**RESEARCH PAPER** 

# 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 exclaiming 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 verities were grown in augmented design with replicating only check verities *viz*., Annigeri

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