evaluated to study genetic divergence by using principal component and cluster analysis. These genotypes were grouped into 6 clusters. Principal component analysis identified four principal components with Eigen values more than the one contributed 88.88 per cent of the cumulative variance. The genotypes selected from the above analysis were Dollar, ICCV- 95334, ICC- 5320 and ICC-4929 which appear to be desirable for inclusion in crossing programme aimed for improvement of *Kabuli* chickpea.

Key words : Cluster Analysis, Genetic Divergence, *Kabuli* chickpea, Principal Component Analysis.

Chickpea is the third most important pulse crop of the world. The clustering of parents based on genetic diversity is a pre requisite for a successful breeding programme. The use of diverse parents gives better opportunities to a breeder for selection and development of superior varieties. Information available on this aspect in Kabuli chickpea is very meager. Thus, in the present study, an attempt has been made to ascertain the nature and magnitude of genetic diversity to identify suitable donors having wider genetic distance in *Kabuli* chickpea

MATERIAL AND METHODS

The material for the investigation comprised 30 *Kabuli* chickpea genotypes (Table 1), collected from different sources. These genotypes of *Kabuli* chickpea were grown in *rabi* season during 2006-07 in 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 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 to used for statistical analysis. The data was subjected to the principal component analysis (Jackson, 1991) and hierarchical cluster analysis (Anderberg, 1993).

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among the 30 *Kabuli* genotypes of bengalgram indicating that the existence of substantial genetic variability for all the characters r/o.

Principal component analysis (PCA) identified four principal components with eigen values more than one which contributed 88.88 per cent of cumulative variance (Table 2). The first principal component (PC_1) contributed maximum towards variability (54.63%) with significant loading of 100 seed weight (-0.831) which was negatively correlated and number of primary branches per plant (0.116) which was positively correlated. The second principal component (PC_2) accounted for 18.28 per cent of total variance and it reflected significant loading of days to 50% flowering (0.688) number of secondary branches per plant (0.418) and plant height (0.364) which were positively correlated. The third principal component (PC_3) was characterized by conspicuously high loading of no. of pods per plant (0.568), protein content (0.503) and seed yield per plant (0.387) which were positively correlated (Table 3). Based on these first three principal components mean genotype scores were computed (Table 4). Principal scores for all the 30 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 81.93 per cent of variability accounted for all the characters (Table 4).

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

S.No.	Genotype/ germplasm accession No.	Source
1	Pusa 1053	IARI, New Delhi
2	HK 3	HAU, Hisar
3	ICC 12331	ICRISAT, Hyderabad (collected by IARI from Syria)
4	ICC 4908	ICRISAT, Hyderabad (collected by RPIP from Turkey)
5	ICCV 89224	ICRISAT, Hyderabad
6	ICC 5320	ICRISAT, Hyderabad developed by PAU, Ludhiana
7	IC 12495	ICRISAT, Hyderabad (collected by ICRI, India)
8	JGK -1	JNKVV, Jabalpur
9	ICC 4929	ICRISAT, Hyderabad (collected by PAU, Ludhiana)
10	ICCV 04312	ICRISAT, Hyderabad
11	ICCV 03407	ICRISAT, Hyderabad
12	ICCV 04301	ICRISAT, Hyderabad
13	ICCV 04309	ICRISAT, Hyderabad
14	ICCV 04305	ICRISAT, Hyderabad
15	ICCV 04308	ICRISAT, Hyderabad
16	ICCV 04311	ICRISAT, Hyderabad
17	ICCV 05306	ICRISAT, Hyderabad
18	ICCV 05310	ICRISAT, Hyderabad
19	ICCV 05311	ICRISAT, Hyderabad
20	ICCV 05313	ICRISAT, Hyderabad
21	ICCV 05314	ICRISAT, Hyderabad
22	ICCV 05315	ICRISAT, Hyderabad
23	Virat	ICRISAT, Hyderabad
24	Dollar	ICRISAT, Hyderabad
25	ICCV 2	ICRISAT, Hyderabad
26	KAK – 2	MPKV, Rahuri
27	Vihar	MPKV, Rahuri
28	ICCV 95334	ICRISAT, Hyderabad
29	LBeG 7	RARS, Lam
30	JGK-2	JNKVV, Jabalpur

Table 2. The Eigen values, per cent variability, cumulative per cent variability for four principal components in Kabuli chickpea *(Cicer arietinum* L.*)*

	Pc_1	Pc_2	Pc_3	Pc_4
Eigen value	33.01	19.09	13.41	11.77
% of variance	54.63	18.28	9.01	6.95
Cumulative variance	54.63	72.91	81.93	88.88

Table 3. Character loading of four principal components in 30 different genotypes of *Kabuli* chickpea (*Cicer arietinum* L.)

Character	PC_1	PC_2	PC_3	PC_4
Days to 50% flowering	0.257	0.688	0.027	0.370
Days to maturity	-0.059	0.178	0.323	-0.559
Plant height (cm)	-0.039	0.364	-0.035	-0.023
No. of. primary branches plant^{-1}	0.116	0.108	-0.101	0.002
No. of. secondary branches plant^{-1}	0.169	0.418	-0.344	-0.410
No. of. pods plant^{-1}	-0.019	0.212	0.568	0.184
100 seed weight (g)	-0.831	0.235	-0.119	-0.208
Harvest index (%)	-0.110	-0.080	0.139	0.145
Biological yield plant^{-1} (g)	-0.409	0.162	-0.066	0.490
Protein content (%)	0.047	0.146	0.503	-0.200
Seed yield plant^{-1} (g)	-0.110	-0.137	0.387	0.031

Table 4. The PCA scores of 30 *Kabuli* genotypes of chickpea *(Cicer arietinum* L.*)*

Genotype	PCA I X Vector	PCA II Y Vector	PCA III Z Vector
PUSA1053	-4.153	39.664	9.501
HK3	-7.630	40.778	12.384
ICC 12231	-8.825	47.190	9.119
ICC 4908	-6.773	45.589	8.737
ICC 89224	-14.324	35.139	10.805
ICC 5320	10.807	41.494	13.541
ICC 12495	-7.650	34.958	11.265
JGK 1	-9.620	36.159	12.868
ICC 492	6.055	33.943	16.951
ICCV 04312	-8.166	36.267	14.881
ICCV 03407	-13.619	39.284	14.339
ICCV 04301	-12.323	38.226	12.909
ICCV 04309	-15.962	39.930	12.035
ICCV 04305	-9.288	40.212	11.117
ICCV 04308	-14.557	38.376	11.172

Genotype	PCA I X Vector	PCA II Y Vector	PCA III Z Vector
ICCV 04311	-10.915	39.022	14.201
ICCV 05306	-10.763	37.461	10.868
ICCV 05310	-13.312	39.705	12.181
ICCV 05311	-12.921	40.552	13.878
ICCV 05313	-14.165	38.146	13.802
ICCV 0514	-10.454	38.068	12.924
ICCV 0515	-11.163	40.112	14.986
Virat	-9.125	37.780	14.247
DOLLAR	-19.143	42.908	18.256
ICCV2	-9.643	29.641	11.609
KAK 2	-11.798	41.906	18.574
VIHAR	-10.573	41.605	17.605
95334	-20.590	35.820	11.886
LBeG 7	-10.662	33.472	12.716
JGK 2	-12.144	37.187	12.296

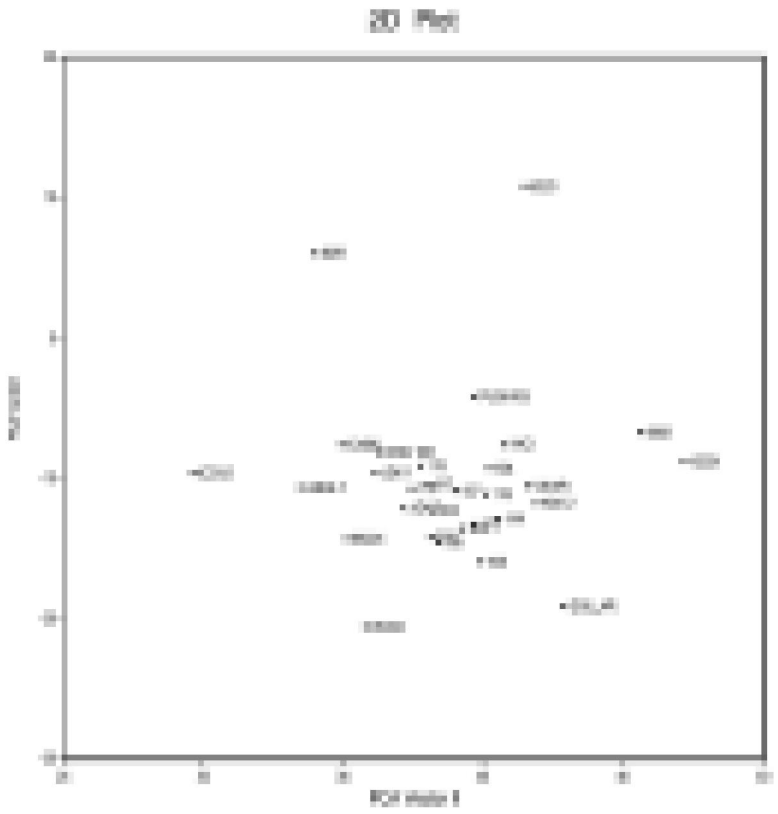

Fig. 1 Two dimensional graph showing relative position of genotypes of *Kabuli* chickpea *(Cicer arietinum* L.*)*

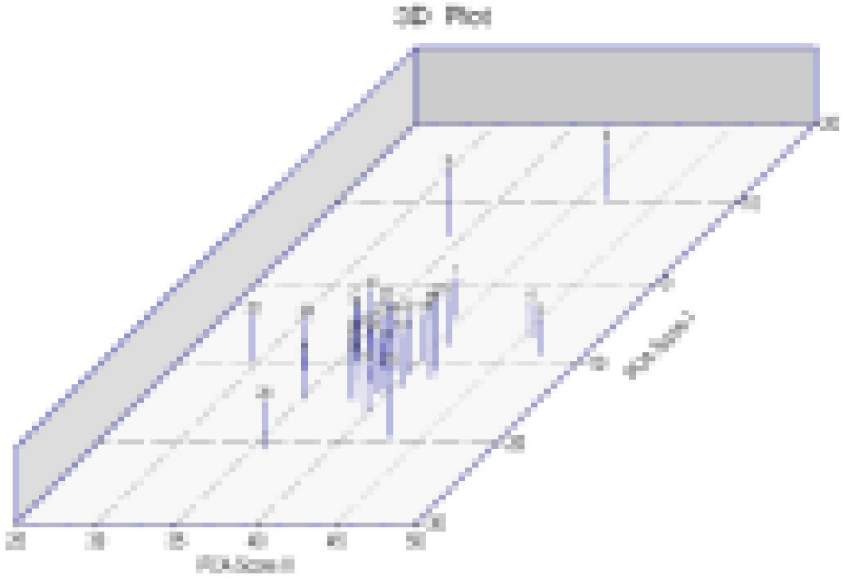

Fig.2 Three dimensional graph showing relative position of genotypes of *Kabuli* chickpea *(Cicer arietinum* L.*)*

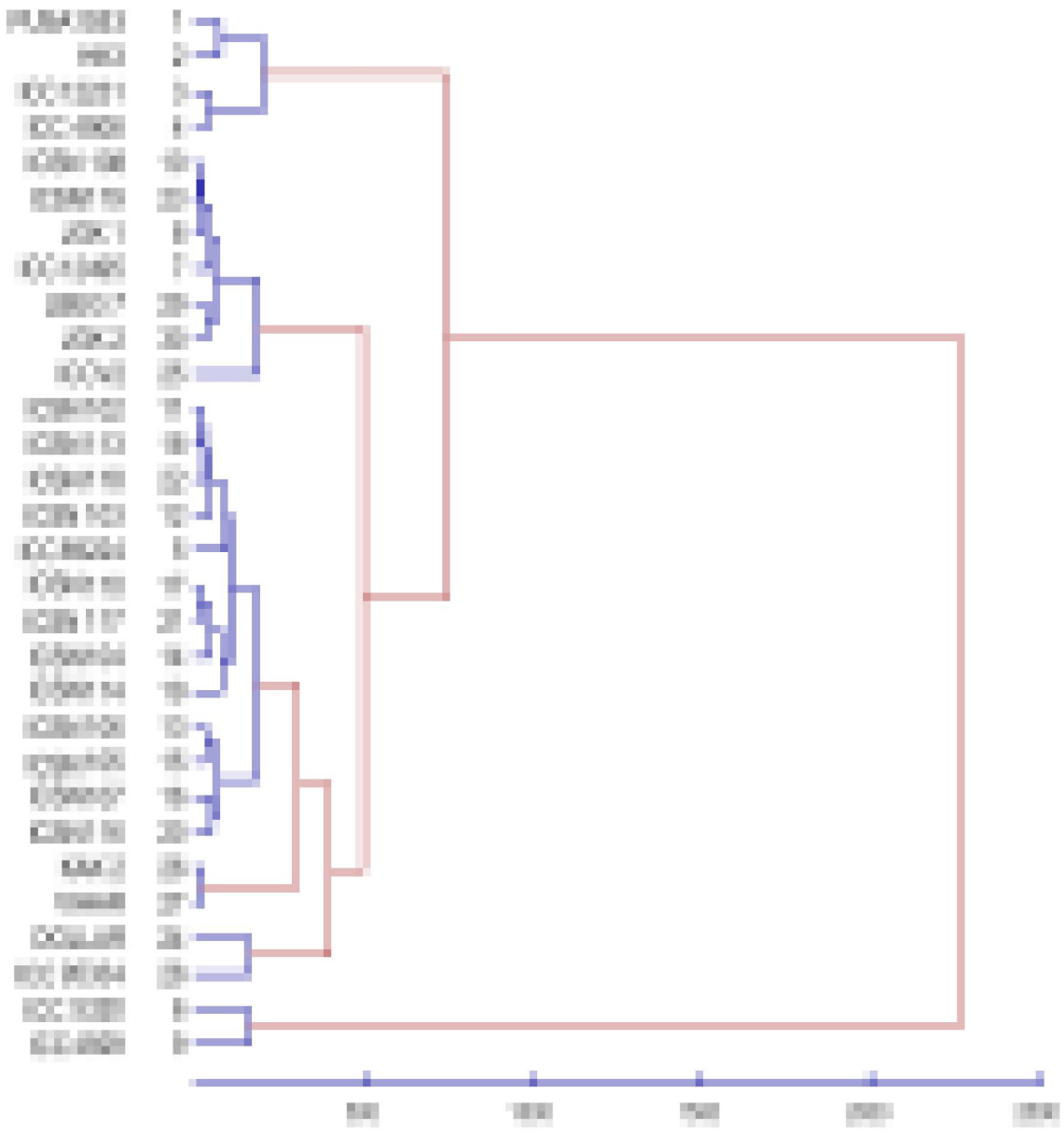

Fig. 3: Hierarchical clustering procedure of the *Kabuli* chickpea (*(Cicer arietinum* L.*)* genotypes using Ward's minimum variance method

Table 5. Distribution of 30 *Kabuli* chickpea (*Cicer arietinum* L.) genotypes in different clusters based on cluster analysis

Cluster	No.of genotypes	Genotypes
I	4	Pusa 1053, HK-3. ICC-12231, ICC 4908
II	7	ICCV-04312,Virat, JGK-1, ICC-12495, LBeG 7, JGK-2, ICCV-2
III	13	ICCV-03407,ICCV- 05310,ICCV- 0515,ICCV-04301, ICCV -05306, ICCV-0514,ICCV-4305,ICCV-05311, ICCV-04309,ICCV-04308,ICCV -04311,ICCV- 05313
IV	2	KAK-2, Vihar
V	2	Dollar, ICC-95334
VI	2	ICC-5320, ICC-4929

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

Cluster	I	II	III	IV	V	VI
I	**209.483**	391.435	341.930	384.337	826.064	1055.107
II		**120.589**	191.749	311.006	554.197	1156.356
III			**125.797**	244.804	369.835	1500.332
IV				**39.278**	445.643	1384.374
V					**325.178**	2587.297
VI						**318.272**

Table 7 : Cluster means for 11 different characters in *Kabuli* chickpea *(Cicer arietinum* L.*)*

Clusters	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	60.33	104.16	51.97	2.43	18.20	35.79	32.22	38.90	31.09	18.96	1.79
II	45.52	86.19	39.88	1.71	9.53	37.40	30.39	44.86	27.34	18.65	12.16
III	52.12	93.64	46.06	1.77	9.01	36.88	36.5	44.68	35.17	18.54	15.56
IV	53.00	101.33	50.50	1.78	10.13	81.66	36.66	49.92	54.51	19.72	27.00
V	48.16	92.66	40.66	1.21	8.68	42.10	48.42	48.37	33.20	20.87	17.02
VI	63.83	104.66	40.83	2.56	14.66	39.88	11.45	33.69	16.96	21.50	4.80

The plot of PC_1, PC_2 and PC_3 showed characters differentiation of genotypes according to 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 6 clusters (Table 5 Fig 3). This reflects that there was no relation between eco-geographical origin and genetic diversity.

The biggest cluster was cluster III consisting of 13 genotypes followed by cluster II comprising of 7 genotypes. Based on cluster analysis the intra-cluster values ranged from 39.27 (Cluster IV) to 325.17 (Cluster V). The maximum inter - cluster distance was observed between cluster V and VI (2587.29) followed by cluster III and VI (1500.33) and cluster IV and VI (1384.37) as shown in Table 6. Cluster VI is characterized by high mean value for days to 50% flowering (63.88), days to maturity (104.66), number of primary branches per plant (2.56), protein content (%) (21.50), cluster IV recorded high mean values for number of pods per plant (81.66), harvest index (49.92), biological yield per plant (54.53) and seed yield per plant (27.00). Where as cluster IV recorded high mean values for 100- seed weight (g) (48.42) (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 in and Narendra Singh (2002) in bengalgram and Altaher and Singh (2003) in cotton.In broad sense, hierarchical cluster analysis is identifying sub clusters of the major groups at different levels so that each small group can be critically analyzed. Genotypes Dollar, ICCV-95334, ICC- 5320, and ICC- 4929 appear to be desirable for inclusion in crossing programme.

Clustering pattern indicated no association between geographical distribution of accessions and genetic divergence as shown in Table 1. 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. Similar results were derived by Sarvaliya and Goyal (1995) and Kumar (1997).

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