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## PROMOTING & REINVIGORATING AGRI-HORTI, TECHNOLOGICAL INNOVATIONS [PRAGATI-2019] (14-15 December, 2019)

### Principal component analysis of Agro-morpho- genetic traits in *Desi* chickpea (*Cicer arietinum* L.)

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Satyendra, Kumari Rajani and PK Singh**

#### Abstract

Chickpea (*Cicer arietinum* L.) is the 2<sup>nd</sup> largest grain-legume crop in the world and is an important rabi pulse crop of Indo Gangetic Plain. 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, 2018-19 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. All the 3PCs exhibited more than 1.0 Eigen value and showed about 91.59% variability. Therefore, these PCs were given due importance for the further explanation. The PC1 showed 59.61% variability among traits, while PC II, and PC III exhibited 24.76% and 7.13% variability respectively. PC1 contributed 59.61% of the total variation and correlated with days to 50% flowering, grain yield per plot and number of pods per plant while PC2 explained an additional 24.76% of the total variation and dominated by days to 50% flowering, 100-seed weight, days to maturity and grain yield per plot. Since, a total of 84.37% 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 BLBG3, BRC-6, BLBG4, DC17-111, PBC546-18 and Sabour chana-1. 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) [6]. 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. 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 (Muniraja *et al.*, 2011) [12, 16]. 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 five genotypes of chickpea in Rabi 2018-19 at Pulse Research Farm, Bihar Agricultural University, Sabour (Bhagalpur). The experiment was laid in randomized complete block design with three replications during Rabi 2018-19 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 Massay (1965) [10] and Jolliffe (1986) 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 proceeding 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 five 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 three 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) [3], 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 59.61% variability among traits, while PC II and PC III exhibited 24.76% and 7.13% 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., 59.61. 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 Mahendra *et al.*, (2015) [9] that the cumulative variance of 77.38% of total variation. Rotated component matrix (Fig. 2) 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 (59.61%) was highly loaded with traits such as days to 50% flowering (0.545), grain yield per plot (0.109), and number of pods per plant (0.060) (Table 2). The PC II accounted for 24.76% of total variability, was highly loaded with trait days to 50% flowering (0.798), 100-seed weight (0.543), days to maturity (0.086) and grain yield per plot (0.077) indicating its importance for altering genotypes with respect to grain yield. The PCIII showed 7.13% of the variability was highly loaded with number of pods per plant (0.685), grain yield per plot (0.637), plant height (0.285), 100-seed weight (0.141) and days to 50% flowering (0.067) representing the significance of this PC for grain yield. Thus, PCA revealed principal discriminatory characteristics such as plant height, days to 50% flowering, grain yield per plot and number of pods per plant 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 programme. Genotype commonly found in more PC, were BLBG3, BRC-6, BLBG4, DC17-111, PBC546-18 and Sabour chana-1. 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) [1], Ojo *et al.*, (2012) [13], Miladinovic *et al.*, (2006) [11], Iqbal *et al.*, (2008) [7], Ghafoor *et al.*, (2000), Tokar and Cagirgan (2004) [15] and Amrita *et al.*, (2014) [2].

**Table 1:** Eigen value, contribution of variability and Eigen vectors for the principal component axes in chickpea

Characters	PC I	PC II	PC III
Eigene Value (Root)	263.80	109.57	31.58
% Var. Exp.	59.61	24.76	7.13
Cum. Var. Exp.	59.61	84.37	91.59
Days to 50% Flowering	0.545	0.798	0.067
Days to maturity	-0.058	0.086	-0.130
Plant Height (cm)	-0.142	-0.113	0.285
Number of pods/ plant	0.060	-0.199	0.685
100-seed weight (g)	-0.814	0.543	0.141
Grain yield/ plot (g)	0.109	0.077	0.637

**Table 2:** Scoring of genotypes in different PC's

Sl. No.	Genotypes	PC I	PC II	PC III
1	BG3043	13.469	21.465	4.908
2	GNG2207	14.748	20.796	3.871
3	ICCV171105	12.965	21.027	3.599
4	NBeG798	16.634	19.746	5.227
5	BDNG2017-1	17.302	18.475	4.664
6	Bidhan Chola	14.217	19.365	4.393
7	JG2018-52	15.631	19.163	4.987
8	BG4001	17.889	20.093	3.835
9	GNG2434	15.686	20.004	4.815
10	RKG13-22	17.495	21.478	4.588
11	PBC538-8	15.375	19.379	5.428
12	PG215	13.959	20.579	6.068
13	DBGV217	17.184	21.436	6.122
14	GL1507	10.658	21.078	5.742
15	RKG18-1	18.308	19.962	4.583
16	JG2018-51	15.136	18.231	4.864
17	CSJ1065	14.882	19.316	5.443
18	RVSSG68	15.810	21.002	4.697
19	H15-27	18.609	19.102	6.119
20	RG2016-134	16.778	19.109	5.647
21	BRC-6	13.962	21.921	5.029
22	RLBG4	18.732	19.252	6.817
23	PhuleG16109	13.572	21.298	4.047
24	BG4000	15.209	23.238	6.128
25	PBC546-18	16.182	22.665	5.089
26	IPC14-51	15.150	19.144	5.485
27	BDNG2015-9	18.926	21.123	5.563
28	GJGI607	14.259	21.052	4.325
29	RVSSG69	14.009	20.813	6.600
30	NDG17-2	13.221	26.044	4.783
31	RLBG3	22.242	22.663	3.346
32	DC17-1115	12.131	21.604	4.431
33	GNG2340	14.679	21.893	3.886
34	RVSSG67	17.365	19.688	3.597
35	GL15020	13.677	19.909	4.760
36	DBGC-2	19.802	20.462	5.191
37	DC17-1111	16.793	22.527	6.232
38	CSJ902	13.269	20.373	4.047
39	PG216	11.392	19.083	3.471
40	IPC14-39	13.126	20.104	5.065
41	GJGI610	13.614	20.896	4.298
42	H14-14	14.089	18.188	4.846
43	NBeG857	15.385	18.231	4.230
44	ICCV171117	9.976	17.314	4.841
45	Sabour chana-1	21.593	23.716	4.839

## 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 91.51% of the total variations, thus suggesting that traits such as 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.

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