Research Article

Genetic diversity and correlation studies in chickpea (*Cicer arietinum* L.) based on morphological traits

S.M. Samyuktha, S. Geethanjali and J.R. Kannan Bapu
Department of Pulses, Centre for Plant Breeding and Genetics,
Tamil Nadu Agricultural University, Coimbatore – 641 003.
E-mail: samyukthaliea@gmail.com

Abstract
The present study was conducted to evaluate the selection criteria in 48 chickpea germplasm accessions using correlation, path analysis, principal component analysis and cluster analysis based on fourteen morphological traits. These traits included seven vegetative traits (*viz.,* plant height, plant width, number of basal primary branches per plant, number of apical primary branches per plant, number of basal secondary branches per plant, number of apical secondary branches per plant and number of tertiary branches per plant), one flowering trait (days to fifty per cent flowering) and six yield related traits (days to maturity, number of pods per plant, number of seeds per pod, number of seeds per plant, hundred seed weight and single plant yield). Basic descriptive statistics showed normal distribution for six morphological traits. However significant and positive skewness were observed for plant width (1.15), number of apical primary branches per plant (1.68), number of basal secondary branches per plant (1.18), number of tertiary branches per plant (1.86), days to maturity (0.91), number of seeds per pod (0.78), number of seeds per plant (0.72) and hundred seed weight (1.48). ANOVA revealed that significant genotypic variation existed for most of the traits. Traits such as plant width (0.346), number of pods per plant (0.788), number of seeds per pod (0.055), number of seeds per plant (0.675) and hundred seed weight (0.477) exhibited significant positive correlation with single plant yield whereas a strong negative association was exhibited by days to fifty per cent flowering (-0.418) and days to maturity (-0.331). Correlation among component traits revealed a strong negative association of hundred seed weight with seeds per pod (-0.36). Path analysis specified that the highest positive direct effect on single plant yield was exerted by number of pods per plant (0.86) and hundred seed weight (0.589). Principal component analysis (PCA) revealed that the first five components with Eigen values more than one contributed to a maximum of 77.58 per cent of the variability. PC1 contributed 26.59 per cent of the total variation and the traits contributing to maximum variation in first component included plant width (0.712), number of pods per plant (0.692), number of seeds per plant (0.621), number of apical secondary branches per plant (0.54) and plant height (0.538). The Wards method of hierarchical cluster analysis grouped the accessions into two major clusters. Cluster I comprised of genotypes with high mean values for hundred seed weight (20.65) whereas cluster II, showed superior contribution for number of pods per plant (40.27), number of seeds per pod (1.06), number of seeds per plant (42.52) and single plant yield (6.88g). The grouping of chickpea germplasm based on various agro-morphological traits would be useful to identify the promising genotypes for effective utilization in future breeding programmes.

Key words
Chickpea, Correlation, Path analysis, Principal Component Analysis, Cluster analysis.

Introduction

Chickpea (*Cicer arietinum* L.) also known as "poor man's meat and rich man's vegetable" is the second most important food legume in the world after beans in terms of area (13.5 million hectares) and production (13.1 million tons) (FAOSTAT 2016). Chickpea contains two to three times more protein and oil in their seeds compared to cereals (Tonk *et al.,* 2010) which eventually fulfill the protein need of the expanding population. Unlike most pulse crops, chickpea is low in anti-nutritional factors and it improves soil nutrition by fixing atmospheric nitrogen. Evolving new varieties with enhanced performance over the existing varieties is the ultimate aim of formulating any dexterous breeding program. Since yield is a complex character and influenced by many environmental factors, direct selection based on yield may not be rewarding. Therefore a basic understanding of the nature and magnitude of correlation among component traits towards yield is essential. While correlation and path analysis depict the nature of association of different traits and their effects on yield, PCA and cluster analysis help in revealing the magnitude of genetic diversity. To obtain efficient recombinants, the identified component traits need to be combined from diverse parents through recombination breeding followed by selection of transgressive segregants. The proficient transgressive segregants for yield increment as well as resistant to various stresses can be obtained by effectively utilizing the chickpea germplasm comprising of diverse land races, exotic and wild relatives in crossing programmes instead of using few closely related lines. Hence the present study was formulated with the objective to assess the genetic diversity for desirable traits among chickpea germplasm lines so as to utilize them in future breeding programmes.

Materials and Methods

Forty eight chickpea germplasm accessions obtained from ICRISAT along with three checks

viz., Co 4, JAKI 9218 and Thuraiyur local were planted in augmented block design during *Rabi* 2015 in Tamil Nadu Agricultural University, Coimbatore, India. The accessions were raised in seven blocks each consisting of seven accessions and the three checks. Each accession was sown in a single row of four meter length in ridges and furrows with a spacing of 30 cm x 10 cm. All the recommended agronomic practices were carried out during the crop growth period. The observations were recorded on five randomly selected plants in each accession based on descriptors of chickpea (ICRISAT, 1988). The observations were recorded for fourteen different traits *viz.,* plant height (cm), plant width (cm), number of basal primary branches per plant, number of apical primary branches per plant, number of basal secondary branches per plant, number of apical secondary branches per plant, number of tertiary branches per plant, days to fifty per cent flowering, days to maturity, number of pods per plant, number of seeds per pod, number of seeds per plant, hundred seed weight(g) and single plant yield(g). The mean data of five randomly selected plants in each accession for each trait were used for determining the range, mean, variance and standard deviation. Analysis of variance (ANOVA) was obtained by using PB-Tools. Correlation and path analysis were performed using TNAUSTAT (Manivannan, 2014). 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) and the accessions were grouped based on similarity matrix as implemented in Darwin software version 6 (Dissimilarity Analysis and Representation for windows) V.6.0.013 (Perrier and Jacquemoud-Collet, 2006).

Results and Discussion
The results of basic descriptive statistics for 14 quantitative traits studied in chickpea germplasm showed considerable diversity (Table 1). Among the fourteen quantitative traits studied eight traits *viz.,* plant width (1.15), number of apical primary branches per plant (1.68), number of basal secondary branches per plant (1.18), number of tertiary branches per plant (1.86), days to maturity (0.91), number of seeds per pod (0.78), number of seeds per plant (0.72) and hundred seed weight (1.48) were significantly and positively skewed. Excess kurtosis was estimated for the fourteen traits, significant leptokurtic distribution was shown by six traits namely plant width (2.02), number of apical primary branches per plant (3.15), number of basal secondary branches per plant (1.48), number of tertiary branches per plant (5.12), days to maturity (1.69) and hundred seed weight (1.68). The traits days to fifty per cent flowering, plant height, number of pods per plant and single plant yield showed platy kurtic

distribution. Analysis of variance (Table 2) revealed that there was highly significant difference among most of the characters *viz.,* plant height, number of basal primary branches per plant, number of apical primary branches per plant, number of basal secondary branches per plant, number of tertiary branches per plant, days to fifty per cent flowering, days to maturity, number of seeds per pod, number of seeds per plant, hundred seed weight and single plant yield where as significant difference was shown by number of pods per plant.

Correlation coefficient is an important biometrical tool for formulating the selection index, as it reveals the strength of relationship among the group of characters. In the present study, number of pods per plant, number of seeds per pod, number of seeds per plant and hundred seed weight showed a highly significant positive association with single plant yield (Table 3). The positive association of number of pods per plant and number of seeds per plant with single plant yield have also been reported by Kobraee *et al.* (2010) whereas Yadav *et al.* (2012) reported positive association of hundred seed weight with single plant yield. The association of number of seed per pod to single plant yield was akin to the findings of Malik *et al.* (2014). On contrary the negative association of seeds per pod with single plant yield was given by Yadav *et al.* (2012). Plant width also exhibited significant positive correlation with single plant yield. Selection of parents based on these traits can help in yield improvement in chickpea.

The traits *viz.,* days to fifty per cent flowering and days to maturity showed a significant negative association with single plant yield. Though early flowering accessions produce reduced yield than the late flowering ones, it is desirable in case of arid and semiarid conditions under which majority of chickpea is grown, using the available soil moisture and also escape from the biotic and abiotic stresses that occurs during the late growing season. Hence evolving early flowering genotypes coupled with high yield remains a key objective in chickpea breeding programmes. But this negative association with yield could be compensated by adopting appropriate breeding methods like bi - parental mating or diallel selective mating.

Correlation among the component characters revealed that days to fifty per cent flowering and days to maturity showed significant positive correlation with each other and significant negative correlation with hundred seed weight. Similar findings were reported by Malik *et al.* (2014). Plant height and plant width exhibited significant positive correlation with each other and also with number of basal secondary branches per plant, number of apical secondary branches per plant,

number of tertiary branches per plant and hundred seed weight. Number of basal primary branches per plant showed significant positive correlation with number of basal secondary branches per plant, number of seeds per pod and number of seeds per plant. Owing to the increase in number of primary branches the number of secondary branches also increase resulting in more vegetative growth of the plant. This in turn results in the production of more number of flowers and pods per plant due to increased photosynthate production. Number of apical primary branches per plant showed significant positive correlation with number of basal secondary branches per plant and significant negative correlation with number of seeds per pod. This indicates that although number of branches per plant increases the number of pods, it results in less number of seeds per pod which reflects the source to sink relation and partitioning of assimilates. Number of basal secondary branches exhibited significant positive correlation with number of pods per plant. The strong association of primary and secondary branches per plant with number of pods per plant was reported by Zali *et al.* (2011) and Malik *et al.* (2014). Tertiary branches per plant showed significant positive correlation with number of apical secondary branches per plant and hundred seed weight. An understanding on branching behavior is important in chickpea as it influences the pattern of flower production, number of flowers produced and pod rentention. In a study under taken to quantify the flower and pod abortion in chickpea, Zaiter and Barakat (1995) found that in general, primary branches, secondary branches and main stem contributed 54 per cent, 27 per cent and l9 per cent respectively to the final pod yield. The yield obtained after stress at flowering and during pod-filling came mainly from flowers on primary and secondary branches compared to flowers on the main stem. Most of the pods produced from primary and secondary branches on the basal nodes 1-3 from the main stem were retained. This explains for the positive correlation exhibited by basal primary and secondary branches with number of pods, number of seeds and overall seed yield per plant.

In the present study, number of pods per plant exhibited significant positive correlation with number of seeds per plant (Monpara and Gaikwad, 2014), while number of seeds per plant exhibited a negative correlation with hundred seed weight (Yadav *et al.,* 2012). The availability of assimilates to the reproductive organs during flowering determines the seed number and weight, both of these traits can be improved by the prioritized separation of dry matter to reproductive parts which in turn influence the yield (Heitholt *et al.,* 1986). A striking balance between quality and the quantity of assimilates partitioned and accumulated in the reproductive parts may explain for the

negative correlation between these two traits as observed from the present study. The competition for moisture and nutrients also leads to reduced seed size and weight.

The results of correlation in the present study indicated that the traits *viz.,* number of pods per plant, number of seeds per plant and hundred seed weight had major contribution towards higher seed yield in chickpea. Apart from these traits there are other traits which contribute indirectly towards seed yield. Correlation measures the nature and degree of association only between pair of traits where as path provides the magnitude and direction of association between component traits. Selection practiced based on path analysis provides better results since improvement can be made in desirable direction.

Grain yield is determined by the number of seeds formed per unit area of the plant and also the average weight of the individual seeds. As the seed size and number plays a vital role in chickpea improvement programmes, knowledge of these traits contributing towards phenotypic variation for both these traits and their direct and indirect share towards yield is essential (Monpara and Gaikwad, 2014). Path coefficient analysis is one of the reliable statistical techniques in quantifying the interrelationships between different yield contributing components, keeping yield as dependent variable (Mushtaq *et al.,* 2013)

Path analysis showed that the maximum positive direct effect contributing to single plant yield was exhibited by number of pods per plant (0.86) followed by hundred seed weight (0.589), which implied that direct selection for these characters would improve the single plant yield (Table 4). These results were in correspondence with the findings made by Hasan and Deb (2014).

The traits days to fifty per cent flowering (-0.141) and number of apical primary branches per plant (-0.139) displayed negative and low direct effect on single plant yield. However Mushtaq *et al.* (2013) using 17 chickpea genotypes with 3 checks reported that days taken to flowering had maximum direct influence on seed yield per plant. Days to maturity exhibited positive and low direct effect on single plant yield. Mushtaq *et al.* (2013) reported positive direct effect of days to fifty per cent flowering and negative effect of days to maturity with single plant yield.

Among the component traits studied, high and significant indirect effect on yield was attributed by number of seeds per plant *via* number of pods per plant (0.794). Such an observation has also been reported by Hasan and Deb (2014). These findings indicate that indirect selection for seed yield in chickpea can be made through number of

pods per plant. The residual effect of path analysis in the present study was low (0.2107), which indicated that the traits included in the study were sufficient enough to explain their pattern of interaction on yield. From the path analysis the traits number of pods per plant and hundred seed weight showed maximum direct effect on single plant yield. Both these traits exhibited highly significant and positive association with single plant yield. Therefore to increase the yield potential in chickpea the emphasis should be given to the selection based on these traits.

The mean data of fourteen quantitative traits were subjected to principal component analysis that follows a data reductionist approach involving a linear combination of optimally-weighted observed variables and helps in identifying the plant traits that contribute most towards the total variation. PCA analysis revealed that the first five components in the PCA analysis contributed to a maximum of 77.58 per cent of the variability among 48 genotypes. These five principal components were retained based on the scree plot and threshold Eigen value greater than 1 (Table 5, Fig. 1 and 2). The Eigen values for PC 1, PC 2, PC 3, PC 4 and PC 5 were 3.72, 2.57, 2.24, 1.28 and 1.05 respectively.

The first principal component PC 1, explained 26.59 per cent of the total variation and was characterized by vegetative and yield contributing characters *viz.,* plant height, plant width, number of secondary branches per plant, number of pods per plant, number of seeds per plant, hundred seed weight and single plant yield. From PC 1 it was evident, that an increase in plant height and width led to an increased branching behaviour in chickpea genotypes, resulting in increased pods and seeds per plant, thereby boosting the single plant yield in a positive direction. However, late flowering and late maturing traits are shown to have a negative influence on yield. Nawab *et al.* (2013) has also reported that the early maturing genotypes might result in more number of secondary branches and increased plant height.

PC 2 accounted for 18.37 per cent of the total variation and was characterized mainly by pod and seed traits. Here, an increase in number of pods per plant and number of seeds per pod resulted in an increase in the number of seeds per plant, but resulted in a corresponding decrease in seed size, which is evident from effect of hundred seed weight in relation to seed yield.

PC 3 accounted for 16 per cent of the total variation and the communalities of PC 3 were attributed to the flowering behaviour of the genotype, wherein an increase in days to 50 per cent flowering always resulted in a corresponding increase in the days to maturity. PC 4 and PC 5

explained about 9.15 and 7.47 per cent of the total variation respectively and were contributed by the branching behaviour of the genotypes. It was evident from PC 4 and PC 5 that, whenever basal primary and secondary branches increased, the production of apical and tertiary branches were reduced and also had an impact either on seeds per pod or pods per plant. Malik *et al.* (2014) reported the major contribution of days to fifty per cent flowering, days to maturity, plant height, pods per plant, single plant yield and biological yield to PC 2 whereas PC4 was attributed by primary branches, secondary branches, seeds per pod and hundred seed weight. Malik *et al.* (2014) also reported that PC 1 was positively contributed by seed yield, biomass yield, number of pods per plant, number of secondary branches per plant and plant height whereas days to flowering, days to maturity and hundred seed weight were positively associated with PC 2.

Cluster analysis is an important technique to classify the data which facilitates for dividing the germplasm 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 14 quantitative trait data using Ward's method resulted in two major clusters (Fig. 3). Comparison of mean values of these clusters revealed that cluster I consisted of 29 accessions which were further subdivided into four sub-clusters *viz.,* Ia, Ib, Ic and Id. Out of these four sub-clusters, the first three sub-clusters were characterized by poor basal branching habit, and showed poor performance for single plant yield and yield attributing traits. A further insight into the sub-clusters identified sub-cluster Ia with low yielding genotypes with mean single plant yield of 3g, sub-cluster 1b with late maturing (102 days) and low yielding (2.1g) genotypes, and sub-cluster Ic exhibiting small seeded genotypes. However sub-cluster Id was predominated by early maturing genotypes and high yielding genotypes especially with higher mean value for hundred seed weight (37.3g) compared to all the seven sub - clusters.

Cluster II comprised of a total of 19 genotypes with high mean values for single plant yield (6.88 g), number of pods per plant (40.27) and number of seeds per plant (42.52). The cluster 2 was further subdivided into three sub-clusters based on yield performance. Sub-cluster IIa possessed genotypes with more number of seeds per plant with a mean of 42.40, coupled with a longer maturity period (96 days) compared to genotypes in other sub-clusters. Sub-cluster IIb comprised of

early maturing genotypes (87 days) with high number of pods per plant (40.28) and high single plant yield (8.08 g). The highest seed bearing genotype ICC 10653 producing about 76 seeds per plant on an average formed a solitary sub-cluster IIc (seeds per plant – 76).

The selection of diverse parents should be based on the component characters of yield that leads to better adaptation of the crop. For example the genotypes grouped under cluster II of the present study, having more number of pods per plant, seeds per pod and single plant yield can be utilized as potential donors for enhancing the yield of other genotypes.

In a study by Malik *et al.* (2014) 11 genotypes with higher mean value for hundred seed weight grouped into a single cluster which is similar to the sub – cluster Id of the present study. A study under taken by Zali *et al.* (2011) using 17 chickpea genotypes obtained three clusters in which genotypes with maximum plant height, more number of secondary branches, seeds per plant, pods per plant and in turn resulted in higher seed yield formed a major cluster which is in correspondence with the cluster II of the present study. In line with the clusters obtained from the present study, Nawab *et al.* (2013), reported that genotypes with better grain yield and yield components grouped under a single cluster, while long duration types with high number of seeds per pod grouped as a separate cluster based on morphological marker based genetic diversity study involving 20 genotypes. Thus, variability among the genotypes was compressed into various heterotic groups which are particularly important for utilizing the germplasm in hybrid breeding programs in chickpea. Crossing programmes involving selected genotypes from cluster Id with cluster II would be useful in breeding for high yielding chickpea varieties.

The present investigation depicts that the chickpea germplasm displayed considerable genetic diversity for most of the traits under consideration. The traits *viz.,* number of pods per plant and hundred seed weight were found to be important yield attributing traits since these traits showed maximum direct effect and significant positive association with single plant yield as well as contributed for maximum variation in first component of PCA. 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.

References

Faostat, F., 2016. Agriculture Organization of the United Nations Statistics Division. Production Available in: http://faostat3. fao. org/browse/Q/QC/S.

Hasan, M.T. and Deb, A.C. 2014. Estimates of direct and indirect effects between yield and yield components and selection indices in chickpea (*Cicer arietinum* L.). *Tropical Plant Research*, **1**(2) : 65-72.

Heitholt, J.J., Egli, D.B. and Leggett, J.E. 1986. Characteristics of reproductive abortion in soybean. *Crop Sci.,* **26** : 589-594.

ICRISAT. 1988. Annual Report, 1987. Patancheru, India: International Crops Research Institute for the Semi- Arid Tropics, 390.

Kobraee, S., Shamsi, K. and Rasekhi, B. 2010. Investigation of correlation analysis and relationships between grain yield and other quantitative traits in chickpea (*Cicer arietinum* L.). *Afr. J. of Biotechnol.*, **9**(16) : 2342-2348.

Malik, S.R., Shabbir, G., Zubur, M., Iqbal, S.M. and Ali, A. 2014. Genetic diversity analysis of morpho-genetic traits in Desi chickpea (*Cicer arietinum* L.). *International Journal of Agriculture and Biology*, **16**(5) : 956-960.

Manivanan, N. 2014. TNAUSTAT-Statistical package. Retrieved from https://sites.google.com/site/tnaustat.

Monpara, B.A. and Gaikwad, S.R. 2014. Combining high seed number and weight to improve seed yield potential of chickpea in India. *African Crop Science Journal*, **22**(1) : 1 – 7.

Mushtaq, M.A., Bajwa, M.M. and Saleem, M. 2013. Estimation of genetic variability and path analysis of grain yield and its components in chickpea (*Cicer arietinum* L.). *International Journal of Science & Engineering Research*, **4**(1) : 1-4.

Nawab, N.N., Subhani, G.M. and Ullah, M.N. 2013. Patterns of morphological diversity and character association in chickpea genotypes through multivariate approach. *Journal of Animal and Plant Sciences,* **23**(4) : 1107-1114.

Perrier, X. and Jacquemoud-Collet, J.P. 2006. DARwin software. Available at http://darwin.cirad.fr/darwin. (The weighted pair group method with arithmetic mean dendrogram was produced using the DARwin software (Perrier and Jacquemoud-Collet 2006)).

Tonk, F.A., Ilker, E. and Tosun, M. 2010. A study to incorporate high protein content from tetraploid wheat (*T. turgidum dicoccoides*) to hexaploid wheat (*T. aestivum vulgare*). Turk. *J. Field Crops*, **15** : 69-72.

Ward, J.H. 1963. Hierarchical groupings to optimize an objective function. *J. Am. Stat. Assoc.,* **58** : 236–244.

Yadav, P., Tripathi, D.K., Khan K.K. and Yadav, A.K. 2012. Character association and path coefficient analysis in chickpea (*Cicer arietinum* L.) under late sown conditions. *Forage Res.,* **37** (4) : 258-262.

Zaiter, H.Z. and Barakat, S.G. 1995. Flower and pod abortion in chickpea as affected by sowing date and cultivar. *Canadian Journal of Plant Science,* **75** : 321-327.

Zali, H., Farshadfar, F. and Sabaghpour, S.H. 2011. Genetic variability and interrelationships among agronomic traits in chickpea (*Cicer arietinum* L.) genotypes. Crop Breeding Journal, 1(2) : 127-132.

Table 1. Basic descriptive statistics for 14 quantitative traits studied in chickpea germplasm

S.No.	Characters	Mean±2SE	Minimum	Genotypes	Maximum	Genotypes	SD	Skewness	Kurtosis
1	Plant height	35.14±1.18	27.10	ICC 5434	43.76	ICC 1052	4.08	0.49	-0.20
2	Plant width	24.21±0.84	18.10	ICC 1356	33.21	ICC 4958	2.90	1.15*	2.02
3	No. of basal primary branches/plant	2.89±0.15	1.60	ICC 8274	4.20	ICC 1052	0.52	0.11	0.79
4	No. of apical primary branches/plant	3.44±0.43	1.80	ICC 10130	8.80	ICC 1392	1.49	1.68*	3.15
5	No. of basal secondary branches/plant	7.49±0.75	4.00	ICC 1356	15.80	ICC 1052	2.58	1.18*	1.48
6	No. of apical secondary branches/plant	4.11±0.53	0.20	ICC 6098	8.60	ICC 8274	1.84	0.34	0.07
7	No. of tertiary branches/plant	2.53±0.62	0.00	ICC 2919 ICC 4567 ICC 5378 ICC 5434 ICC 6098 ICC 6920	11.00	ICC 1392	2.16	1.86*	5.12
8	Days to 50 per cent flowering	52.27±2.42	32.00	ICC 4951	69.00	ICC 2919 ICC 6920	8.39	-0.16	-0.03
9	Days to maturity	92.95±2.01	80.00	ICC 4951	115.00	ICC 2919	6.95	0.91*	1.69
10	No. of pods/plant	29.28±3.34	8.40	ICC 10685	59.80	ICC 10653	11.58	0.29	-0.27
11	No. of seeds/pod	1.01±0.05	0.77	ICC 1356 ICC 16903 ICC 2210 ICC 4495 ICC 4814 ICC 5679 ICC 6098 ICC 10448	1.45	ICC 3512	0.17	0.78*	0.13
12	No. of seeds/plant	29.96±3.95	8.00	ICC 2919	76.00	ICC 10653	13.71	0.72*	1.21
13	Hundred seed weight	18.94±2.14	10.23	ICC 13892	41.73	ICC 4958	7.41	1.48*	1.68
14	Single plant yield	5.23±0.79	1.12	ICC 10685	12.24	ICC 13464	2.72	0.53	-0.20

Table 2. ANOVA test for significance of genotypic effect on trait variation for fourteen quantitative traits in chickpea

Trait	Degrees of freedom	Sum of squares	Mean sum of squares	F value	Probability (>F)
Plant height	47	1157.36	24.62**	5.24	0.0025
Plant width	47	420.52	8.95	2.24	0.0322
No. of basal primary branches/ plant	47	14.00	0.30**	4.32	0.0038
No. of apical primary branches/ plant	47	91.47	1.95**	16.84	0.0000
No. of basal secondary branches/ plant	47	357.01	7.60**	43.98	0.0000
No. of apical secondary branches/ plant	47	155.82	3.32	2.00	0.0959
No. of tertiary branches/ plant	47	236.50	5.03**	3.80	0.0016
Days to 50 per cent flowering	47	4122.64	87.72**	28.27	0.0000
Days to maturity	47	2463.12	52.41**	17.75	0.0000
No. of pods per plant	47	7004.24	149.03*	3.08	0.0180
No. of seeds per pod	47	1.35	0.03**	3.99	0.0054
No. of seeds per plant	47	9218.21	196.13**	3.61	0.0085
Hundred seed weight	47	4280.28	91.07**	59.77	0.0000
Single plant yield	47	604.07	12.85**	4.41	0.0034

**Significance (1% level)   *Significance (5% level)

Table 3. Simple correlation coefficients among the 14 quantitative characters in chickpea

	PH	PW	BPB	APB	BSB	ASB	TB	DFF	DM	PPP	SPP	SPPT	HSW	SPY
PH	1													
PW	0.570**	1												
BPB	0.261	0.237	1											
APB	0.248	0.281	0.014	1										
BSB	0.388**	0.427**	0.340*	0.313*	1									
ASB	0.368**	0.493**	-0.073	-0.004	0.254	1								
TB	0.340*	0.412**	-0.151	0.271	0.083	0.512**	1							
DFF	0.079	-0.196	0.130	0.091	0.141	-0.0253	0.042	1						
DM	0.071	-0.236	0.079	0.117	-0.003	-0.194	-0.055	0.782**	1					
PPP	0.054	0.176	0.212	-0.041	0.305*	0.185	0.073	-0.250	-0.217	1				
SPP	0.060	-0.003	0.291*	-0.354*	0.011	-0.037	0.041	0.025	0.165	0.226	1			
SPPT	0.061	0.139	0.316*	-0.160	0.243	0.140	0.056	-0.210	-0.121	0.924**	0.553	1		
HSW	0.355*	0.433**	-0.088	0.223	-0.040	0.166	0.385**	-0.350*	-0.345*	-0.084	-0.360*	-0.219	1	
SPY	0.282	0.346*	0.166	-0.045	0.184	0.247	0.210	-0.418**	-0.331*	0.788**	0.055**	0.675**	0.477**	1

**Significance (1% level)   *Significance (5% level)

PH=Plant height, PW=Plant width, BPB=Basal primary branches/plant, APB=Apical primary branches/plant, BSB=Basal secondary branches/plant, ASB=Apical secondary branches/plant, TB= Tertiary branches/plant, DFF=Days to 50 per cent flowering, DM=Days to maturity, PPP=No. of pods/plant, SPP=No. of seeds/pod, SPPT=No. of seeds/plant, HSW=Hundred seed weight, SPY=Single plant yield.

Table 4. Direct and indirect effect of component characters on single plant yield as revealed from path analysis

	PH	PW	BPB	APB	BSB	ASB	TB	DFF	DM	PPP	SPP	SPPT	HSW	Correlation
PH	**0.091**	-0.042	0.013	-0.034	-0.005	0.020	-0.015	-0.011	0.011	0.047	0.000	-0.002	0.209	0.281
PW	0.052	**-0.073**	0.011	-0.039	-0.005	0.027	-0.018	0.028	-0.038	0.151	0.000	-0.005	0.255	0.345
BPB	0.024	-0.017	**0.048**	-0.002	-0.004	-0.004	0.007	-0.018	0.013	0.184	0.001	-0.012	-0.050	0.169
APB	0.023	-0.020	0.001	**-0.139**	-0.004	0.000	-0.012	-0.013	0.019	-0.036	-0.001	0.006	0.131	-0.047
BSB	0.035	-0.031	0.016	-0.043	**-0.012**	0.013	-0.004	-0.020	-0.001	0.263	0.000	-0.009	-0.023	0.185
ASB	0.034	-0.036	-0.004	0.001	-0.003	**0.053**	-0.023	0.004	-0.031	0.159	0.000	-0.005	0.098	0.247
TB	0.031	-0.030	-0.007	-0.038	-0.001	0.027	**-0.044**	-0.006	-0.009	0.063	0.000	-0.002	0.227	0.211
DFF	0.007	0.014	0.006	-0.013	-0.002	-0.001	-0.002	**-0.141**	0.125	-0.215	0.000	0.008	-0.206	-0.419
DM	0.006	0.017	0.004	-0.016	0.000	-0.010	0.002	-0.110	**0.160**	-0.188	0.001	0.005	-0.204	-0.333
PPP	0.005	-0.013	0.010	0.006	-0.004	0.010	-0.003	0.035	-0.035	**0.860**	0.001	-0.035	-0.048	0.789
SPP	0.007	0.000	0.014	0.046	0.000	-0.001	-0.002	-0.012	0.032	0.149	**0.004**	-0.019	-0.215	0.003
SPPT	0.006	-0.010	0.015	0.022	-0.003	0.008	-0.003	0.030	-0.019	0.794	0.002	**-0.038**	-0.129	0.675
HSW	0.032	-0.031	-0.004	-0.031	0.001	0.009	-0.017	0.049	-0.055	-0.071	-0.001	0.008	**0.589**	0.477

*Bolded values indicate the direct effects to yield (path coefficients)
*Other values indicate the indirect effects via different pathways to yield except the correlation values.

PH=Plant height, PW=Plant width, BPB=Basal primary branches/plant, APB=Apical primary branches/plant, BSB=Basal secondary branches/plant, ASB=Apical secondary branches/plant, TB= Tertiary branches/plant, DFF=Days to 50 per cent flowering, DM=Days to maturity, PPP=No. of pods/plant, SPP=No. of seeds/pod, SPPT=No. of seeds/plant, HSW=Hundred seed weight, SPY=Single plant yield.

Table 5. Eigen values, percent of total variation and component matrix for the principal component axes

	PC 1	PC 2	PC 3	PC 4	PC 5
Eigen value	3.722	2.571	2.241	1.281	1.046
Variance%	26.586	18.367	16.004	9.151	7.473
Cumulative%	26.586	44.954	60.957	70.108	77.581

Component matrix

| Characters	Component				
	1	2	3	4	5
Plant height	0.538	-0.338	0.470	0.012	-0.287
Plant width	0.712	-0.370	0.220	-0.017	-0.258
No. of basal primary branches/plant	0.276	0.337	0.437	-0.411	-0.475
No. of apical primary branches plant	0.154	-0.501	0.307	-0.434	0.404
No. of basal secondary branches/plant	0.467	-0.011	0.508	-0.388	0.094
No. of apical secondary branches/ plant	0.540	-0.267	0.148	0.515	0.060
No. of tertiary branches plant	0.454	-0.433	0.179	0.538	0.212
Days to 50% flowering	-0.410	-0.012	0.775	0.119	0.211
Days to maturity	-0.433	0.093	0.712	0.092	0.213
No. of pods/plant	0.692	0.583	-0.076	-0.082	0.384
No. of seeds/pod	0.088	0.601	0.316	0.418	-0.368
No. of seeds/plant	0.621	0.741	0.034	0.060	0.185
Hundred seed weight	0.448	-0.627	-0.311	-0.070	-0.141
Single plant yield	0.826	0.213	-0.251	-0.065	0.155
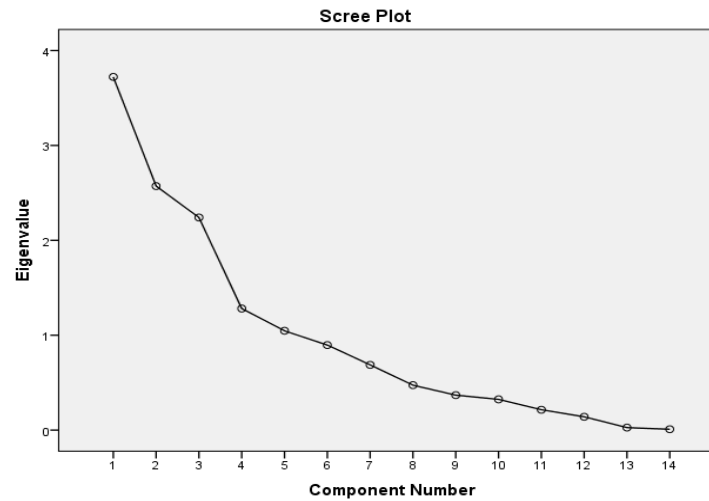
Figure 1. Scree plot for 14 quantitative traits in chickpea germplasm
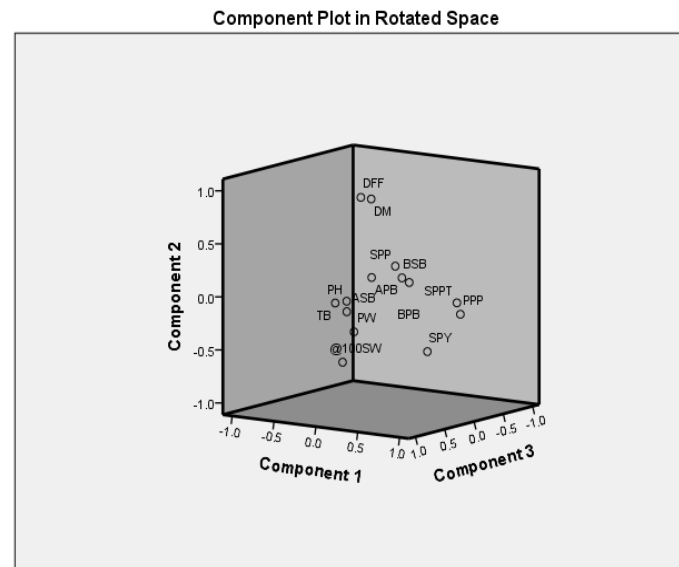

Figure 2. Three dimensional component plots for 14 quantitative traits in chickpea germplasm
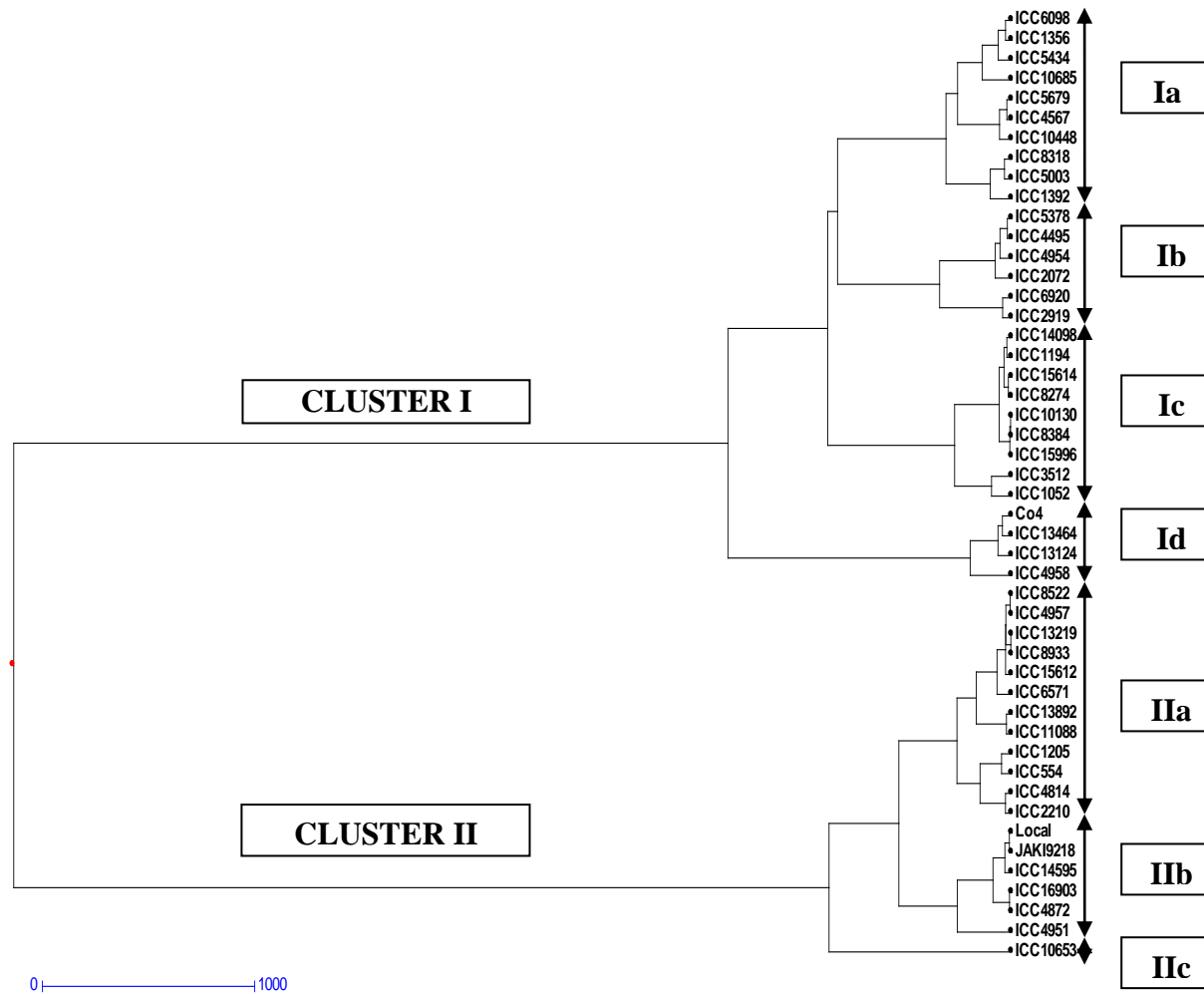
Figure 3. Dendrogram based morphological traits in chickpea germplasm accessions