



ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2021; 10(5): 1076-1080
© 2021 TPI

www.thepharmajournal.com

Received: 07-02-2021

Accepted: 18-03-2021

Halavath Sai Kumar

Ph.D., Scholar, Department of Genetics and Plant Breeding, Naini Agricultural institute, Sam Higginbottom University of Agriculture Technology & Sciences, Prayagraj, Uttar Pradesh, India

GR Lavanya

Associate Professor, Department of Genetics and Plant Breeding, Naini Agricultural institute, Sam Higginbottom University of Agriculture Technology & Sciences, Prayagraj, Uttar Pradesh, India

G Babithraj Goud

Ph.D., Scholar, Department of Crop Physiology, PJTSAU, Rajendranagar, Hyderabad, Telangana, India

Shivashish Verma

Ph.D., Scholar, Department of Genetics and Plant Breeding, Naini Agricultural institute, Sam Higginbottom University of Agriculture Technology & Sciences, Prayagraj, Uttar Pradesh, India

Sindhuja Yerrabala

Department of Agricultural Entomology, Naini Agricultural institute, Sam Higginbottom University of Agriculture Technology & Sciences, Prayagraj, Uttar Pradesh, India

Corresponding Author:

Halavath Sai Kumar

Ph.D., Scholar, Department of Genetics and Plant Breeding, Naini Agricultural institute, Sam Higginbottom University of Agriculture Technology & Sciences, Prayagraj, Uttar Pradesh, India

Principal component analysis for seed yield and other attributing traits in Chickpea (*Cicer arietinum* L.)

Halavath Sai Kumar, GR Lavanya, G Babithraj Goud, Shivashish Verma and Sindhuja Yerrabala

Abstract

To determine the selection criteria, the genotypes of chickpeas were evaluated during the *rabi* season of the year 2019-2020 for twenty five characteristics including biochemical and physiological characteristics. Selection of genotypes and traits based on Principal component analysis. The first of the 12 PCS identified is 83.9% of the variation of the 9 PCS. PC1 explained 21.45% of the total diversity. While PC2, PC3, PC4, PC5, PC6, PC7, PC8 and PC9 have displayed variability of 11.61, 10.61, 9.89, 9.05, 6.66, 6.01, 4.47, 4.32 and all PCs have 1 to 1 respectively. More Eigen values are shown. Results regarding PCA revealed that first three PCS's showed maximum variation and cumulative variance percent. Principle component analysis extracted from first principal component PC1 showed high positive loading for days to maturity (0.373), days to 50% flowering (0.370), grain yield per plant (0.357), chlorophyll content (0.338), starch content (0.293), biological yield (0.282), number of seeds per plant (0.244), plant height (0.213). where as it showed high negative loading for canopy temperature at vegetative stage (-0.047), trypsin inhibitor (-0.053), crude fiber (-0.105), and protein content (-0.150). Principal factor two PC2 enabled high positive loading for leaf area index at 108th and 55th day (0.380) (0.306), number of secondary branches (0.323), biological yield (0.252). where as it showed high negative loading for plant height (-0.333), specific leaf weight at 110th day (-0.423), harvest index (-0.286), and days to 50% flowering (-0.197). which exhibited most significant contributions to genetic variability among chickpea genotypes in this study.

Keywords: Chickpea, genetic variation, Eigen value, PCA

Introduction

Among pulses chickpea (*Cicer arietinum* L.) is an important bean crop grown during *rabi* season. On average, it produces 126 kg of protein per hectare and makes perhaps the highest protein-giving legume next to peanuts and soybeans. Genetic variability is a basic prerequisite for improvement of any crop species for characters of economic importance. 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 genotypes available with the plant breeders (Upadhyay *et al.*, 2002; 2007) [15]. Principal component analysis involves a mathematical process that converts a number of unrelated variables into a number of unrelated variables called Principal components. The first major component has a share of variability in as much data as possible and each subsequent component is responsible for as much variability as possible. The Principal component analysis is the multivariate analysis, which is used to study the diversity 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. The present study is envisaged to measure the genetic variability and effects of yield, biochemical and physiological characters on seed yield in chickpea to identify diverse genotype for their further utilization in hybridization programme for yield improvement.

Materials and Methods

A study on evaluation of best chickpea genotypes using Principal component analysis was conducted during *Rabi* 2019-20 at Center for Experimental Experiment Center, Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University, Agriculture, Technology and Science, Prayagraj. Randomized block design with three Replications. The experimental material comprised of 25 different chickpea genotypes

evaluated for 25 traits in that quantitative, biochemical and physiological traits are taken, received from IIPR, Khanpur and Department of Genetics and Plant Breeding SHUATS. The size of each plot is 1 * 1 m² row to row spacing 30 cm. And plant to plant distance 10 cm. The soil in this region is of sandy loam and alkaline nature. According to Masae (1965) [9] and Joll Liffey (1986), PCA is a well-known method of reducing parameters that can be used to reduce a large set of variables to a small set, which still contains most of the information in a large set. The purpose of the present investigation was to evaluate chick genotypes to identify and sequence important traits and genotypes based on principal component analysis for better hybrid development in chickpeas.

Results and Discussion

Principal component analysis is a simple non-parametric method for extracting information related to confusing data sets. With minimal effort, this one provides a guide to minimizing how complex data is set to a lower dimension, which is often laid out on hidden, simple structures. PCA is a statistical process that uses the orthogonal transformation to convert a set of observations of potentially correlated variables into a set of values of linear unrelated variables known as the principal components whose number of original 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 highest possible variation and in turn each subsequent component has as many variations as possible under the limit that the orthogonal components are preceding components. The resulting vectors are an unrelated orthogonal base set. The principal components are orthogonal because they are the eigen vector of the co-variance matrix, which is symmetrical. In the present investigation PCA was done for the yield and yield related characteristics of chickpea. In present investigation PCA was performed for yield and yield attributing traits of chickpea.

In this experimental study PCA was performed for quantitative, biochemical and physiological traits of chickpea. Out of 12 only 9PC's exhibited more than 1.0 Eigen value and showed 83.9% variability. Therefore these 9 PC's were given due important for the further explanation.

The PC1 explained total variation 21.45% followed by respectively among the genotypes for the traits under study. PC1, PC2 and PC3 showed maximum contribution to the total variation are presented table1. In present investigation PCA was performed for yield and yield attributing traits of chickpea.

In this experimental study PCA was performed for quantitative, biochemical and physiological traits of chickpea. Out of 12 only 9PC's exhibited more than 1.0 Eigen value and showed 83.9% variability. Therefore these 9 PC's were given

due important for the further explanation.

The PC1 explained total variation 21.45% followed by respectively among the genotypes for the traits under study. PC1, PC2 and PC3 showed maximum contribution to the total variation are presented table1. In present investigation PCA was performed for yield and yield attributing traits of chickpea. In this experimental study PCA was performed for quantitative, biochemical and physiological traits of chickpea. Out of 12 only 9PC's exhibited more than 1.0 Eigen value and showed 83.9% variability. Therefore these 9 PC's were given due important for the further explanation. The PC1 explained total variation 21.45% followed by respectively among the genotypes for the traits under study. PC1, PC2 and PC3 showed maximum contribution to the total variation are presented table1.

PC1, PC2, and PC3 showed the maximum contribution to the total diversity that Table 1 presents. PC1 is responsible for the maximum amount of total variability in the set of all variables and the remaining components account for the proportion of the difference in successive less and less. PC1 accounted for the maximum variability i.e. 21.45% which gradually increased to PC2 (11.61), PC3 (10.61), PC4 (9.89), PC5 (9.05), PC6 (6.66), PC7 (6.01), PC8 (4.47), PC9 (4.32)%. In nine PC's. From the above results it can be concluded that PC1 has the greatest difference in yield attribute characteristics after PC2 and PC3.

The purpose of the PCA is to identify the minimum number of components, which can explain the maximum variation from the total variation based on the PC scores. The findings similar to the Mahendra *et al.*, (2015) that the cumulative variance of 84.1% of total variance. Component 1 had 21.45 variability and the remaining of 11.6, 10.61, 9.89, 9.05, was consolidated in component 2,3,4 and 5. That first principal component PC1 showed high positive loading for days to maturity (0.373), days to 50% flowering (0.370), grain yield per plant (0.357), chlorophyll content (0.338), starch content (0.293), biological yield (0.282), number of seeds per plant (0.244), plant height (0.213). where as it showed high negative loading for canopy temperature at vegetative stage (-0.047), trypsin inhibitor (-0.053), crude fiber (-0.105), and protein content (-0.150).

Principal factor two PC2 enabled high positive loading for leaf area index at 108th and 55th day (0.380) (0.306), number of secondary branches (0.323), biological yield (0.252). where as it showed high negative loading for plant height (-0.333), specific leaf weight at 110th day (-0.423), harvest index (-0.286), and days to 50% flowering (-0.197). Principal factor three PC3 enabled high positive loadings for hundred seed weight (0.440), specific leaf weight at 60th day (0.402), relative water content at 45th day (0.154), plant height (0.141), biological yield (0.104). whereas it showed high negative loading for trypsin inhibitor (-0.455), number of seeds per pod (-0.366), chlorophyll content (-0.241), and crud fiber (-0.231).

Table 1: PC Values of rotation component matrix for twenty five variables of chickpea

Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
Days to 50% flowering	0.370	-0.197	0.015	0.105	0.031	0.184	-0.094	0.023	0.024
Days to maturity	0.373	-0.166	-0.008	0.128	-0.024	0.154	-0.114	0.006	0.068
Plant height	0.239	-0.333	0.141	0.065	0.135	0.063	0.086	0.179	-0.134
No. of primary branch	0.142	-0.065	-0.005	0.313	-0.159	-0.443	-0.192	0.010	-0.127
No. of secondary branch	0.117	0.323	-0.040	0.113	-0.135	-0.442	-0.139	-0.145	-0.074
No. of seeds per plant	0.244	0.172	-0.135	-0.186	-0.169	-0.002	0.230	0.098	-0.251
No. of seeds per pod	0.029	-0.019	-0.366	0.161	0.147	0.300	0.088	-0.211	-0.457
100 seed weight	0.039	-0.045	0.440	0.164	0.156	-0.112	0.127	0.003	-0.137

Biomass	0.282	0.252	0.104	-0.164	-0.191	0.143	0.206	-0.005	0.133
Harvest index	0.213	-0.286	-0.169	0.105	0.043	-0.207	-0.178	0.165	-0.294
Chlorophyll index	0.338	-0.103	-0.241	-0.099	0.021	0.117	-0.160	-0.047	0.131
Canopy temperature depression at vegetative stage	-0.047	0.046	-0.015	0.413	0.029	-0.186	0.043	-0.066	-0.089
Canopy temperature depression at pod filling stage	0.145	0.054	-0.154	-0.086	0.154	-0.415	0.385	0.395	0.121
Leaf area index at 55 days	0.122	0.306	0.001	-0.254	0.210	-0.016	-0.428	0.129	-0.070
Leaf area index at 108 days	0.060	0.380	0.072	0.044	0.099	0.175	-0.222	0.312	-0.387
Specific leaf weight at 60 days	0.082	-0.063	0.405	-0.033	0.348	-0.004	-0.240	0.025	0.147
Specific leaf weight at 110 days	0.038	-0.423	0.099	-0.275	0.003	-0.146	0.127	-0.010	-0.078
Relative water content at 45 days	0.088	0.177	0.154	-0.067	0.462	-0.079	0.190	-0.067	-0.105
Relative water content at 105 days	0.120	0.104	-0.164	0.185	0.402	0.029	-0.008	-0.385	0.158
Protein	-0.150	-0.151	0.000	-0.262	-0.252	-0.056	-0.373	0.009	-0.166
Starch	0.293	0.079	0.077	0.009	-0.155	-0.110	-0.206	-0.245	0.336
Fibre	-0.105	-0.091	-0.231	-0.359	0.343	-0.179	-0.173	0.108	0.061
Trypsin Inhibitor	-0.053	0.001	-0.455	0.180	0.123	0.004	-0.029	0.281	0.346
Phytic acid content	0.100	-0.049	-0.124	-0.340	0.068	-0.228	0.104	-0.524	-0.197
Grain yield per plant	0.357	0.134	0.031	-0.132	-0.155	0.041	0.153	0.097	-0.005
Eigenvalue	5.363	2.904	2.655	2.474	2.263	1.665	1.505	1.118	1.080
variance percent	21.451	11.615	10.618	9.894	9.053	6.661	6.018	4.470	4.321
Cumulative variance percent	21.451	33.065	43.684	53.578	62.631	69.292	75.310	79.780	84.102

Table 2: Total variance explained by different principal components in chickpea genotypes

Principal components	Eigenvalue	Variance percent explained (%)	Cumulative variance percent explained (%)
1	5.36	21.45	21.45
2	2.90	11.61	33.06
3	2.65	10.61	43.68
4	2.47	9.89	53.57
5	2.26	9.05	62.63
6	1.66	6.66	69.29
7	1.50	6.01	75.31
8	1.11	4.47	79.78
9	1.08	4.32	84.10

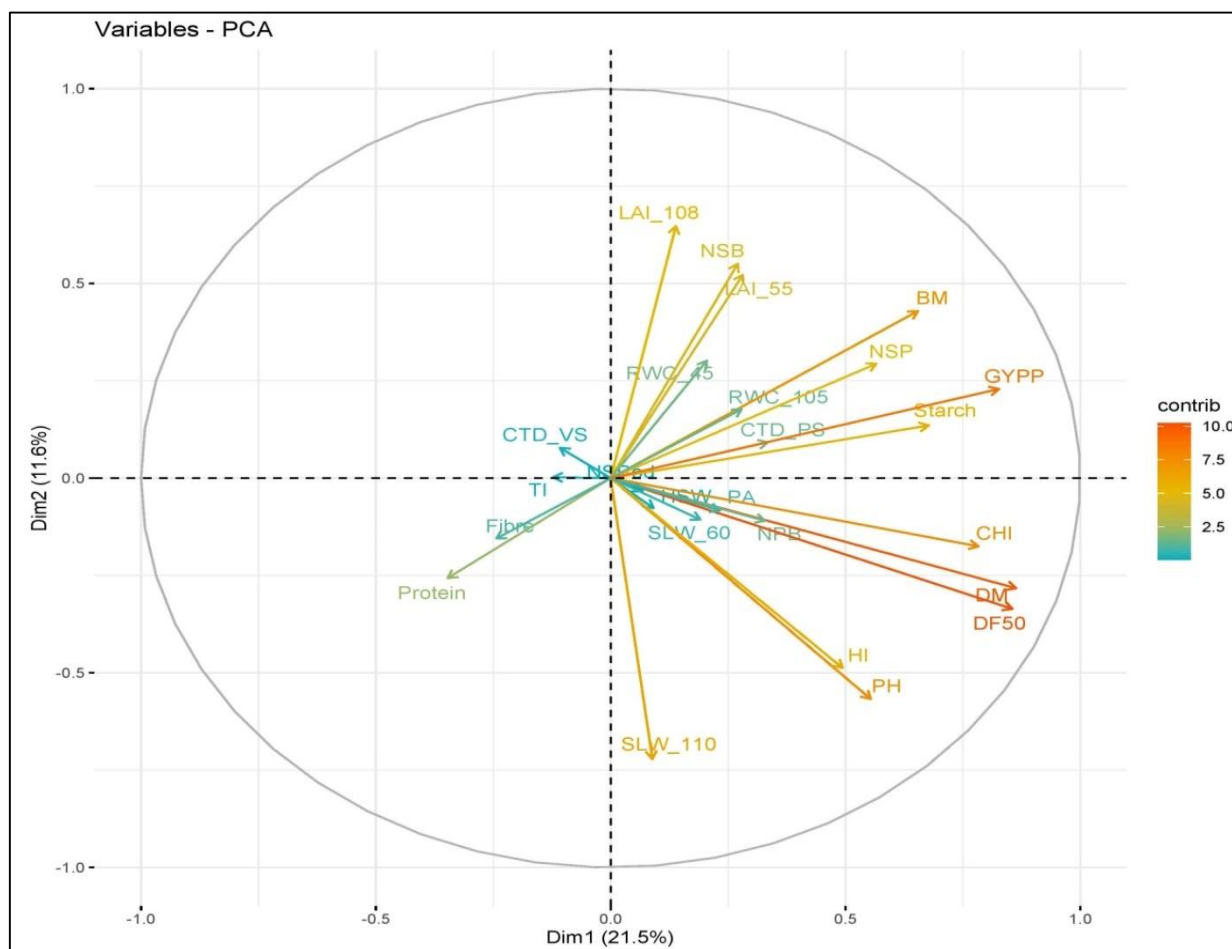


Fig 1: Distribution of 25 traits of chickpea based on principal component PC1 and PC2

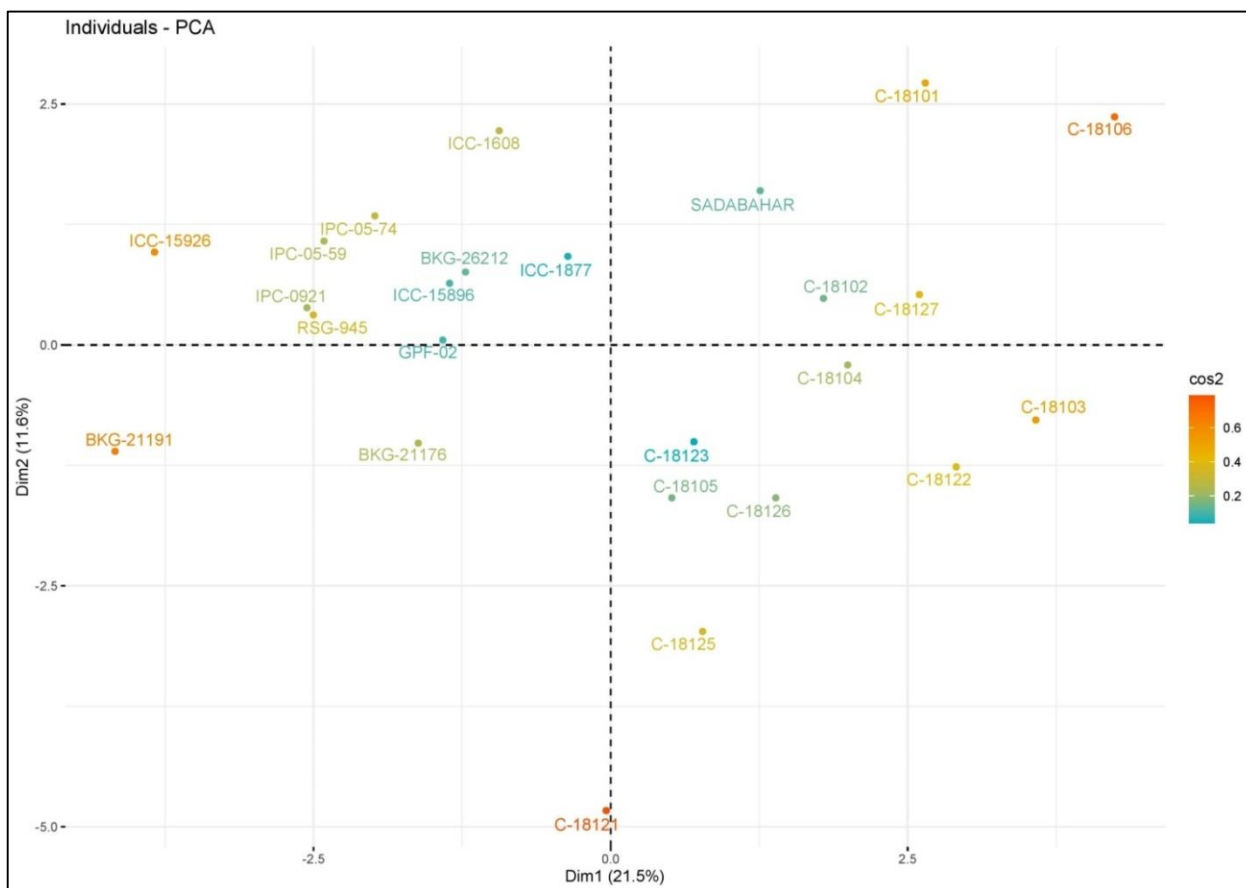


Fig 2: Distribution of 25 chickpea genotypes based on principal component PC1 and PC2

In figure 1. Twenty five traits of chickpea are distributed on the bases of their relative performance with respect to principal factor one and two. All the traits showed significant relation to the variance, post of the traits showed positive loading and few are showed negative loadings, depending on the distance from center of origin represent the variance of a particular trait. Trait enabled high positive loading for days to maturity, days to 50% flowering, and grain yield per plant and high negative loading for canopy temperature at vegetative stage, trypsin inhibitor, and crude fiber.

In figure 2. Twenty five strains of chickpea are distributed on the bases of their relative performance with respect to principal factor one and two. Genotypes C-18104, C-18103, C-18123, C-18105, C-18126, C-18122, C-18125, C-18102, C-18127, C-18106, C-18101 and SADABAHAR cluster towards positive side of PC1, so they were better in terms of grain yield. The genotypes ICC-1608, ICC-15926, IPC-05-74, IPC-05-59, IPC-0921, BKG-26212, RSG-945, ICC-15896, ICC-1877, GPF-02, BKG-21191, BKG-21176, C-18121, were clusters towards negative side of PC2, so they were less effective on grain yield. Earlier scientist reported that a high value of PC scores can be used for selection and for further utilization in future breeding programme. These genotypes which are common in more than IPC's are indicated that selection of genotypes from these PC's is useful in further crop improvement programme. These findings are also confirmation with Akande *et al.*, (2007) [2], Ojo *et al.*, and Amrita *et al.*, (2014).

Conclusion

Principal component analysis revealed that traits *viz* days to maturity, days to 50% flowering, grain yield /plant,

chlorophyll index Contributed greatly to the total variation in yield which is in the first three main components. These characteristics contributed 43.684% of the total diversity. Thus, PC1 PC2 and PC3 can be allowed for simultaneous selection of yielding characteristics in chickpeas. These characters can be given due consideration for further improvement and development of chickpea.

References

1. Annicchiarico P, Nazzicari N, Pecetti L, Romani M. Genomic Selection for Biomass Yield of Perennial and Annual Legumes. Springer International Publishing, Cham 2018, 259-264.
2. Akande SR. Multivariate analysis of the genetic diversity of pigeon pea germplasm from south-west Nigeria. Journal of Food Agriculture and Environment 2007;5(1):224.
3. Babar MM, NuSS Zaidi, Azooz MM, Kazi AG. Genetic and molecular responses of legumes in a changing environment. Legumes under Environmental Stress. John Wiley & Sons, Ltd 2015, 199-214.
4. Ghafoor A, Sharif A, Ahmad Z, Zahid MA, Rabbani MA. Genetic diversity in blackgram (*Vigna mungo* L. Hepper). Field Crops Research 2001;69(2):183-190.
5. Hammed MY, Albadrany MM. Stability of chickpea (*Cicer arietinum* L.) varieties under rainfed conditions in northern Iraq. Afric. crop. sci. 2009;8:219-224.
6. Jones C, De Vega J, Lloyd D, Hegarty M, Ayling S, Powell W, Skot L. Population structure of red clover ecotypes collected from Europe and Asia. Springer International Publishing, Cham 2018, 20-26.
7. Jolliffe I. Principal component analysis. John Wiley & Sons, Ltd 2002.

8. Malik SR, Shabbir G, Zubir M, Iqbal SM, Ali A. Genetic diversity analysis of morpho-genetic traits in Desi chickpea (*Cicer arietinum* L.). Int. J. Agric. Biol 2014;16:956-960.
9. Massey WF. Principal components regression in exploratory statistical research. J. Amer. Statist. Assoc. 1965;60:234-246.
10. Miladinovic Jegor, Hideki Kurosaki, Joe W Burton, Milica Hrustic, Dragana Miladinovic. The adaptability of short season soybean genotypes to varying longitudinal regions. European journal of Agronomy 2006;25:243-9.
11. Rekha R, Prasanthi L, Sekhar MR, Priya MS. Principal Component and Cluster Analysis in Pigeonpea (*Cajanus cajan* L. Mill Sp). International journal of Applied Biology and Pharmaceutical Technology 2013;4(4):424-430.
12. Roorkiwal M, Jain A, Thudi M, Varshney RK. Advances in chickpea Genomic Resources for Accelerating the Crop Improvement. In: Varshney, R.K., Thudi, M., Muehlbauer, F.(Eds), The chickpea Genome. Springer International Publishing, Cham 2017, 53-67.
13. Saeed A, Hovsepyan H, Darvishzadeh R, Imtiaz M, Panguluri SK, Nazaryan R. Genetic diversity of Iranian accessions, improved lines of chickpea (*Cicer arietinum* L.) and their wild relatives by using simple sequence repeats. Plant Mol. Biol. Report 2011;29:848-858.
14. Toker C, Ilhan Cagirgan M. The use of phenotypic correlations and factor analysis in determining characters for grain yield selection in chickpea (*Cicer arietinum* L.). Hereditas 2004;140(3):226-228.
15. Upadhyaya HD, Dwivedi SL, Gowda CLL, Singh S. Identification of diverse greiplasm lines for agronomic traits in a chickpea (*Cicer arietinum* L.) core collection for use in crop improvement. Field Crops Res 2007;100:320-326.