

# Principal component analysis among genotypes of chickpea (*Cicer arietinum* L.)

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## ABSTRACT

Principal component analysis among genotypes showed that the first two PC axes explained 44.2% of total multivariate variation with first five PC axes explaining 74.2%. The PC 1 separates genotypes on number of pods per plant, seed yield per plant, plant height and number of secondary branches per plant, while PC2 separated on days to maturity, days to 50 per cent flowering and per cent pod damage. All 12 characters were statistically significant among the genotypes and three clusters were selected based on the graph plotted by using first two principal components, which contain extreme genotypes for four important contributing characters, which also provide useful criteria for further evaluation of chickpea genotypes.

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**Key words :** *Cicer arietinum*, Principal components, Clusters analysis, Multivariate variation

## INTRODUCTION

Principal component analysis (PCA) involves a mathematical procedure that transforms a number of (possibly) correlated variables into a (smaller) number of uncorrelated variables called principal components. The first principal component accounts for as much of the variability in the data as possible, and each succeeding component accounts for as much of the remaining variability as possible. The main applications of factor analytic techniques are: to reduce the number of variables and to detect structure in the relationships between variables, that is to classify variables. Therefore, factor analysis is applied as a data reduction or structure detection method. The principle component analysis is a multivariate analysis used to study kind of variation present in the selected population. In chickpea more PCA studies is made on pure breeding lines like germ plasm lines, while these are not reported in segregating population.

Among pulses chickpea (*Cicer arietinum* L.) is one of the important pulse crops grown during *Rabi* season. On an average, it produces 126 kg of protein from one hectare and probably the highest protein yielding legume next to groundnut and soybean. The genetic variability for the characters of economic importance is the basic prerequisite for improvement of any crop species. There is good scope to improve productivity of crop through varietal improvement programme, but which needs the

information regarding the range of existing genetic variability, relationship of the various economically important characters and extent of genetic diversity in the promising genetic stocks available with the plant breeders (Upadhyay *et al.*, 2002; 2007).

Realizing the importance of diversity, the plant breeders are now looking for more diverse forms from various sources to augment the yield potential. Hence, the present study is envisaged to measure the genetic diversity among core collections of chickpea (*Cicer arietinum* L.) to explain multivariate polymorphism of core collections and to identify diverse genetic stock for their further utilization in hybrid programme for yield improvement.

## MATERIALS AND METHODS

The experimental material for the present investigation comprised of 215 core collections of chickpea core collections collected from international center for research in semi arid tropics (ICRISAT), Hyderabad. The material included both *Kabuli* and *Desi* types of different geographical origin and 5 checks *viz.*, Annigere-1, KAK-2, Vishal, JG-11 and HIR-50. The detailed description of these core collections is furnished in Table 1.

Two hundred and fifteen genotypes of chickpea along with five local; check varieties were grown in augmented design with replicating only check varieties *viz.*, Annigere

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Table 1 : List of genotypes used for study								
Sr. No.	ICC Number	Source country	Sr. No.	ICC Number	Source country	Sr. No.	ICC Number	Source country
1.	ICC 67	India	49.	ICC 3325	Cyprus	97.	ICC 7323	Russia and CISs
2.	ICC 95	India	50.	ICC 3362	Iran	98.	ICC 7441	India
3.	ICC 283	India	51.	ICC 3421	Israel	99.	ICC 7554	Iran
4.	ICC 440	India	52.	ICC 3512	Iran	100.	ICC 7571	Israel
5.	ICC 456	India	53.	ICC 3631	Iran	101.	ICC 7668	Russia and CISs
6.	ICC 506	India	54.	ICC 3761	Iran	102.	ICC 7819	Iran
7.	ICC 637	India	55.	ICC 3776	Iran	103.	ICC 7867	Iran
8.	ICC 708	India	56.	ICC 3946	Iran	104.	ICC 8058	Iran
9.	ICC 762	India	57.	ICC 4182	Iran	105.	ICC 8151	USA
10.	ICC 791	India	58.	ICC 4418	Iran	106.	ICC 8195	Pakistan
11.	ICC 867	India	59.	ICC 4463	Iran	107.	ICC 8261	Turkey
12.	ICC 1052	Pakistan	60.	ICC 4495	Turkey	108.	ICC 8318	India
13.	ICC 1083	Iran	61.	ICC 4533	India	109.	ICC 8350	India
14.	ICC 1098	Iran	62.	ICC 4567	India	110.	ICC 8384	India
15.	ICC 1161	Pakistan	63.	ICC 4593	India	111.	ICC 8522	Italy
16.	ICC 1164	Nigeria	64.	ICC 4639	India	112.	ICC 8607	Ethiopia
17.	ICC 1180	India	65.	ICC 4657	India	113.	ICC 8621	Ethiopia
18.	ICC 1194	India	66.	ICC 4814	Iran	114.	ICC 8740	Afghanistan
19.	ICC 1205	India	67.	ICC 4841	Morocco	115.	ICC 8855	Afghanistan
20.	ICC 1230	India	68.	ICC 4872	India	116.	ICC 8950	India
21.	ICC 1356	India	69.	ICC 4918	India	117.	ICC 9002	Iran
22.	ICC 1392	India	70.	ICC 5135	India	118.	ICC 9137	Iran
23.	ICC 1397	India	71.	ICC 5337	India	119.	ICC 9402	Iran
24.	ICC 1398	India	72.	ICC 5383	India	120.	ICC 9586	India
25.	ICC 1422	India	73.	ICC 5434	India	121.	ICC 9643	Afghanistan
26.	ICC 1431	India	74.	ICC 5504	Mexico	122.	ICC 9755	Afghanistan
27.	ICC 1510	India	75.	ICC 5613	India	123.	ICC 9848	Afghanistan
28.	ICC 1710	India	76.	ICC 5639	India	134.	ICC 9862	Afghanistan
29.	ICC 1715	India	77.	ICC 5845	India	125.	ICC 9895	Afghanistan
30.	ICC 1882	India	78.	ICC 5878	India	126.	ICC 9942	India
31.	ICC 1915	India	79.	ICC 5879	India	127.	ICC 10341	Turkey
32.	ICC 1923	India	80.	ICC 6263	Russia and CISs	128.	ICC 10393	India
33.	ICC 2065	India	81.	ICC 6279	India	129.	ICC 10399	India
34.	ICC 2072	India	82.	ICC 6293	Italy	130.	ICC 10755	Turkey
35.	ICC 2210	Algeria	83.	ICC 6306	Russia and CISs	131.	ICC 10885	Ethiopia
36.	ICC 2242	India	84.	ICC 6537	Iran	132.	ICC 10945	India
37.	ICC 2263	Iran	85.	ICC 6571	Iran	133.	ICC 11121	India
38.	ICC 2277	Iran	86.	ICC 6579	Iran	134.	ICC 11198	India
39.	ICC 2507	Iran	87.	ICC 6802	Iran	135.	ICC 11284	Russia and CISs
40.	ICC 2580	Iran	88.	ICC 6811	Iran	136.	ICC 11378	India
41.	ICC 2629	Iran	89.	ICC 6816	Iran	137.	ICC 11498	India
42.	ICC 2720	Iran	90.	ICC 6874	Iran	138.	ICC 11584	India
43.	ICC 2884	Iran	91.	ICC 6877	Iran	139.	ICC 11627	India
44.	ICC 2919	Iran	92.	ICC 7184	Turkey	140.	ICC 11664	India
45.	ICC 2969	Iran	93.	ICC 7255	India	141.	ICC 11764	Chile
46.	ICC 2990	Iran	94.	ICC 7272	Algeria	142.	ICC 11879	Turkey
47.	ICC 3218	Iran	95.	ICC 7308	Peru	143.	ICC 11944	Nepal
48.	ICC 3230	Iran	96.	ICC 7315	Iran	144.	ICC 12028	Mexico

Contd.... Table 1

Table 1 Contd....

Sr. No.	ICC Number	Source country	Sr. No.	ICC Number	Source country	Sr. No.	ICC Number	Source country
145.	ICC 12037	Mexico	169.	ICC 13524	Iran	193.	ICC 15518	Morocco
146.	ICC 12155	Bangladesh	170.	ICC 13599	Iran	194.	ICC 15567	India
147.	ICC 12299	Nepal	171.	ICC 13628	Unknown	195.	ICC 15606	India
148.	ICC 12307	Myanmar	172.	ICC 13764	Iran	196.	ICC 15610	India
149.	ICC 12328	Cyprus	173.	ICC 13816	Russia and CISs	197.	ICC 15612	Tanzania
150.	ICC 12492	ICRISAT	174.	ICC 13863	Ethiopia	198.	ICC 15618	India
151.	ICC 12537	Ethiopia	175.	ICC 13892	Ethiopia	199.	ICC 15697	Syria
152.	ICC 12654	Ethiopia	176.	ICC 14051	Ethiopia	200.	ICC 15802	Syria
153.	ICC 12726	Ethiopia	177.	ICC 14077	Ethiopia	201.	ICC 15868	India
154.	ICC 12824	Ethiopia	178.	ICC 14098	Ethiopia	202.	ICC 15888	India
155.	ICC 12851	Ethiopia	179.	ICC 14199	Mexico	203.	ICC 16207	Myanmar
156.	ICC 12866	Ethiopia	180.	ICC 14402	ICRISAT	204.	ICC 16261	Malawi
157.	ICC 12916	India	181.	ICC 14595	India	205.	ICC 16269	Malawi
158.	ICC 12928	India	182.	ICC 14669	India	206.	ICC 16374	Malawi
159.	ICC 12947	India	183.	ICC 14778	India	207.	ICC 16487	Pakistan
160.	ICC 13077	India	184.	ICC 14799	India	208.	ICC 16524	Pakistan
161.	ICC 13124	India	185.	ICC 14815	India	209.	ICC 16796	Portugal
162.	ICC 13187	Iran	186.	ICC 14831	India	210.	ICC 16903	India
163.	ICC 13219	Iran	187.	ICC 15264	Iran	211.	ICC 16915	India
164.	ICC 13283	Iran	188.	ICC 15294	Iran	212.	ICC 4948	Punjab
165.	ICC 13357	Iran	189.	ICC 15333	Iran	213.	ICC 4973	Punjab
166.	ICC 13441	Iran	190.	ICC 15406	Morocco	214.	ICC 12968	ICRISAT
167.	ICC 13461	Iran	191.	ICC 15435	Morocco	215.	ICC 15996	ICRISAT
168.	ICC 13523	Iran	192.	ICC 15510	Morocco			

Checks

1 Annigeri 1      2 JG 11      3 Vishal      4 KAK 2      5 HIR 50

1, JG11, Vishal, KAK 2 and HIR 50 at regional research station, Hiriyyur during *Rabi* 2006. Each plot consisted of 3 row of 1 m length spaced 30 cm apart. Distance between plants to plant was maintained at 10cm. Recommended agronomic practices were followed to raise the experimental material. The data was recorded on 5 randomly selected plant in each plot for plant height, number of primary branches per plant, number of secondary branches per plant, number of pod per plant, per cent pod damage, number of seeds per pod, test weight, days to 50% flowering, days to maturity, incidence of Fusarium wilt protein content and seed yield per plant. The mean observations for each genotype were standardized by subtracting mean value of the character from each observation and subsequently dividing by its respective standard deviation. This resulted in standardized values for each trait with mean zero and SD of one or less. The standardized values were used to perform PCA using statistical package called MINTABLE to know the importance of different traits in explaining multivariate polymorphism.

## RESULTS AND DISCUSSION

Principal component analysis to explain the per cent variation / multivariate polymorphism for the first five principal components (PC) and vector loading for each character and principal components (PC) are presented in the Table 2. The first five principal components (PC) explained 74.2% of variation in the core collection of the chickpea and reduced the original 12 characters. The first principal component is most important and the number of pods per plant, plant height, number of secondary branches per plant, seed yield per plant and Fusarium wilt incidence were most important traits contributing to variation that explained about 27.8 % of total variance. The eigen value of PCI was 3.34.

In second principal component which describe about 16.3 % of total variance originated mainly from days to minority, days to 50 per cent flowering, per cent pod damage and test weight constituted a large part of total variance among chickpea genotypes. The eigen value of PC was 1.96.

The first principal component had maximum vector

**Table 2 : Vector loadings and percentage of variation explained by the first five principal components after assessing morphological characteristics in subsets of chickpea core collections**

Characters	PC 1	PC 2	PC 3	PC 4	PC 5
Plant height (cm)	0.411302	0.174652	0.194278	-0.078634	0.037699
Primary branches	0.245984	0.174759	0.046814	0.252320	-0.132538
Secondary branches	0.408200	0.190207	0.210250	-0.068614	-0.105477
No. of pods per plant	0.451340	0.163240	0.149105	-0.098803	-0.040592
Pod damage (%)	-0.270900	0.295714	0.466915	0.018051	-0.281379
No. of seeds per pod	-0.028995	0.034877	0.188402	0.066055	0.879732
Test weight (g)	0.018136	-0.028440	-0.303094	0.700657	-0.204061
Days to 50 % flowering	0.087380	-0.591082	0.353327	0.116472	-0.080913
Days to maturity	0.108604	-0.616403	0.303534	0.020294	-0.067337
Wilt incidence (%)	-0.341149	0.187424	0.499180	-0.010357	-0.153215
Seed yield/plant (g)	0.433488	-0.18642	-0.028648	-0.012127	-0.033367
Protein content (%)	0.041312	0.147823	0.285100	0.637056	0.194493
Eigen values	3.34447	1.96086	1.44545	1.12203	1.03421
Per cent of total variance explained	27.8 %	16.3 %	12.04 %	9.3%	8.6 %
Cumulative per cent of total variance explained	27.8 %	44.2 %	56.2 %	65.60 %	74.2 %

PH- Plant height (cm) DM- Days to maturity PB- Primary branches SB- Secondary branches  
 PRO- Protein content (%) DF- Days to 50 % flowering PPD- Pod damage (%) NSSP- No. of seeds per pod  
 FWI- Fusarium wilt incidence (%) TW- Test weight (g) NPP- No. of pods per plant SY- Seed yield/plant (g)

loadings for number of pods per cent plant and PC 2 had for days to maturity. By considering these two characters graph was plotted by calculating graph values for both PC 1 and PC 2 in to each genotypes. A graph was plotted by considering PC1 in X-axis and PC 2 in axis. The details of graph were shown in Fig.1. Based on the distribution of different genotypes with respect to PC1 and PC2, we had selected three clusters, which include extreme genotypes for number of pods per plant, which had maximum vector loading in PC 1 and days to maturity, which had maximum vector loading in PC 2.

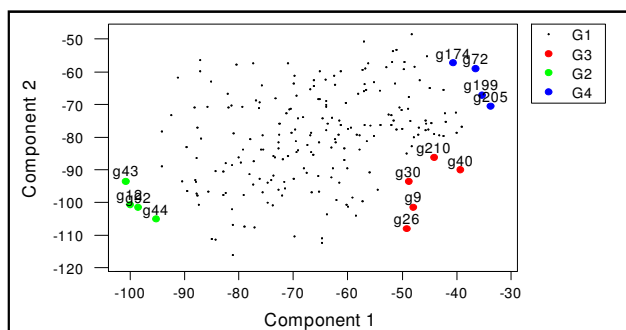
The clusters I, II and III had four, five and four genotypes, respectively. Characters which had maximum vector loading in PC1 viz., number of pods per plant and

seed yield per plant and in PC2 days to maturity and per cent pod damage were selected and mean and standard deviation for genotypes which fall under different clusters were calculated and graph was plotted against the clusters. An over view of the results of three clusters indicated that genotypes which comes under cluster I were superior to number of pods per plant, seed yield per plant with considerable tolerance to pod borer, but they had delayed maturity. The genotypes of clusters II were inferior to all the characters when compared to cluster III with medium duration (Table 3).

#### Student 't' test:

To confirm the significant difference among three clusters with respect to all characters student t test was followed. This indicated that there was significant difference between cluster I and II, cluster I and III for number of pods per plant, seed yield per plant and days to maturity (Table 4). As revealed by principal component analysis indicates that number of pods per plant, per cent pod damage, days to maturity and seed yield per plant were the most important traits contributing to total variation in first two principal components. The first five principal components explained 74.2 % of variation in the core collections of chickpea and reduced the original twelve characters to four characters.

Selection of clusters based on the extreme genotypes with respect to number of pods per plant which had maximum vector loading in PC 1 and days to maturity with maximum vector loading in PC 2, indicated that the



**Fig 1. Scatter diagram of first two principal components showing relative proportions of core collections of chickpea**

G1 – Remaining genotypes

G2 – Cluster I

G3 – Cluster II

G4 – Cluster III

**Table 3 : Mean values of three clusters for four important characters in chickpea core collections**

Genotypes	No. of pods per plant	Pod Damage (%)	Days to maturity	Seed yield/plant (g)	Source country
<b>Cluster I</b>					
ICC 1052	72.60	3.42	139.00	42.1	Pakistan
ICC 2884	72.50	4.12	127.00	42.5	Iran
ICC 2919	69.80	4.63	141.00	37.2	Iran
ICC 7184	70.00	10.00	131.00	42.2	Turkey
Mean	71.23	5.54	134.50	41.00	
SD	1.53	3.01	6.60	2.53	
<b>Cluster II</b>					
ICC 762	37.00	6.97	129.00	24.1	India
ICC 1431	42.00	12.78	138.00	25.8	India
ICC 1882	41.50	11.00	130.00	28.4	India
ICC 2580	35.80	11.60	122.00	19.8	Iran
ICC 16903	40.00	8.00	115.00	21.5	India
Mean	39.26	10.07	126.80	23.92	
SD	2.74	2.47	8.70	3.40	
<b>Cluster III</b>					
ICC 5383	39.50	16.50	95.00	21.5	India
ICC 13863	49.80	15.60	97.00	14.6	Ethiopia
ICC 15697	23.00	13.60	102.00	25.1	Syria
ICC 16269	36.50	7.40	101.00	19.3	Malawi
Mean	37.20	13.28	98.75	20.13	
SD	11.04	4.09	3.30	4.39	

**Table 4 : Student 't' test values of three clusters for four important traits in chickpea**

Clusters	Table 't' value	No. of pods per plant	Pod damage (%)	Days to maturity	Seed yield/ plant (g)
CI v/s CII	1.895	4.02**	-0.616	0.070	15.81**
CI v/s CIII	1.943	3.56**	-0.319	0.288	12.72**
CII v/s CIII	1.895	0.147	-0.794	0.333	0.96

genotypes which fall under cluster I were superior to all the characters with delayed maturity. But the genotypes of cluster III, which were inferior to all the characters with early maturity and cluster II genotypes, had average mean values for all the characters. Based on the PCA and clustering the genotypes viz., ICC 1052, ICC 2884, ICC 2919 and ICC 7184 for number of pods per plant and the genotypes viz., ICC 5383, ICC 13863, ICC 15697 and ICC 16269 for early maturity and superior to local check varieties. The hybridization between these genotypes may expect good results in future.

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