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Principal Component and Genetic Diversity Analysis for Seed Yield and Its Related Components in the Genotypes of Chickpea (*Cicer arietinum* L.)

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ABSTRACT

Background: The seed yield of chickpea can be improved by selection of superior genotypes on the basis of different yield and yield component traits. These genotypes exclusively utilize in breeding programs. Yield is a complex trait which is affected by several factors, hence, a well-known technique known as principal component analysis was used to identify and minimize the number of traits for effective selection. To obtain efficient recombinants, the identified component traits need to be combined from diverse parents through recombination breeding followed by selection of transgressive segregants. Hence, the present study is envisaged to measure the genetic diversity among genotypes of chickpea.

Methods: The experimental material comprised of 40 chickpea genotypes evaluated in randomized block design with three replications. The experimental unit was four rows per plot with 4 m length and spacing between row to row and plant to plant maintained as 30 x 10 cm. NPK (20:40:00) fertilizers was applied as basal doses. The data were recorded for each genotype on nine quantitative traits as per standard methods. Descriptive statistics and PCA analysis was performed by using the statistical package SPSS 16.0 version and cluster analysis was done using the Wards method of hierarchical clustering technique.

Result: Out of nine PCs only three PCs exhibited more than 1.0 Eigen value and showed about 73.4% variability. PC1 contributed 28.6% of the total variation and correlated with days to flowering, days to maturity, plant height, first pod height, seeds per pod and number of pods per plant while PC2 explained 21.00% of the total variation and dominated by plant height, first pod height and seed yield. PC3 explained an additional 13.00% of the total variation and dominated by primary branches per plant. Genotype commonly found in more PC, were BG 4016, IPCB 2015-165, IPC 2011-247, GNG2459 and RKG 19-4. Hierarchical clustering technique grouped 40 genotypes into two main clusters (A and B) and nine sub clusters. The present investigation depicted that the chickpea germplasm displayed considerable genetic diversity for most of the traits under consideration.

Key words: *Cicer arietinum* L., Descriptive statistics, Genetic diversity, Principal component analysis.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is the second largest food legume produced globally, after common bean. India is the largest chickpea producing country (72.0 %) in the world followed by Australia, Turkey and USA (FAOSTAT, 2020). Chickpea is usually grown throughout India covering North Hill (dry and cool), North East Hills (wet and mild hot), North West plains (wet and cool), North East plains (humid/wet and cool) and Central and Southern part (dry and hot). But some of the states like Punjab, Haryana, Uttar Pradesh and Bihar have lost considerable area of chickpea due to expansion of irrigated wheat cultivation where as other states like Madhya Pradesh andhra Pradesh, Maharashtra, Karnataka have brought additional area under chickpea cultivation (Arya *et al*., 2019). Among all the pulses, chickpea is the most important *rabi* crop with high acceptability and wider use in India. More availability of quality seed of improved varieties being made available to the famers and it is one of the factors contributing to better harvest of chickpea in recent years. 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.

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Yield and yield contributing parameters are the most widely targeted traits for chickpea improvement program worldwide. Yield is a complex trait which 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). To obtain efficient recombinants, the identified component traits need to be combined from diverse parents through recombination breeding followed by selection of transgressive segregants. Hence, the present study is envisaged to measure the genetic diversity among genotypes of chickpea to explain multivariate polymorphism of diverse genotypes and to identify diverse genetic stock for their further utilization in breeding programme for yield improvement. We also carried out a PCA to identify agronomic attributes whose selection would lead to improvement in seed yield in chickpea.

MATERIALS AND METHODS

The study pertaining to the evaluation of superior chickpea genotype using principal component analysis and hierarchical cluster analysis was conducted at experimental farm, Rajasthan Agricultural Research Institute, Durgapura, Jaipur (Rajasthsan) during Rabi 2019-20. The experimental material comprised of 40 different chickpea genotypes evaluated in randomized block design (RBD) with three replications. The genotypes were sown in first week of December under late sown conditions. The experimental unit was four rows per plot with 4 m length and spacing between row to row and plant to plant maintained as 30 x 10 cm. NPK (20:40:00) fertilizers was applied as a basal dose. The data were recorded from 5 randomly selected plants for each genotype on nine quantitative traits as per standard methods *viz*., days to flowering, total plant height (cm), height from ground to first pod (cm), days to maturity, number of primary branches plant^{-1}, 100 seed weight (g), number of pods plant^{-1}and grain yield kg ha^{-1}.Mean values were taken for analysis of variance and descriptive statistics deliberated as per Panse and Sukhatme (1978). PCA was performed using the statistical package SPSS 16.0 version. Cluster analysis was done using the Wards method of hierarchical clustering technique (Ward, 1963)

RESULTS AND DISCUSSION

The results of basic descriptive statistics for nine quantitative traits showed considerable diversity in chickpea genotypes under studied (Table 1). Principal component analysis is a simple non parametric method for extracting relevant information from confusing data sets. According to the Massay (1965) and Jolliffie (2002) 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 breeding lines 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 crosses in chickpea. 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 the present investigation PCA was performed for quantitative traits of chickpea. Out of nine PCs only 3 PCs exhibited more than 1.0 Eigen values and showed about 73.4% variability (Table 2 and Fig 1). Therefore, these three PCs were given due importance for the further explanation in the present study. The PC1 explained total variation 28.6 % followed by respectively among the genotypes for the traits under study. PC 1 and PC 2 showed maximum contributed to the total variation are presented in Table 2. The PC 1 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. The PC 1 accounted for maximum variability *i.e.* 28.6 % which reduced gradually to PC 2 (21.00%) and PC 3 (13.00%). It can be concluded from the above results that yield contributing traits were having the highest variation in PC 1 followed by PC 2 and PC 3. 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 are akin with to the Malik *et al.* (2014) and Kumari Rajani *et al.,* (2020).Rotated component matrix (Fig 2) revealed that each PC separately loaded with various phenological and yield attributing traits. PC 1 which accounted for the highest variability were mostly related yield contributing traits like days to flowering, days to maturity, plant height, first pod height, seeds per pod and number of pods per plant were given important contributions for

Table 1: Descriptive Statistics for yield and yield relative traits in chickpea.

	SY	DF	DM	PH	HPP	PB	PP	SP	SW
Mean	947.408	66.208	112.490	57.196	29.846	2.238	61.858	1.821	21.642
Variance	25,737.344	54.024	70.228	64.667	32.204	0.098	225.279	0.109	26.296
S.D	160.429	7.350	8.380	8.042	5.675	0.313	15.009	0.330	5.128

SY: Seed yield (kg/ha); DF: Days to flowering; DM: Days to maturity; PH: Plant height (cm); HPP: Plant heights up to first pod (cm); PB: Primary branches per plant; PP: Pods per plant; SP: seeds per pod; SW: 100-Seed weight (g).

variability while PC 2 dominated by plant height, first pod height and seed yield. Thus the PC 1 and PC 2 was constituted by most of the yield attributing traits, a intensive selection procedure can be designed to bring out rapid improvement of dependent traits *i.e*. yield by selecting the lines of PC 1 and PC 2. These results are getting support from the findings of Shivwanshi and Babbar (2017) and Anand Kumar *et al*., (2019). In the present study PC 3 explained an additional 13.00% of the total variation and dominated primary branches per plant. Since, 73.4% of the total variation was contributed by PC1, PC 2 and PC 3, therefore, these three principal components can be allowed for simultaneous selection of yield contributing traits in chickpea.

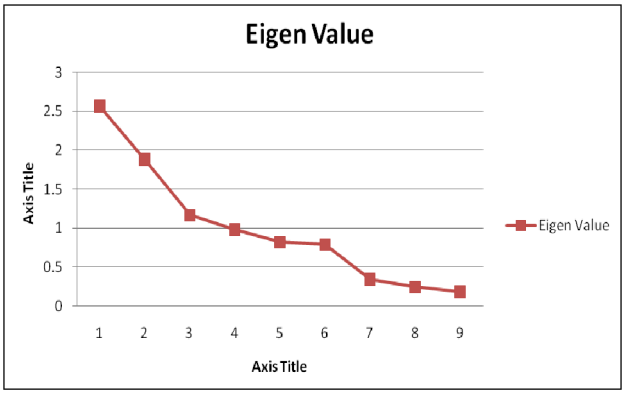
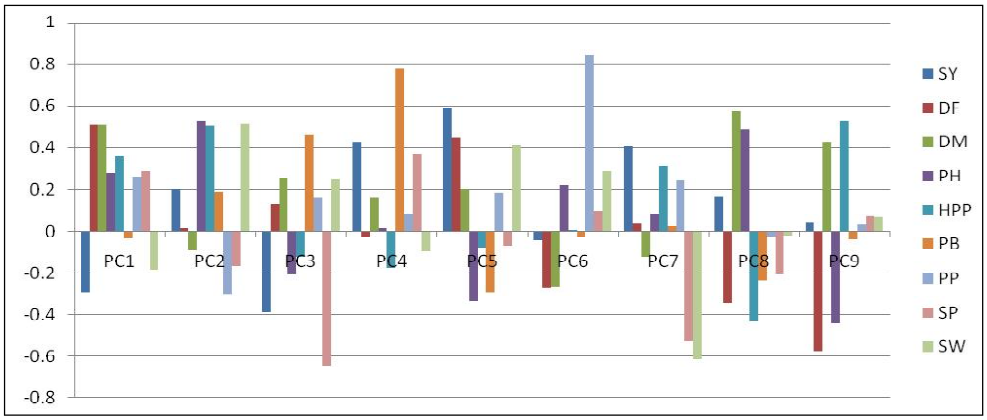


Fig 1: Screen plot constructed based on nine principal component and their Eigen values.

Genotype commonly found in more PC, were BG 4016, IPCB 2015-165, IPC 2011-247, GNG 2459 and RKG 19-4 (Table 3). 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.* days to flowering, days to maturity, plant height, first pod height, seeds per pod and number of pods per plant. Genotype BG 4016 was common in PC 2, PC 3, PC 4 and PC 7, genotype IPCB 2015-165 in PC 1, PC 2, PC 3 and PC 6, genotype IPC 2011-247 in PC 1, PC 2 and PC 8, genotype GNG 2459 in PC 3, PC 4 and PC 6 while RKG 19-4 was common in PC 3, PC 6 and PC 8are



SY: Seed yield (kg/ha); DF: Days to flowering; DM: Days to maturity; PH: Plant height (cm); HPP: Plant heights up to first pod (cm); PB: Primary branches per plant; PP: Pods per plant; SP: seeds per pod; SW: 100-Seed weight (g).

Fig 2: Rotated component matrix.

Table 2: Eigen value, contribution of variability and Eigen vectors for the principal component axes in chickpea.

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
Eigen values	2.571	1.888	1.168	0.983	0.824	0.792	0.344	0.245	0.185
Proportion	0.286	0.210	0.130	0.109	0.092	0.088	0.038	0.027	0.021
Cumulative Proportion	0.286	0.495	0.625	0.734	0.826	0.914	0.952	0.979	1.000
SY	-0.291	0.201	-0.390	0.427	0.588	-0.046	0.404	0.167	0.042
DF	0.509	0.014	0.128	-0.034	0.448	-0.269	0.038	-0.344	-0.575
DM	0.512	-0.094	0.249	0.164	0.201	-0.268	-0.123	0.575	0.427
PH	0.278	0.526	-0.206	0.014	-0.338	0.220	0.085	0.489	-0.441
HPP	0.360	0.506	-0.123	-0.176	-0.079	0.005	0.314	-0.430	0.528
PB	-0.036	0.189	0.462	0.778	-0.291	-0.032	0.025	-0.237	-0.040
PP	0.263	-0.303	0.161	0.081	0.184	0.844	0.242	-0.022	0.034
SP	0.288	-0.165	-0.643	0.370	-0.073	0.097	-0.528	-0.205	0.072
SW	-0.185	0.514	0.245	-0.097	0.410	0.288	-0.614	-0.020	0.066

SY: Seed yield (kg/ha); DF: Days to flowering; DM: Days to maturity; PH: Plant height (cm); HPP: Plant heights up to first pod (cm); PB: Primary branches per plant; PP: Pods per plant; SP: seeds per pod; SW: 100-Seed weight (g)

presented in Table 3. On the basis of PC scores which is found to be common in all the principal components the maximum positive score (>1.0) is found by nine genotypes in PC 1 (NDG 18-13, IPCB 2015-165 Pant Gram 5, DC 19-2, GL 17032, H16-08, DC 19-1 GL 16081, IPC 2011-247), 4 genotypes in PC 2 (BG 4017, IPCB 2015-165, BG 4016, IPC 2011-247), 9 genotypes in PC 3 (Pant Gram 5, IPCB 2015-165 , DC 19-2, JG 2019-151-09, GNG2459,BG 4016, GL16081,RKG 19-4, RSG-945), 7 genotypes in PC 4 (GNG 2144, Pant Gram 5, GNG 2459, BG 4016, PG 248, RSG 902, RSG 974), 5 genotypes in PC 5 (NDG 18-13, RVSSG-84, Phule G 1216-6, GNG 2475, Phule G 1215-1),6 genotypes in PC 6 (RKG 19-3, IPCB 2015-165, NBeG 1633, NDG 18-5, GNG 2459, RKG 19-4), 6 genotypes in PC 7 (RSGD-1080, JG 2019-1214, BG 4016), GL 16081, BRC 9-14, RSG-902), 4 genotypes in PC 8 (RKG 19-3, RKG 19-4,

Table 3: PCA scores of chickpea genotypes having positive >1 values in each PCs.

Principal Components	Number of genotypes	Genotypes having positive >1 values
PC1	9	NDG 18-13 (1.049), IPCB 2015-165 (1.573), Pant Gram 5 (1.674), DC 19-2 (1.726), GL17032 (1.011), H16-08 (1.200), DC 19-1 (1.080), GL 16081 (1.306), IPC 2011-247 (1.290)
PC2	4	BG 4017 (1.515), IPCB 2015-165 (2.304), BG 4016 (1.582), IPC 2011-247 (1.664)
PC3	9	Pant Gram 5 (1.347), IPCB 2015-165 (1.899), DC 19-2 (1.142), JG 2019-151-09 (1.234), GNG 2459 (1.143), BG 4016 (1.367), GL16081 (1.080), RKG 19-4 (1.393), RSG-945 (2.125)
PC4	7	GNG 2144 (1.352), Pant Gram 5 (1.941), GNG 2459 (1.141), BG 4016 (1.317), PG 248 (2.086), RSG-902 (1.088), RSG-974 (1.683)
PC5	5	NDG 18-13 (1.345), RVSSG-84 (1.698), Phule G 1216-6 (1.010), GNG 2475 (1.038), Phule G 1215-1 (2.250)
PC6	6	RKG 19-3 (2.447), IPCB 2015-165 (1.230), NBeG 1633 (1.975), NDG 18-5 (1.137), GNG 2459 (1.426), RKG 19-4 (1.247)
PC7	6	RSGD-1080 (1.269), JG 2019-1214 (2.389), BG 4016 (1.312), GL16081 (1.533), BRC 9-14 (1.220), RSG-902 (1.567)
PC8	4	RKG 19-3 (1.594), RKG 19-4 (1.261), IPC 2011-247(1.336), BRC 9-14 (2.623)
PC9	3	IPC 2015-123 (1.381), H16-17(1.049), RG 2016-31(1.517)

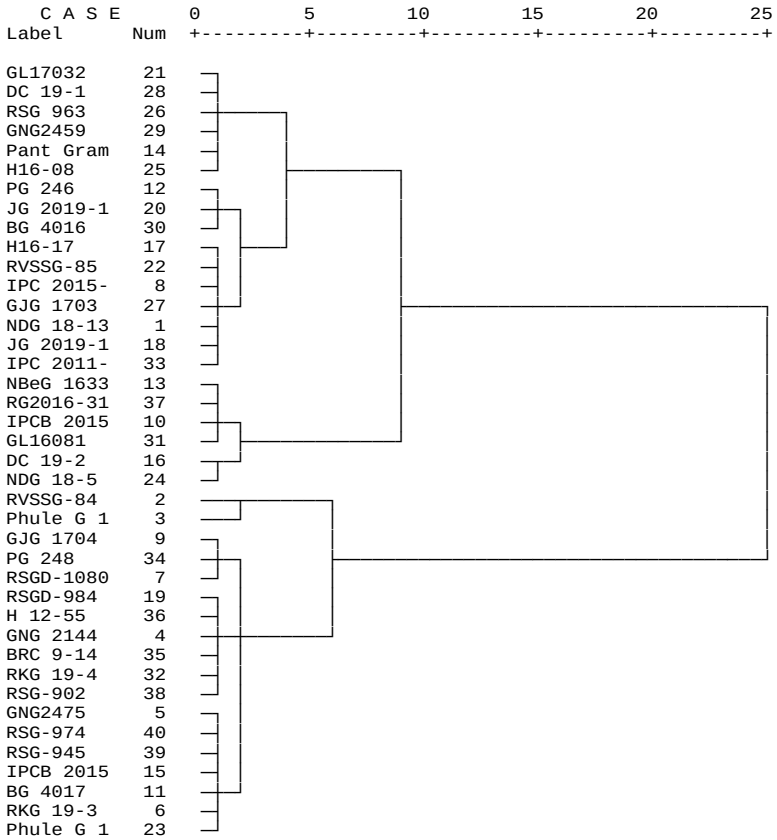


Fig 3: Dendrogram by hierarchical cluster analysis using Ward Method.

IPC 2011-247, BRC 9-14) and 3 genotypes in PC 9 (IPC 2015-123, H16-17, RG2016-31) are explain in Table 3. This indicated the presence of fair amount of genetic diversity and is useful for future breeding program. Earlier scientist reported that that a high value of PC scores can be used for selection and further utilization in future breeding programme. These genotypes which are common in more than one PCs are indicated that selection of genotype from these PCs is useful in further crop improvement program. These findings are also confirmation with Ojo *et al.,* (2012) and Amrita *et al.,* (2014). PC 2 was dominated by phenological traits *viz*., days to flowering and days to maturity. The main variables of PC 3 were plant height, first pod height and seed yield. Thus, PC1, PC 2 and PC 3 allowed for simultaneous selection of yield related traits and it can be regarded as yield factor from this study it was clear that PC 1, PC 2 and PC 3 were mostly related to seed yield traits.

Cluster analysis is an important technique to classify the data which facilitates for dividing the genetic material into various homogenous groupings. Cluster analysis facilitates to group the genotypes on the basis of morpho-genetic traits. Cluster analysis assists in minimizing of the variance within the group whereas, maximizing of the variance among groups and also helps in identifying of outliers. Hierarchical clustering technique based on nine quantitative trait data using Ward's method grouped 40 genotypes into two main groups (A and B) and nine clusters (Fig 3). Group A was comprised of 22 genotypes and further divided into five clusters (I, II, III, IV and V). Cluster I contained six genotypes, cluster II comprised of three genotypes, cluster III comprised of seven genotypes. Cluster IV comprised of four genotypes, cluster V comprised of two genotypes. Group B was comprised of 18 genotypes and further divided into four clusters (VI, VII, VIII and IX). Cluster VI comprised of 2 genotypes, cluster VII comprised 3 genotypes and VIII consists of 6 genotypes while IX clusters included seven genotypes. Similar type of diversity also observed by Ghafoor *et al*. (2001) and Malik *et al*. (2014), Jayalakshmi *et al*., (2014) and Vishnu *et al*., (2020) in chickpea. Thus in the present study the chickpea germplasm displayed considerable genetic diversity for most of the traits under considerations.

CONCLUSION

The present investigation depicts that the chickpea germplasm displayed considerable genetic diversity for most of the traits under consideration. Clustering of germplasm based on various morphological traits has also helped in identifying suitable parents to get better recombinants and the chickpea germplasm can be effectively utilized in future breeding programs for developing high yielding varieties.

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