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Detection of most diverse and high yielding strains of chickpea (*Cicer arientinum* L.)

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Abstract: Genetic variability is of prime importance for conservation of plant genetic resources. Existence of considerable amount of diversity for various valuable traits in genetic material of crop plants guarantees the world food security. The present investigation was carried out during 2018-19 at Gram Breeding Research Station, Kallurkot, Pakistan, to estimate the extent of variability and to identify the elite chickpea strains with better genetic constitution. Twenty elite genotypes were evaluated to sort out the better strains possessing valuable genetic makeup. The collected data was subjected to analysis of variance, principle component analysis (PCA) and cluster analysis. PCA revealed that first two principle components extracted more than 1 Eigen values contributing 56.63 and 22.90 percent respectively in total variability. Higher positive loadings were expressed by number of pods, 100 seed weight and yield kg ha^{-1}. Cluster analysis distinguished genotypes into four clusters. Dendrogram constructed on the basis of Euclidean distance showed that the members of cluster I and II possess higher genetic variation. Results also confirmed that the genotypes D-17006, D-17016 and Punjab-08 falling in cluster II were more diverse and high yielding. Therefore, genotypes of both clusters may be utilized in breeding program however, the members of cluster-II may be prefered for use as parents in chickpea hybridization program.
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Introduction

Chickpea (*Cicer arientinum* L.) commonly known as gram, is also familiar with local names as Garbenzo bean, Bengal gram, Hamaz and Channa around the world (Ladizinsky and Adler, 1976; Lev-Yadun *et al*., 2000). Its grains are rich sources of various minerals, carbohydrates and several essential amino acids (Upadhyaya *et al*., 2007; Rajeev *et al*., 2019; Mohammdi, 2019 and Rybinski *et al.,* 2019). Chickpea plays a very important role in the farming system and is being grown in various tropical and sub-tropical countries around the globe (Islam *et al*., 2008; Govindaraj *et al*., 2015; Muehlbauer et al., 2017; Annicchiarico *et al*., 2018). Traditional chickpea varieties have narrow genetic base, less adaptable to wide range of environments and vulnerable to various abiotic and biotic stresses therefore, continuous breeding efforts are required to evolve new improved, better performing varieties (Atta *et al*., 2008; Gupta *et al*., 2011; Islam *et al*., 2008; Talebi and Rokhzadi, 2013; Chen *et al*., 2017 and Mahmood *et al.,* 2018).

Pattern of genetic variability differ among genotypes, so extent of diversity and its sources is direly needed for effective utilization of such genomic resources in crop breeding programs (Gupta *et al*., 2011; Pavan *et al*., 2017; Nadeem *et al*., 2018; Varshney *et al*., 2018). Variability among genetic resources of crop plants in performance of various valuable traits serves as important resource for evolution of new varieties through hybridization program (Sharifi *et al*., 2018 and Rybinski *et al.,* 2019).

Genetic diversity among parental material provides fundamental basis to help the researchers in classification of genetic resources and to identify the appropriate types from a mixed population (M. Farshadfar and E. Farshadfar, 2008; Parameshwarappa *et al*., 2011; Talebi and Rokhzadi, 2013; Varshney et al., 2019). Variability studies among genotypes helps the breeders by providing more choices for selection of desired plant types and to devise effective crop improvement strategies (Chowdhury *et al*., 2002; Gupta *et al*., 2011).

Several researchers extensively utilized the principle component analysis (PCA) and cluster analysis techniques to estimate the variability and to identify the groups of genotypes contributing towards genetic variation (Upadhyaya *et al*., 2007; Gupta *et al*., 2011; Talebi and Rokhzadi, 2013; Chen *et al*., 2017; Sharifi *et al*., 2018 and Arora *et al.,* 2018). The present study was planned to generate information on genetic variability and to identify the promising chickpea genotypes with desirable genetic constitution.

Materials and Methods

Present research on genetic variability was conducted at Gram Breeding Research Sub-Station, Kallurkot, Punjab, Pakistan (71.153°E, 32.923°N) during the rabi season of 2018-19. Experimental content of 18 elite strains (D-17002, D-17003, D-17005, D-17006, D-17007, D-17009, D-17010, D-17014, D-17015, D-17016, D-17019, D-17027, D-17028, D-17029, D-17030, D-17031, D-17035) and two standard varieties (Punjab-08 and Bittle-2016) was sown under tri-replicated randomized complete block design during the first week of November in 2018. Each entry was sown in experimental plot measuring 4 meter in length with 4 rows having 30 cm row to row spacing. Sowing was done manually by dibbler by maintaining 10 cm plant to plant spacing. At pod formation stage Insecticide Emamectin @ 750 ml ha^{-1} was sprayed twice to avoid pod borer (*Helicoverpa armigera*) attack. Data for primary branches, secondary branches, days to 90% maturity, pods plant-1, 100 seed weight (g) and yield kg ha^{-1} was recorded for each experimental genotype.

Data recoded were subjected to analysis of variance following steel et al., 1997. While principal component analysis (PCA) and cluster analysis by STAR (Statistical Tool for Agricultural Research version 2.0.1)

Results and Discussion

Results concerning the mean performance of various chickpea traits have been shown in Table 1. The final grain yield ranged between 270-706 kg ha^{-1}. The other morpho-yield traits i.e. 100 seed weight ranged among 23.33-27 grams and pods $plant^{-1}$ were recorded from 31.33-75.65. Highest final grain yield was recorded in D-17006 (706 kg ha^{-1}) followed by D-17016 (653 kg ha^{-1}) and Punjab 2008 (633 kg ha^{-1}). Variance analysis revealed significant differences among all the included traits (Table 2). Higher values of coefficient of variation indicated that a considerable amount of variation exists among the studied genotypes. Results are in line with Dwevedi and Lal (2009) and Syed *et al*. (2012).

Table 1. Mean performance various elite chickpea strains

Genotypes	PB	SB	DM	NPP	SW	YLD
Bittle-2016	4.33	4.33	164.67	39.67	23.33	376
D-17002	3.67	6.33	160.00	64.00	25.33	590
D-17003	3.33	5.67	159.67	62.00	25.00	626
D-17005	2.67	5.33	163.33	53.00	24.67	536
D-17006	4.33	7.33	165.67	75.67	27.00	706
D-17007	3.67	5.67	166.67	32.67	23.33	536
D-17009	2.33	4.67	160.33	31.33	21.67	270
D-17010	3.33	5.33	162.67	56.00	23.67	243
D-17014	3.67	4.33	161.33	50.00	24.67	588
D-17015	3.67	5.67	163.33	57.33	24.67	453
D-17016	2.67	6.33	167.00	64.33	26.67	653
D-17019	3.33	5.33	158.67	59.33	26.33	613
D-17021	2.67	4.67	161.00	43.33	23.67	400
D-17027	2.67	5.67	167.00	48.67	24.67	486
D-17028	2.33	4.67	166.67	45.67	23.00	408
D-17029	2.33	5.33	167.00	51.33	24.00	478
D-17030	3.33	4.33	164.33	46.33	23.67	380
D-17031	3.67	5.33	163.67	58.00	25.33	560
D-17035	3.67	5.33	163.00	55.00	25.67	546
Punjab-08	4.33	6.33	164.67	59.67	26.00	633
CV	20.96	13.26	4.78	5.32	2.50	10.29

(PB = Primary branches, SB = Secondary branches, DM= Days to maturity, PH = Plant height at maturity, NPP= number of pods $plant^{-1}$, SW= 100 Seeds weight, YLD = Yield kg ha^{-1})

Table 2. Mean Square values of different traits of chickpea strains.

Source	DF	Primary Branches	Secondary Branches	Days to Maturity	Pods plant^{-1}	100 Seed Weight	Yield Kg ha^{-1}
Reps	2	3.05000	6.06667	5.0667	7.0565	0.81667	3343
Genotypes	19	21.6632**	1.84561**	21.6632**	273.378**	5.48333**	160841**
Error	38	0.4359	0.2095	61.200	5.461	0.2321	752
Total	59						

Principle component analysis employed for exploration of genetic diversity classified the genotypes into six PCs. Results regarding PCA revealed that a sufficient amount of variation was contributed by first two components (Table 3). Similar conclusions were previously reported by Ghafoor *et al*., 2003; Malik *et al*., 2014 and Arora *et al.,* 2018. First and second components extracted > 1 Eigen values (3.2980 and 1.3742 respectively) denoting that maximum variation was added by these both PCs (Fig 1). PC1 and 2 cumulatively explained 79.54 percent among 20 genotypes. Results are in line with previous researchers who reported more than 70 percent contribution of first two PCs in total variation (Upadhyaya *et al*., 2007; Talebi and Rokhzadi, 2013; Sharifi *et al*., 2018).

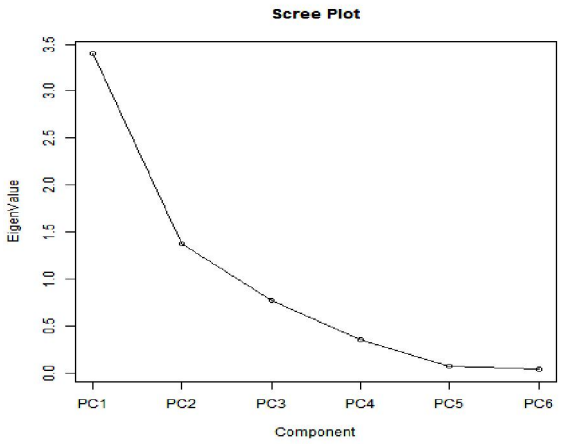

Fig 1. Scree plot showing Eigean values against the respective PCs

Table 3. Principal component analysis of chickpea strains.

Principal component	Eigen value	Percentage of variance	Cumulative percentage of variance
PC 1	3.3980	56.63	56.63
PC 2	1.3742	22.90	79.54
PC 3	0.7714	12.86	92.39
PC 4	0.3493	5.82	98.21
PC 5	0.0716	1.19	99.41
PC 6	0.0355	0.60	100

Scores of principle components against studied traits have been given in Table 4. Results also showed that 100 seed weight (g), yield kg ha^{-1}and pods plant^{-1} extracted significant positive loading (0.523, 0.507 and 0.470 respectively) in PC1. Moreover, extracted positive loadings in PC2 indicating that these traits are more influential in contribution of genetic variability. Biplot among PC1 and PC2 also depicted that the vectors for 100 seed weight (g), yield kg ha^{-1}and pods plant^{-1} reflect that these traits have considerable contribution in determination of variability (Fig 2). From PCA results it is also evident that selection of parental types from first two components will be more beneficial for a successful chickpea breeding program.

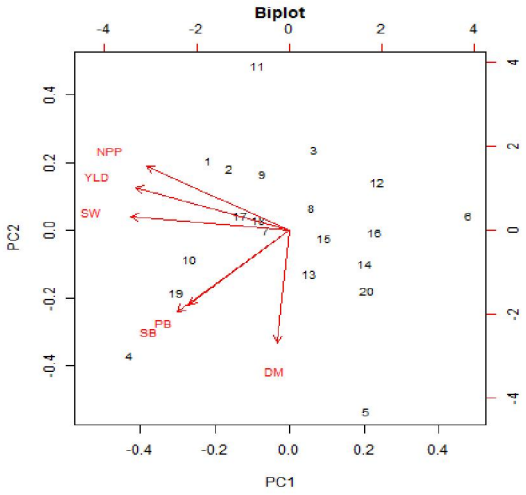

Fig 2. Biplot among PC1 and PC2

Table 4. Extraction method of variable in PCA

Trait	PC1	PC2	PC3	PC4	PC5	PC6
Primary branches	-0.332	-0.423	0.567	-0.615	-0.108	-0.004
Secondary branches	-0.371	-0.463	0.226	0.752	-0.107	-0.102
Days to maturity	-0.041	-0.639	-0.737	-0.205	-0.073	0.009
Pods plant^{-1}	0.470	-0.363	-0.219	-0.115	0.456	-0.616
100 seed weight	0.523	0.081	-0.118	-0.027	0.831	-0.122
Grain yield	0.507	0.247	-0.153	0.003	0.251	0.772

Cluster analysis distributed the genotypes in four separate clusters on the basis of similarity in performance of studied traits (Table 5). Studies revealed that eight genotypes (D-17002, D-17003, D-17005, D-17010, D-17015, D-17019, D-17031, D-17035) were grouped in Cluster-I. Similarly D-17006, D-17016 and Punjab-08 were assembled in cluster-II. Cluster-III included six genotypes (D-17007, D-17009, D-17014, D-17021, D-17030 and Bittle-2016) while three genotypes (D-17027, D-17028, D-17029) were grouped under cluster-IV.

Dendrofram was also constructed on the basis of Euclidean distance (Fig 3). Dendrogram illustrated that members of cluster-I and II were more diverse in performance of various traits therefore selection of genotypes from these clusters will be more valuable for chickpea improvement program. Similar results were previously reported by Ghafoor *et al*., 2003; Pavan *et al*., 2017; Mahmood *et al.,* 2018 and Sharifi *et al*., 2018 in agreement to this study. Results also revealed that the members of cluster-II (D-17006, D-17016 and Punjab-08) were divese and high yielding therefore they may given preference while making selections for a successful breeding program.

Table 5. Cluster membership of various chickpea elite strains

Cluster	Members
I	D-17002, D-17003, D-17005, D-17010, D-17015, D-17019, D-17031, D-17035
II	D-17006, D-17016 and Punjab-08
III	D-17007, D-17009, D-17014, D-17021, D-17030 and Bittle-2016
IV	D-17027, D-17028, D-17029

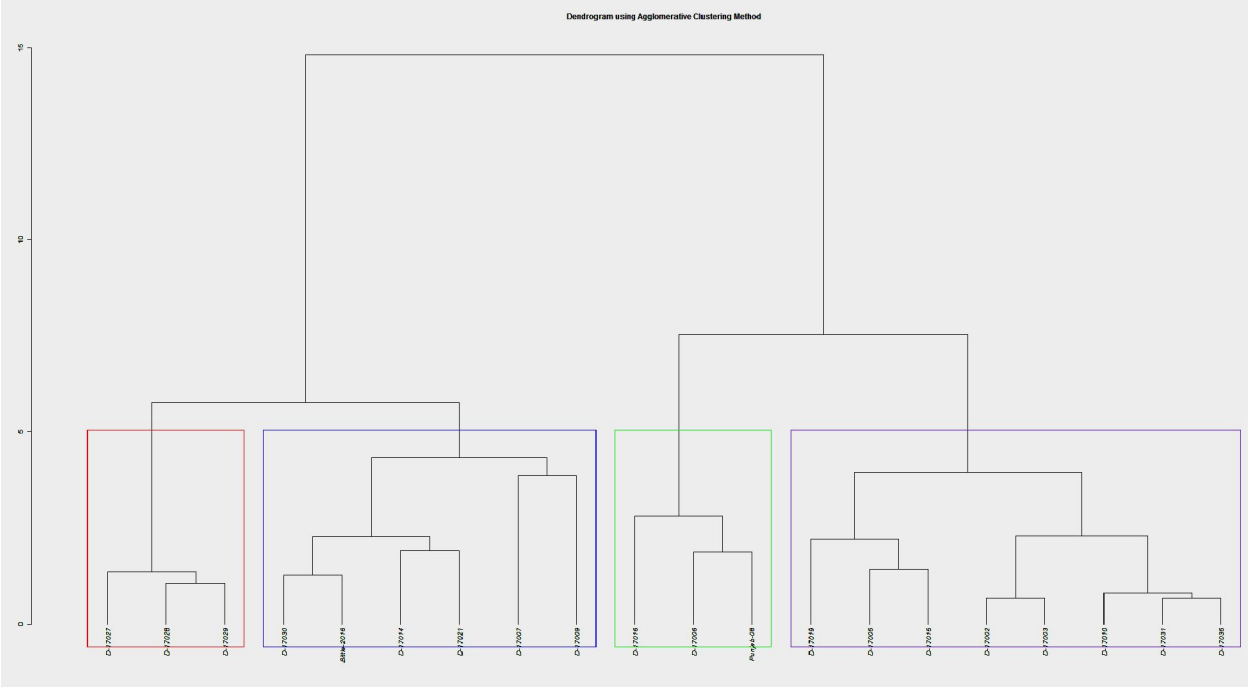

Fig 3. Ward's Dendrogram showing the member of various clusters.

Conclusion

In conclusion, our findings on principle component analysis are evident that maximum amount of genetic variability was contributed by first two components and selection of parental types from these components will be more beneficial. Cluster analysis of genotypes demonstrated that the members of cluster-I and II are most diverse. However, the genotypes in cluster-II (D-17006, D-17016 and Punjab-08) are diverse and high yielding so they may be favored while making selections for a successful chickpea breeding program.

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