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Evaluation of Chickpea Genotypes for Genetic Diversity through Multivariate Analysis

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Abstract: Fifteen chickpea genotypes (*Cicer arientinum* L.) were evaluated for genetic diversity through principal component analysis and cluster analysis. The experiment was conducted at Gram Breeding Research Sub-Station, Kallurkot during Rabi season of the year 2016-17. Results regarding PCA revealed that first three PCs showed more than 1 Eigen values accounting for 50.5%, 19.99% and 15.86% respectively in total variation and collectively share 86.15 % of total variation. Principle component analysis extracted higher loadings for grain yield, harvest index, pods plant^{-1}, 100-seed weight (g), days to 50 % flowering and plant height which exhibited most significant contributions to genetic variability among chickpea genotypes in this study. Through cluster analysis, genotypes were distinguished in three clusters based on similarity in characters. Dendrogram was constructed on the basis of similarity by Euclidean distance among genotypes. Dendrogram showed that members falling in clusters I and III are genetically most divergent. Data certified that considerable genetic variation exists in chickpea genotypes in performance of various attributes in this study and these genotypes can potentially be utilized for chickpea breeding program.

Keywords: Chickpea, genetic variation, PCA, cluster analysis.

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1 Introduction

Legumes, ecologically as well as economically important plants, are considered vital for global food security especially under predicted climatic conditions (Considine et al., 2017; Cullis and Kunert, 2017; Dakora et al., 2015; Rubiales and Mikic, 2015). Global efforts were initiated by United Nations to promote legume production under the banner of "Nutritious seeds for a sustainable future" (FAO, 2016; Foyer et al., 2016). Chickpea (*Cicer arientinum* L.) is one of the most important pulse crop widely grown in almost all the continents of world and help in provision of nutritious food for expanding global population (Millan et al., 2015; Muehlbaur and Sarkar, 2017; Rachwa-Rosiak et al., 2015). In Pakistan productivity of the crop per unit area is far below (276 kg ha^{-1}) than the average world's production of 952 kg ha^{-1} (FAO STAT, 2014).

Both biotic and abiotic stresses significantly influence the overall production of the crop (Roorkiwal et al., 2017; Upadhyaya et al., 2007; Vrignon-Brenas et al., 2016). There is dire need to evolve high yielding varieties capable for better performance under biotic and abiotic stresses to fill this yield gap (Lobell et al., 2009; Rubiales et al., 2018; Varshney et al., 2017). Diversity among parental material provides maximum chances to researchers to devise desirable breeding strategies (Aaujo et al., 2015; Babar et al., 2015; Nawaz et al., 2017a; Wang et al., 2017). Assessment and exploration of diversity among genotypes is importance for a successful breeding program

(Annicchiarico et al., 2018; Boukar et al., 2018; Ojiewo et al., 2018; Renganayaki et al., 2001).

Patterns of genetic diversity and its inheritance significantly vary among genotypes (Govindaraj et al., 2015; Karakoyet al., 2012; Nawaz et al., 2017b; Ye et al., 2018). Assessment of such patterns and amount of diversity is of great importance for the researchers providing maximum chances for the development of most suitable plant genotypes (Ghafoor et al., 2001; Varshney et al., 2018). Collection of diverse genetic material and its characterization is a pre-requisite for all the breeding programs (Jones et al., 2018; Nadeem et al., 2018; Saeed et al. 2011; Zabala et al., 2018). Therefore, exploration of genetic diversity is of much importance for success of a breeding program.

Multivariate analysis involves principal component analysis (PCA) and cluster analysis. Both PCA and cluster analysis were found most efficient for assessment of genetic variation in chickpea genotypes (Chen et al., 2017; Gupta et al., 2011; Nihal and Adak, 2012; Sharifi et al., 2018). The current study was planned to evaluate genetic diversity among elite genotypes and their further utilization in chickpea breeding program.

2. Materials and Methods

2.1 Study Area

The experiment was carried out at Gram Breeding Research Sub-Station, Kallurkot, Bhakkar, Punjab, Pakistan (71.153^{o}E and 32.923^{o}N) during Rabi season of the year 2016-17. Fifteen chickpea genotypes viz; CH-60/10, CH-73/10, CH-86/10, K-010-10, K-044-11, K-065-11, CC-9899, CH-85/06, DO-80-10, DO-72-11, DO-88-11, Bhakkar-11, CM-2008, Noor-2013 and Bittle-2016 were sown in randomized complete block design in three replications. Each entry was sown in experimental plot of 30 cm apart 4 rows of 4 meter length. Sowing was done by dibbler and plant to plant distance was maintained at 10 cm. Insecticide Emamectin @ 600 ml ha^{-1} was sprayed twice to prevent pod borer attack with an interval of 15 days at pod formation stage of the crop. Data was recorded for days to 50% flowering, days to 90% maturity, plant height (cm), pods plant^{-1}, 100 seed weight (g) , harvest index and yield kg ha^{-1}. Data regarding days to 50% flowering, days to 90% maturity were recorded by counting number of days from date of sowing to date of completion of 50% flowering and 90% maturity. While plant height and pods plant^{-1}were recorded from ten consecutive plants from each replication of every genotype and averaged across replications. Harvest index was calculated by total economic yield divided by total biological yield and expressed in percentage.

Data were subjected to principal component analysis and cluster analysis by STAR (Statistical Tool for Agricultural Research version 2.0.1).

3. Results and Discussion

3.1. Principal Component Analysis

Principal component analysis revealed seven PCs among which first three PCs expressed more than 1 Eigen values (Table1). A Scree plot (Fig. 1) between Eigen values and principal components was also constructed for summarizing the contribution of PCs. Graph showed that maximum variation was present in PC1 with highest Eigen value of 3.93 followed by PC2 (1.39) and PC3 (1.09).. Data showed that PC1, PC2 and PC3 contributed 50.5%, 19.99% and 15.66% respectively and 86.15% cummulative variation. Similar results were reported earlier (Ghafoor et al., 2003; Talebi and Rokhzadi, 2013; Upadhyaya et al., 2007) contribution of more than two PCs in variability.

Results also showed that in PC1 significant positive values were exhibited by yield kg ha^{-1} (0.512) followed by harvest index (0.501), pods plant^{-1}(0.457) and 100-seed weight (0.306)while days to 90% maturity and plant height contributed negative loadings. 2nd component was associated positively to days to 50% flowering (0.462) while all other traits expressed negative loadings. In 3rd component positive contribution of pods plant^{-1}, days to 90% maturity, harvest index and yield kg ha^{-1}was noted while negative share was observed by days to 50% flowering and days to 90% maturity.

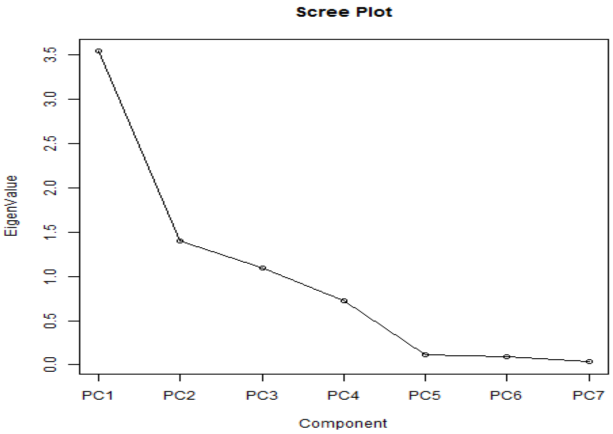

Fig. 1. Scree plot showing contributions of PCs in variability.

Table 1. Principal component analysis of various traits in chickpea

Variable	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Days to 50% Flowering	0.077	0.462	-0.604	0.619	0.161	-0.047	0.071
Plant height	-0.088	-0.735	-0.237	0.428	-0.381	-0.212	-0.149
Days to 90 % of Maturity	-0.415	-0.245	0.346	0.42	0.604	0.294	0.146
Pods plant^{-1}	0.457	-0.019	0.403	0.218	0.175	-0.672	0.314
100-Seed weight	0.306	-0.421	-0.508	-0.38	0.526	0.032	0.223
Harvest Index	0.501	-0.086	0.129	0.205	-0.317	0.615	0.452
Yield	0.512	-0.041	0.148	0.153	0.239	0.187	-0.774
Eigen value	3.535	1.399	1.096	0.725	0.113	0.096	0.034
Percent of variance	50.5	19.99	15.66	10.35	1.61	1.37	0.51
Cumulative percentage of variance	50.5	70.49	86.15	96.51	98.12	99.49	100

Table 2. Cluster analysis of various traits of chickpea genotypes

Variables	Cluster I	Cluster II	Cluster III
DFF	90.75	88.00	87.75
Plant height	53.38	51.00	48.75
DM	155.12	160.00	149.00
NPP	84.25	74.00	103.25
100 seed weight	23.34	20.86	23.11
HI	48.52	44.35	50.81
Yield	1788	1536	2041

DFF, days to 50% flowering; DM, days to 50% maturity; HI, Harvest index; NPP, number of pods plant^{-1};

From Fig. 2 and Fig. 3 it is obvious that distance of variables to PCs show their contributions to genotypes.PCA plot and biplot among PC1 and PC2 also depicted that yield kg ha^{-1}, harvest index, pods plant^{-1} and 100-seed weight expressed most significant contributions to genetic variability in studied chickpea genotypes. Selection of genotype from first three PCs will be more valuable for the success of a breeding program for chickpea improvement. Ghafoor et al. (2003) and Malik et al. (2014) also reported similar findings in agreement to this study.

3.2 Cluster Analysis

Cluster analysis distributed the genotypes into three clusters on the basis of similarity in characters (Table 3). Cluster I comprised of eight genotypes viz; CH-60/10, CH-73/10, CH-86/10, K-065-11, Noor-13, CC-9899, DO-72-11 and DO-88-11.Cluster II had three member viz; CM-08,K-010-10 and K-044-11 while cluster III consisted of four member viz; CH-85/06, Bhakkar-11, DO-80-10 and Bittle-16. Talebi and Rokhzadi (2013) also reported three clusters of 40 genotypes. Dendrogram distributed the genotypes on the basis of distance among the clusters (Fig. 4) which depicted that members of cluster III and I were the most diverse and hybridization between their members could generate a significant diversity for selection process.

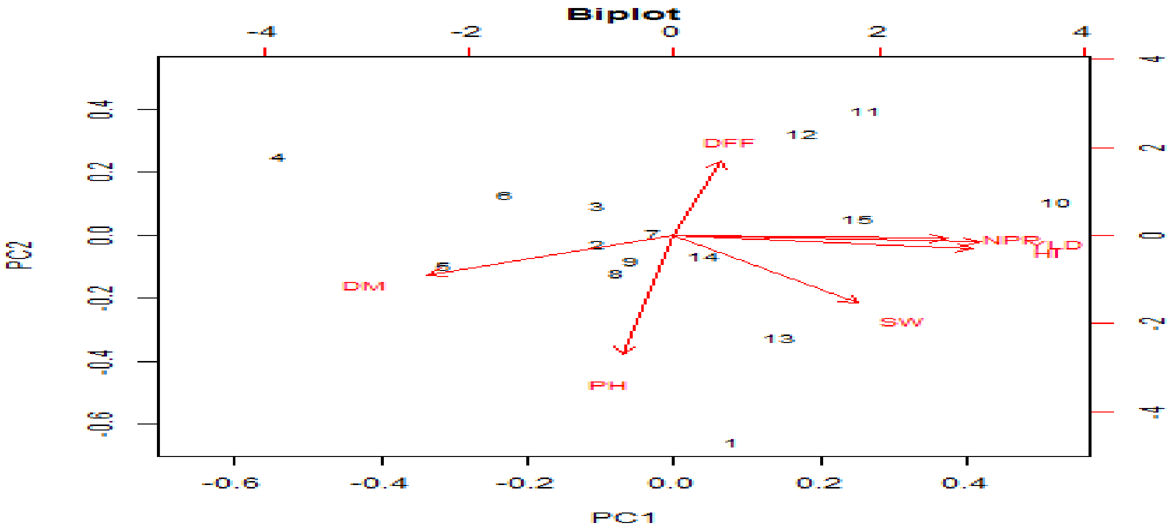

Fig. 2. Biplotof PC1 and PC2 showing contribution of various traits in variability of chickpea genotypes.

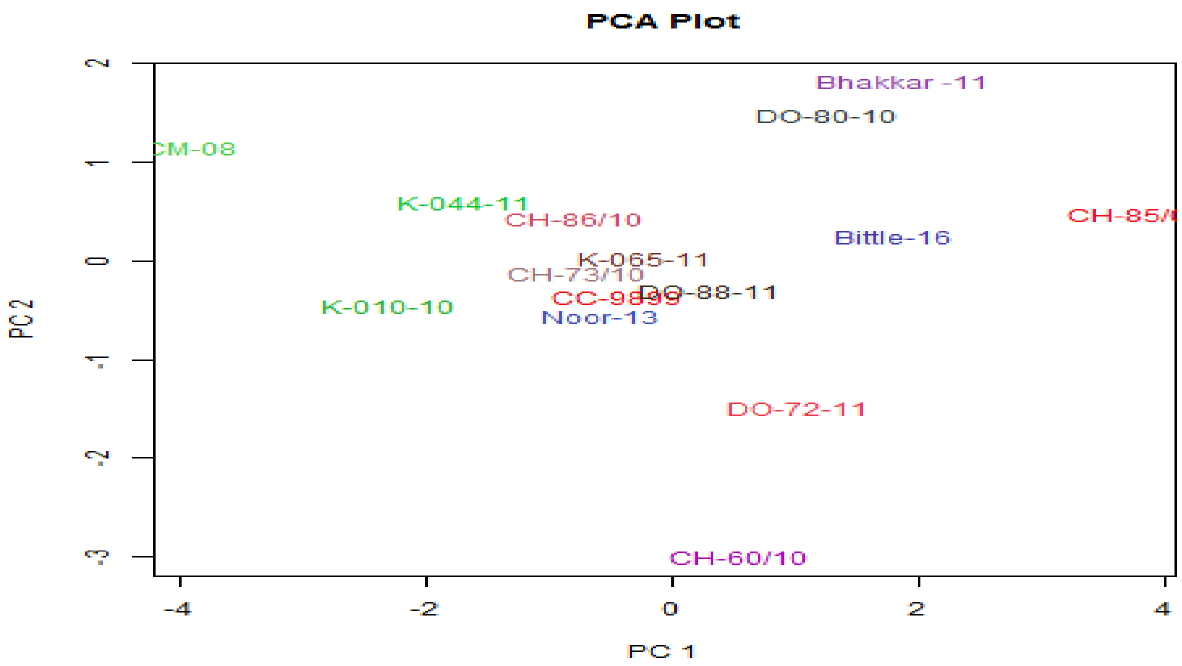

Fig. 3.PCA Plot between Ist and 2nd component showing contribution of variability among.

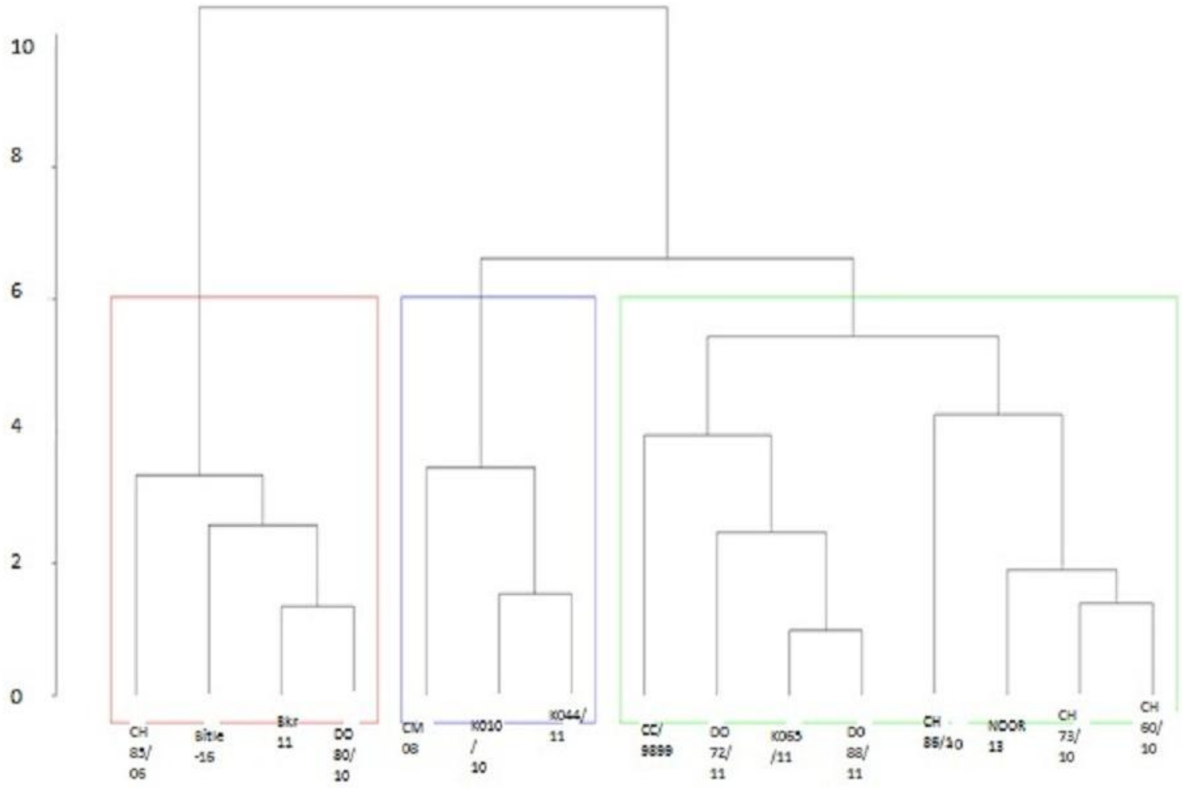

Fig. 4. Wards Dendrogram for Agglomerative clustering of chickpea genotypes.

Table 3. Cluster Membership of Chickpea Genotypes

Cluster I	Cluster II	Cluster III
CH-60/10	CM-08	CH-85/06
CH-73/10	K-010-10	Bhakkar-11
CH-86/10	K-044-11	DO-80-10
K-065-11		Bittle-16
Noor-13		
CC-9899		
DO-72-11		
DO-88-11		

It is evident that genotypes in cluster-I showed higher values for days to 50% flowering (90.7) and plant height (53.4) indicating that selection of genotypes for late flowering and maximum plant height can be made from this cluster (Table 2). Genotypes in cluster II expressed higher values for days to 90% maturity (160.0) and lower values for pods plant^{-1}, 100 seed weight, harvest index and yield kg ha^{-1} indicating that genotypes for breeding of delayed maturity may be done from this cluster. Genotypes in cluster III exhibited higher values for pods plant^{-1} (103.2), harvest index (50.8), yield kg ha^{-1} (2041) and lower values for days to flowering, plant height and days to 90 % maturity indicated that genotypes in this cluster can be further utilized for breeding programs based on higher yield, maximum number of pods plant^{-1} and early maturity that is desirable in most cases. Ghafoor et al. (2003) and Malik et al. (2014) also narrated similar results.

4. Conclusion

From present studies it is evident that considerable genetic variation exists in chickpea genotypes for grain yield, harvest index, pods plant^{-1}, 100-seed weight, days to maturity and plant height which are highly desirable in breeding programs. Results of this study suggest that these genotypes may be employed in future chickpea breeding program to evolve genetically improved chickpea varieties.

List of Abbreviations: FF, Days to 50 percent flowering; DM, days to maturity; FAO, Food and Agriculture Organization; HI, harvest index; NPP, number of pods per plant; PCA, principal component analysis; SW, seed weight; YLD, yield.

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Authors Contribution: M.T.M., M.A. and I.A., involved in the conception, design of the study. M.T.M., A.L., M.Z. performed experiment; all authors were involved in data collection, analysis interpretation and manuscript writing.

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