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Principal component analysis in kabuli chickpea (*Cicer arietinum* L.)

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Abstract
The present study was undertaken using fifty genotypes of *kabuli* chickpea planted in a randomized block design with three replications at the research farm of CCSHAU, Hisar during *Rabi*, 2014-15 to determine the contribution of eight morphological traits to the total variability in *kabuli* chickpea using Principal component analysis. Results revealed that the two principal components (PC1 and PC2) accounted for 72.65% of the total variation. PC1 contributed 48.97% of the total variation and correlated with number of pods per plant, number of seeds per pod, number of branches per plant and 100-seed weight while PC2 explained an additional 23.68% of the total variation and dominated by plant height and seed yield per plant. Since, a total of 72.65% of the total variation was contributed by PC1 and PC2, therefore, these two principal components can be allowed for simultaneous selection of yield contributing traits in *kabuli* chickpea.

Keywords: principal component analysis, *kabuli* chickpea (*Cicer arietinum* L.)

Introduction
Chickpea (*Cicer arietinum* L.) is an important pulse crop of India which is grown during *Rabi* season. India is largest producer of chickpea in the world sharing 65.2% of area and 65.4% of production. Chickpea was grown in 9.93 million ha area, with production of 9.53 million tons and productivity of 960 kg/ha during 2013-14 (Anonymous, 2014) [1]. The major chickpea producing states are Madhya Pradesh, Rajasthan, Maharashtra, Karnataka and Andhra Pradesh which contributed more than 90 per cent of the national production. Chickpea seeds contain 17.7 per cent protein, 0.49 per cent lysine, 0.11 per cent methionine (Katiyar, 1982) [7], 56.6 per cent carbohydrates, considerable amount of calcium, phosphorus, iron and vitamin B (Thakur, 1980) [12]. Assessment of existing genetic diversity following multivariate analysis like D^2 statistics and factorial analysis in the primary gene pool is the most crucial step in any crop improvement programme (Rahman and Al-Mansur, 2009) [10]. Yield and yield contributing parameters are the most widely targeted traits for chickpea improvement programme worldwide. Yield is a complex trait which is affected by several factors and environment, hence, a well-known technique known as principal component analysis was used to identify and minimize the number of traits for effective selection. PCA is a standard tool in modern data analysis because it is a simple, non-parametric method for extracting relevant information from confusing data sets. It involves a mathematical procedure that transforms a number of (possibly) correlated variables into a (smaller) number of uncorrelated variables called principal components (Chatfield *et al*. 1980 and Muniraja *et al.* 2011) [2, 8]. It reduces the dimensionality of the data, while retaining most of the variation in the data set. PCA accomplishes this reduction by identifying directions, 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. For the choice of diverse parents in any hybridization programme, multivariate analysis (Principal component analysis) has been extensively used. Dasgupta and Das (1984) [3] considered multivariate analysis best for choosing parents for hybridization and to study kind of variation present in the selected population. In the present study, we carried out a PCA to identify agronomic attributes whose selection would lead to improvement in seed yield of *kabuli* chickpea.

Materials and Methods
The experiment was carried out at the field research area of Pulses Section, Department of

Genetics and Plant breeding, CCSHAU, Hisar during *Rabi*, 2014-15. Fifty *kabuli* chickpea genotypes were evaluated for some important agronomic traits. The experiment was planted in randomized block design with three replications, keeping row to row distance of 45 cm and plant to plant distance of 10 cm. Five plants randomly selected from each plot were used to record data for 8 different morphological characters viz., days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, number of seeds per pod, 100-seed weight and seed yield per plant. The principal component analysis was performed by using the computer software "SPSS" for windows.

Results and Discussion

Principal component analysis (PCA) is done to estimate the effective contribution of different traits on the basis of respective variation. The first principal component (PC1) accounted for maximum proportion of total variability in the set of all variables and remaining components accounted for progressively lesser and lesser amount of variation. In the present investigation, all three principal components (PCs) have eigen values more than one which contributed 85.61% of the cumulative variance (Table 1). Similar results were reported by Ghafoor *et al.* (2003) [5] and Iqbal *et al.* (2008) [6]. First principal component (PC1) contributed maximum towards variability (48.97%) was correlated with number of pods per plant, number of seeds per pod, number of branches per plant and 100-seed weight (Table 1). As PC1 was contributed by most of the yield attributing traits, an intensive selection procedure can be designed to bring out rapid improvement of dependent traits i.e., seed yield per plant by selecting the lines of PC1. These results are getting support from the findings of Rekha *et al.* (2013) [11] that the first principal component (PC1) had high significant positive loading of number of branches per plant and number of pods per plant. The second principal component (PC2) accounted 23.68 per cent of total variance and it reflected positive loading of plant height and seed yield per plant whereas; the third principal component (PC3) accounted 12.94 per cent of total variance and dominated by phenological traits *viz*, number of days to 50% flowering and number of days to maturity. Characters with high variability are expected to provide high level of gene transfer during breeding programs (Gana *et al.* 2013 and Nachimuthu *et al*. 2014) [4, 9].

Conclusion

In the present study, the traits viz., number of pods per plant, number of seeds per pod, number of branches per plant, 100-seed weight and plant height contributed greater variation to the total variance in yield which is present in first two principal components (Table 1). A total of 72.65% of the total variation was contributed by these traits. Thus, PC1 and PC2 can be allowed for simultaneous selection of yield contributing traits in *kabuli* chickpea.

Table 1: Eigen values, variability and component loading of eight morphological traits in *kabuli* chickpea

	PC1	PC2	PC3
Eigen Value (Root)	4.968	2.175	1.096
% Var. Exp.	48.978	23.687	12.942
Cum. Var. Exp.	48.978	72.665	85.607
Days to 50% flowering	-0.057	0.121	0.225
Days to maturity	0.012	0.782	0.193
Plant height (cm)	-0.041	0.112	0.040
Number of branches/plant	0.136	-0.055	0.174
Number of pods/plant	0.292	0.489	-0.092
Number of seeds/pod	0.267	-0.045	0.018
100-seed weight (g)	0.108	-0.034	-0.091
Seed yield/plant (g)	0.168	0.219	0.083

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