

Principal component analysis in Desi chickpea (*Cicer arietinum* L.) under normal sown condition of Bihar

ABSTRACT

Chickpea (*Cicer arietinum* L.) is the second most important food legume crop after common bean (*Phaseolus vulgaris* L.). It is one of the most important *rabi* pulse crop in India and contributes to 20% of the total pulse production in the world. India ranks first in chickpea production in the world followed by Australia, Myanmar and Pakistan. It is one of the major pulse crops in Bihar. The present investigation was undertaken using forty genotypes of desi chickpea sown in a randomized block design with three replications at the Pulse research model Bhatti farm of Bihar Agricultural University, Sabour (Bhagalpur) during Rabi, 2016-17 to determine the contribution of six morphological traits to the total variability in desi chickpea using Principal component analysis. In the present investigation PCA was performed for six quantitative traits of chickpea. Out of six, only 2PCs exhibited more than 1.0 Eigen value and showed about 79.86% variability. Therefore, these 2 PCs were given due importance for the further explanation. The PC1 showed 28.96% variability among traits, while PC II, PC III and PC IV exhibited 21.93%, 16.35% and 13.87% variability respectively. PC1 contributed 28.96% of the total variation and correlated with days to 50% flowering, days to maturity and 100-seed weight while PC2 explained an additional 21.93% of the total variation and dominated by plant height, grain yield per plot, days to maturity, days to 50% flowering and number of pods per plant. Since, a total of 50.91% 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 desi chickpea. Genotype commonly found in more PC, were KWR108, JG2016-44, Sabour chana-1, IPC 2013-21, HI12-63, AKG1303, PG214J and RKG13-380. Similar type of genotypes on a common principal component permitting to designate them as seed yield factors. These genotypes may further be utilized in breeding programmes for improving seed yield and these genotypes can be considered an ideotype breeding material for selection of traits *viz* more total number of seed per plant and 100-seed weight further utilization in precise breeding programme.

Keywords: Genetic diversity, Principal component analysis, *Cicer arietinum* L.,

INTRODUCTION

The area under chickpea cultivation decreased due to lack of high yielding varieties and susceptibility to insects and diseases (Hameed *et al.*, 2009). The yield of chickpea can be improved by selection of superior genotypes which is directly related with the seed yield and utilize these genotypes exclusively in breeding programs to enhance grain yield. 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 (Agrawal *et al.*, 2018). 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. 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. Thus the primary benefit of PCA arises from quantifying the importance of each dimension for describing the variability of a data set. It involves a mathematical procedure that transforms a number of (possibly) correlated variables into a (smaller) number of uncorrelated variables called principal components (Muniraja *et al.*, 2011). In the present study, we carried out a PCA to identify agronomic attributes whose selection would lead to improvement in seed yield of *Desi* chickpea.

MATERIALS AND METHODS

The experimental material comprised of forty genotypes of chickpea in Rabi 2016-17 at Pulse Research Farm, Bihar Agricultural University, Sabour (Bhagalpur). The experiment was laid in randomized complete block design with three replications during Rabi 2016-17 with inclusion of the recommended packages and practices needed for a healthy crop. Data for six quantitative traits were recorded viz. days to 50% flowering, days to maturity, plant height (cm), number of pods per plant, 100 seed weight (g) and grain yield per plot. The days to 50% flowering, days to maturity, and seed yield per plot were accounted on a plot basis and plant height, number of pods per plant and 100 seed weight (g) were documented from random sample of five plants in each plot. According to the Barbara and Tabachnick (2019) PCA is a well-known method of dimension reduction that can be used to reduce a large set of variables to a small set that still contains most of the information in the large set. Therefore, the present investigation was aimed to evaluate the germplasm of chickpea for identify and rank important traits and genotype on the basis of principal component analysis before taking up hybridization programme for evolving better hybrid in chickpea.

RESULTS AND DISCUSSION

Principal component analysis is a simple non parametric method for extracting relevant information from confusing data sets. With minimum efforts, this provide a roadmap for how to reduce a complex data set to a lower dimension to sometimes hidden, simplified structures that often underlines it. PC is a statistical procedure that uses an orthogonal transformation to convert a set of observations of possibly correlated variables into a set of values of linearly uncorrelated variables called principal components the number of principal components is less than or equal to the number of original variables. This transformation is defined in such a way that the first principal component has the largest possible variance (that is accounts for as much of the variability in the data as possible) and each succeeding component in turn has the highest

variance possible under the constraint that it is orthogonal to the preceding components. The resulting vectors are an uncorrelated orthogonal basis set. The principal components are orthogonal because they are the Eigen vectors of the covariance matrix, which is symmetric. In present investigation principal component analysis was performed for yield and yield contributing traits of chickpea

Analysis of variance revealed significant differences among the genotypes for all the characters under this investigation. Thus, it indicated considerable amount of genetic variability among forty chickpea genotypes. Principal component analysis was performed to reveal the pattern of data matrix for determination and identification of selection criteria. The result of PCA explained the genetic diversity among the chickpea genotypes. The current research, PCA was performed for six yield and yield attributing traits in chickpea genotypes. Eigen values of four principal component axes and percentage of variation accounting for them obtained from the principal component analysis are presented in Table-1. According to Brejda et al. (2000), data were considered in each components with Eigen value >1 which determined at least 10% of the variation. The higher Eigen values were considered as best representative of system attributes in principal components. Only two components (PCs) showed more than 1 Eigen value and exhibited about 79.86% cumulative variability, therefore these two PCs were given due important for the further explanation. PCs were used for further explanation. The PC1 showed 28.96% variability among traits, while PC II, PC III, and PC IV exhibited 21.93%, 16.35% and 13.87% variability respectively (Table-1). The PC1 accounts for as more variability in data and each subsequent components accounts for much of the remaining variability possible. Only highly loaded traits (having absolute value within 10% of the highest factor loading) within each principal components, were retained for factor clarification. Rotated component matrix revealed that the PC 1 which accounts for the highest variability percentage i.e., 28.96. Within each PC, only highly loaded factors or traits (having absolute values within 10% of the highest factor loading) were retained for further explanation. The objective of principal component analysis is to identify the minimum number of components, which can explain maximum variability out of the total variability and also to rank germplasm on the basis of PC scores. These finding similar to the Nachimuthu *et al.* (2014), Mahendra *et al.*, (2015), Arora *et al.* (2018) and Shivwanshi and Babbar (2017) that the cumulative variance of 77.38% of total variation. Rotated component matrix (Fig. 1) revealed that each PC separately loaded with various phenological and yield

attributing traits. Rotated component matrix revealed that the PC1 which accounted for the highest variability (28.96%) was highly loaded with traits such as days to 50% flowering (0.550), days to maturity (0.516) and 100-seed weight (0.328). The PC II accounted for 21.939% of total variability, was highly loaded with trait plant height (0.659), grain yield per plot (0.599), days to maturity (0.308), days to flowering (0.225) and number of pods per plant (0.219) indicating its importance for altering rice genotypes with respect to grain yield. The PCIII showed 16.351% of the variability was highly loaded with grain yield per plot (0.415) and days to 50% flowering (0.265) representing the significance of this PC for grain yield. The fourth principal component exhibited 13.875 % of total variability and variable i.e., days to maturity (0.428), plant height (0.159), days to 50% flowering (0.157) and number of pods per plant (0.111) showed significant variation in flowering time which can be play important role for selection of genotypes on the basis of their duration. Thus, PCA revealed principal discriminatory characteristics such as plant height, days to 50% flowering, days to maturity, number of pods per plant and grain yield per plot, in diverse PCs which are responsible for the observed genotypic variation within a group of genotypes. Important characters coming together in different PCs have tendency to remain together, which may be kept into consideration during utilization of these characters in breeding programme to bring about rapid improvement for yield and other associated traits. In this study number of phenotypic traits can be identified with the help of principal component analysis, which are responsible for the observed genotypic variation present within each component. Consequently, traits coming collectively in various principal components and contributing towards elucidation the variability and have the propensity to remain together this may be kept into consideration during utilization of these characters in breeding program. Distribution of forty genotypes of chickpea in PCs are presented in Fig.-2. Genotype commonly found in more PC, were KWR108, JG2016-44, Sabour chana-1 (BRC-1), IPC 2013-21, HI12-63, AKG1303, PG214J and RKG13-380. Similar type of genotypes on a common principal component permitting to designate them as seed yield factors. These genotypes may further be utilized in breeding programmes for improving seed yield these genotypes can be considered an ideotype breeding material for selection of traits viz more total number of seed per plant and 100-seed weight further utilization in precise breeding programme. These genotypes which are common in more than 1 PCs are indicated that selection of genotype from these PCs is useful in further crop improvement programme. These findings are also confirmation with Akande (2007), Ojo *et al.*,

(2012), Miladinovic *et al.*, (2006), Iqbalet *al.*, (2008), Ghafooret *al.*, (2000), Toker and Cagirgan (2004), Amrita *et al.*, (2014) and Kumar *et al.* (2017), Kumar *et al.* (2019)

CONCLUSIONS

The sufficient amounts of variability present in the chickpea genotypes. The morpho-grain value of the each trait measures the importance and contribution of each component. The results of PCA revealed that the first six principal components explained 81.126% of the total variations, thus suggesting that traits such as canopy plant height, days to 50% flowering, days to maturity, 100-seed weight, number of pods per plant and grain yield per plot were the principal discriminatory characteristics. Therefore, the important characters coming collectively in various PCs and contributing towards explaining the variability and have the tendency to remain together this may be kept into consideration during utilization of these traits in breeding programme of chickpea.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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Table-1: Eigen value, contribution of variability and Eigen vectors for the

principal component axes in chickpea

Characters	PC I	PC II	PC III	PC IV
Eigene Value (Root)	1.738	1.316	0.981	0.832
% Var. Exp.	28.962	21.939	16.351	13.875
Cum. Var. Exp.	28.962	50.900	67.252	81.126
Days to 50% Flowering	0.550	0.225	0.265	0.157
Days to maturity	0.516	0.308	-0.282	0.428
Plant Height (cm)	-0.215	0.659	-0.372	0.159
Number of pods/ plant	-0.527	0.219	-0.259	0.111
100-seed weight (g)	0.328	-0.117	-0.687	-0.614
Grain yield/ plot (g)	0.021	0.599	0.415	-0.614

Fig.: Fig.1 Rotated component matrix

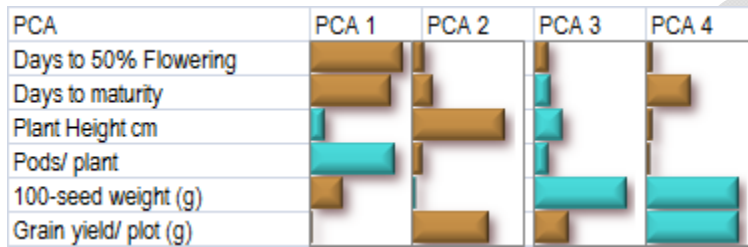
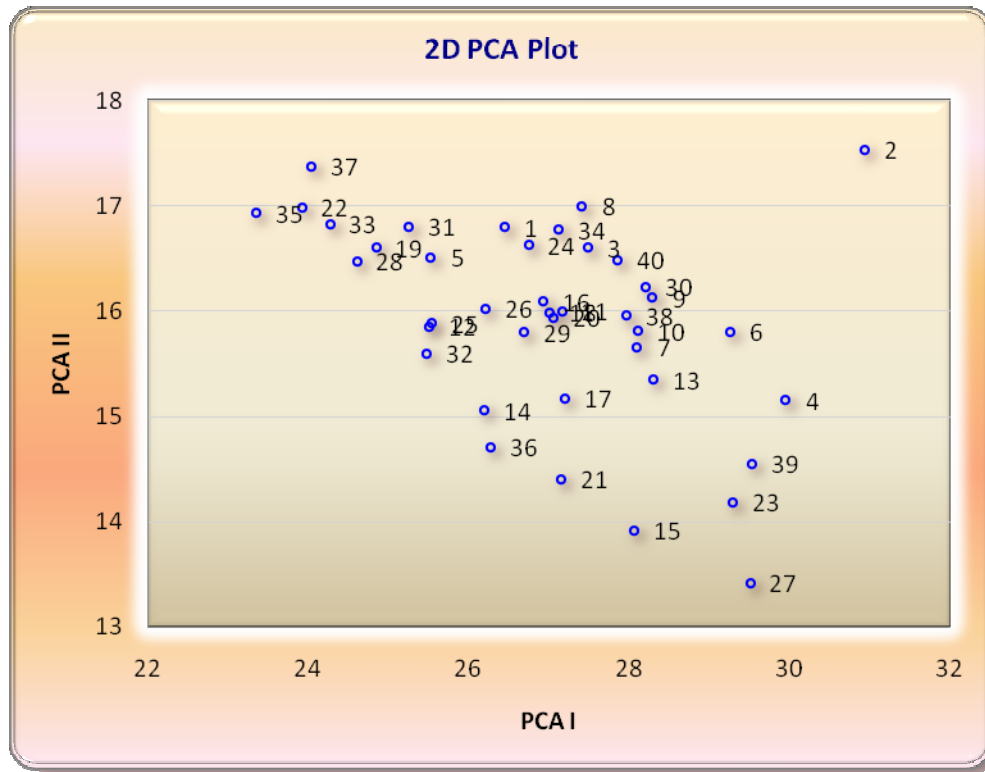


Fig.-2: Scattered distribution of forty genotypes of chickpea



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