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Research Article

Multivariate Analysis for QuantitativeCharacteristics of Chickpea (*Cicer arietinum* L.) Genotypes at Central Highland of Ethiopia

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Forty-nine kabuli chickpea experimental materials were studied at Debre Zeit and Akaki, Ethiopia with the objective of estimating genetic divergence among the genotypes and clustering them into genetically divergent class using multi-variate analysis technique in 2019 cropping season. Cluster analysis showed the 49 genotypes grouped into three clusters and one solitary. This implies that the genotypes used for the study were moderately divergent. The maximum distance was found between clusters II and IV followed by cluster III and IV. The minimum distance was found between cluster II and I. The first four principal components with eigenvalues greater than one explain about 74.3% of the total variation. Genotype DZ-2012-CK-0290 from cluster I for grain yield and number of primary branch, DZ-2012-CK-0242 for high biological yield from cluster II; DZ-2012-CK-0249 for seed size from cluster III; DZ-2012-CK-0309 for early flowering and maturity from cluster III and DZ-2012-CK-0291 for number of seeds per pod, number of seeds per plant could be utilized in hybridization program for kabuli chickpea improvement.

Key words: Chickpea, genetic diversity, cluster analysis, principal component analysis

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INTRODUCTION

Chickpea (*Cicer arietinum* L.) is a self-pollinated, diploid (2n = 2x = 16) chromosome and belongs to the family *Leguminoseae*. It is the only cultivated species within genus *Cicer* and grown in the cool semi-arid areas of the tropics, sub-tropics as well as the temperate areas (Van der Maesen, 1987; Atta and Shah, 2009).Two types of chickpea are known, namely kabuli and desi. The desi type chickpeas are characterized by small seed size of various colors, angular seed shape, pink flowers, anthocyanin pigmentation of stem, rough seed surface, either semi-erect or semi-spreading growth habit (Wood et al., 2012). whereas the Kabuli types generally characterized by large seed size with whitish-cream or beige color, have large owl shaped seeds, white flowers, smooth seed surface, lack of anthocyanin pigmentation and semi-spreading growth habit (Moreno and Cubero, 1978; Pundir et al., 1991).

Chickpea is one of the major pulses grown in Ethiopia usually under rain fed conditions. It is grown widely across the highlands and semi-arid regions of the country (Bejiga and van der Maesen, 2006; CSA, 2019). The crop provides an important source of food and nutritional security for the rural poor, especially those who cannot afford costly livestock products as source of essential proteins (Legesse et al., 2005). The consumption of chickpea is also increasing among the urban population mainly because of the growing recognition of its health benefits(Milner, 2000; Hasler, 2002; Kerem et al.,2007;

Jukanti et al., 2012). Chickpea contributes about 25 % of the pulse export volume.The exported volume accounts about 22.74 % of the total quantity of chickpea production while the balance remains for food, feed or seed and local market (ERCA, 2017; Ferede et al., 2018)..

Major constraints in achieving high yield potential are the low genetic diversity for yield, yield components, resistance against major diseases and abiotic stresses (Gaur et al., 2014). In any plant breeding program aimed at genetic amelioration of yield, the knowledge of genetic diversity is the basic requirement for the improvement of crop plants and used for efficient parental genotype selection to exploit maximum heterosis (Arumuganathan and Earle, 1991; Singh, 2002; De Vicente et al., 2005). Principal component and cluster analysis procedures were found to be efficient to assess genetic diversity for agro-morphological traits.Cluster analysis refers to a multivariate statistical analysis technique used to partition a set of objects into groups based on the characteristics they possess.PCA used to identify and minimize the number of traits for effective selection and improvement of yield and its related trait (Chahal and Gosal, 2002; Singh, 2002).

The extent of diversity present between genotypes determines the extent of improvement gained through selection and hybridization (Singh, 2002).Therefore, the present study was carried out to assess the amount of the genetic diversity in kabuli chickpea genotypes using multivariate techniques based on morpho-genetic parameters and to identify the potential genotypes for future utilization in chickpea breeding programs

MATERIALS AND METHODS

The experiment was conducted under field condition during 2019 main cropping season at Debre Zeit Agricultural Research Center and Akaki research station. Forty-nine genotypes of kabuli chickpea (Table 1.) obtained from Highland Pulse Research Program, Debre Zeit Agricultural Research Center (DZARC) were grown in a simple lattice design. Planting was done by hand drilling with spacing of 0.3m and 0.1m between rows and plants, respectively. Each plot had four rows of 4m length and 1.2m width. The spacing between blocks was 1m and 0.6m distance was kept between plots to separate two genotypes. Thinning after emergency was done to maintain intra-row spacing. Fertilizer was not applied while recommended crop management practices were done throughout the growing season.

Data were recorded on randomly tagged plants and plot basis for days to 50% flowering, grain filling period, days to maturity, biological yield, hundred-seed weight, grain yield, harvest index, plant height, number of primary branches, number of secondary branches, number of pods per plant, number of seeds per pod and number of seeds per plant. Genetic divergence analysis were computed based on D^2 statistic (Mahalanobis, 1936) and the genotypes were grouped into different clusters according to Tocher's method as described by Rao (1952) using SAS statistical software. The intra and inter-cluster distances were estimated according to the method described by Singh and Choudhary (1985). The principal component analysis was done to identify the characters contributing more to the total variation using correlation matrix.

Table 1. List of experimental material used for the study

No	Genotypes	Status	No	Genotype	Status
1	DZ-2012-CK-0260	Pipeline	26	DZ-2012-CK-0259	Pipeline
2	DZ-2012-CK-0261	Pipeline	27	DZ-2012-CK-0264	Pipeline
3	DZ-2012-CK-0265	Pipeline	28	DZ-2012-CK-0263	Pipeline
4	DZ-2012-CK-0268	Pipeline	29	DZ-2012-CK-0271	Pipeline
5	DZ-2012-CK-0273	Pipeline	30	DZ-2012-CK-0287	Pipeline
6	DZ-2012-CK-0275	Pipeline	31	DZ-2012-CK-0282	Pipeline
7	DZ-2012-CK-0277	Pipeline	32	DZ-2012-CK-0276	Pipeline
8	DZ-2012-CK-0279	Pipeline	33	DZ-2012-CK-0266	Pipeline
9	DZ-2012-CK-0281	Pipeline	34	DZ-2012-CK-0291	Pipeline
10	DZ-2012-CK-0283	Pipeline	35	DZ-2012-CK-0243	Pipeline
11	DZ-2012-CK-0284	Pipeline	36	DZ-2012-CK-0309	Pipeline
12	DZ-2012-CK-0285	Pipeline	37	DZ-2012-CK-0274	Pipeline
13	DZ-2012-CK-0286	Pipeline	38	DZ-2012-CK-0278	Pipeline
14	DZ-2012-CK-0288	Pipeline	39	DZ-2012-CK-0300	Pipeline
15	DZ-2012-CK-0242	Pipeline	40	DZ-2012-CK-0290	Pipeline
16	DZ-2012-CK-0244	Pipeline	41	DZ-2012-CK-0280	Pipeline
17	DZ-2012-CK-0061	Pipeline	42	DZ-2012-CK-0310	Pipeline
18	DZ-2012-CK-0305	Pipeline	43	DZ-2012-CK-0272	Pipeline
19	DZ-2012-CK-0246	Pipeline	44	DZ-2012-CK-0303	Pipeline

Continuation of Table 1

20	DZ-2012-CK-0065	Pipeline	45	DZ-2012-CK-0294	Pipeline
21	DZ-2012-CK-0249	Pipeline	46	DZ-2012-CK-0306	Pipeline
22	DZ-2012-CK-0064	Pipeline	47	DZ-2012-CK-0220	Pipeline
23	DZ-2012-CK-0178	Pipeline	48	Ejere	Released variety
24	DZ-2012-CK-0248	Pipeline	49	Hora	Released variety
25	DZ-2012-CK-0269	Pipeline			

RESULTS AND DISCUSSION

Clustering analysis

The D^2 values based on pooled mean of genotypes over the two location resulted in classifying the 49 chickpea genotypes into three clusters and one solitary (Table 2 and Figure 1). This indicate the tested genotypes were moderately divergent. This must probably stems from the fact that most genotypes were developed through limited hybridization and selection. This finding is similar to that of Hajibarat et al. (2014) who classified forty-eight chickpea genotypes in to four clusters.

Cluster I was the largest which consist of maximum twenty-five genotypes; that is 51% of the genotypes evaluated. The genotypes in this cluster had narrow genetic divergence among them. These may be due to the similarity in the base population from which they had been involved. The second cluster comprised twenty kabuli chickpea test genotypes with 40.8 percent proportion. Three genotypes with proportion of 6.12% made cluster III while genotype DZ-2012-CK-0291 remain solitary and form cluster IV.

Table 2. Distributionof chickpea genotypes in different clusters based on quantitative traits

Cluster	Number of genotypes	Proportion	Name of the genotypes
I	25	51.02	DZ-2012-CK-0269,Hora, DZ-2012-CK-0281, DZ-2012-CK-0305, DZ-2012-CK-0248, DZ-2012-CK-0274, DZ-2012-CK-0283, DZ-2012-CK-0284, Ejere , DZ-2012-CK-0265, DZ-2012-CK-0288, DZ-2012-CK-0306, DZ-2012-CK-0290, DZ-2012-CK-0303, DZ-2012-CK-0294, DZ-2012-CK-0259, DZ-2012-CK-0287,DZ-2012-C K-0285, DZ-2012-CK-0286, DZ-2012-CK-0275, DZ-2012-CK-0272, DZ-2012-CK-0065, DZ-2012-CK-0220, DZ-2012-CK-0277, DZ-2012-CK-0282

Table 2. continuation

II	**20**	**40.82**	**DZ-2012-CK-0264, DZ-2012-CK-0178, DZ-2012-CK-0061, DZ-2012-CK-0278, DZ-2012-CK-0246, DZ-2012-CK-0273 DZ-2012-CK-0280, DZ-2012-CK-0279, DZ-2012-CK-0064, DZ-2012-CK-0261, DZ-2012-CK-0242, DZ-2012-CK-0243 DZ-2012-CK-0249, DZ-2012-CK-0244, DZ-2012-CK-0276, DZ-2012-CK-0263, DZ-2012-CK-0271, DZ-2012-CK-0266, DZ-2012-CK-0268, DZ-2012-CK-0260**
III	3	6.12	DZ-2012-CK-0300, DZ-2012-CK-0310, DZ-2012-CK-0309
IV	1	2.04	DZ-2012-CK-0291

Distance analysis

The distance analysis reveal that there was statistically significant difference among all the clusters as tested by chi-square distribution (Table 3.). The maximum distance was found between clusters II and IV followed by between cluster III and IV. This implies that crosses between parents extracted out of them are expected to result in good level of genetic recombination and generate desirable segregants with broad genetic base. Therefore selection in segregating generations of these crosses seems to give promising results. The minimum distance was found between cluster II and Ifollowed by cluster III and I indicating minimal difference among genotypes between those clusters.

Table 3. Average intra and inter cluster distance values in chickpea genotypes

Cluster	CL I	CL II	CL III	CL IV
CL I	**1.35**	24.60*	31.22**	51.30**
CL II		**1.79**	54.10**	115.96**
CL III			**5.59**	78.88**
CL IV				**0.00**

* and ** significant at 0.05 and 0.01 probability level of chi-square(x^2) test, respectively.

Mean values of clusters

The mean performance of genotypes in each cluster for the 13 quantitative characters is presented in Table 4. The first cluster (CL I) was characterized by the highest grain yield, number of pod per plant, number of secondary and primary branches. The second cluster (CL II) was characterized by the highest biological yield, plant height, days to maturity and days to flowering. This cluster was also characterized by lowest grain filling period, number of seeds per pod and harvest index. The third cluster (CL III) was characterized by the highest harvest index and hundred seed weight. This cluster was also characterized by the lowest number of days to flowering, days to maturity, number of pod per plant and number of seed per plant. The fourth cluster (CL IV) was characterized by the highest number of seed per pod, number of seeds per plant and grain filling period. And also this cluster had the lowest number of primary branch, number of secondary branch, biomass and grain yield.

Generally these results indicated that parents for different desirable traits can be easily chosen from clusters based on their merit. For example, genotype DZ-2012-CK-0290 can be chosen from cluster I for grain yield and number of primary branch; DZ-2012-CK-0242 for high biological yield from cluster II; DZ-2012-CK-0249 for maximum hundred seed weight (seed size) from cluster III; DZ-2012-CK-0309 for early flowering and maturity time from cluster III and DZ-2012-CK-0291 for number of seeds per pod, number of seeds per plant. These genotypes could be utilized in hybridization program for kabuli chickpea improvement.

Table 4. Cluster mean values for different traits in chickpea genotypes

Traits	CL I	CL II	CL III	CL IV
DF	53.71	61.46	45.67	51.75
DM	121.07	124.94	116.42	119.50
GFP	65.53	63.31	66.83	67.25
PLHT	48.73	51.11	43.48	45.00
NPB	3.21	3.06	2.77	2.63
NSB	8.43	8.30	8.40	4.15
NPP	34.94	30.21	22.47	33.55
NSPP	41.39	33.79	25.27	46.45
NSP	1.18	1.12	1.15	1.24
BY	5840.67	6121.56	4737.50	4533.21
HSW	33.79	36.41	37.95	25.20
GY	3082.36	2544.07	2713.56	2181.67
HI	52.55	41.14	57.07	48.12

DF =days to flowering, DM = days to maturity, GFP = grain filling period, PLHT= plant height, NPB = number of primary branches, NSB = number of secondary branches, NPP = number of pod per plant, NSPP = number of seed per plant, NSP = number of seed per pod, BY = biological yield, HSW = hundred seed weight, GY = grain yield, HI = harvest index.

Principal component analysis

Principal component analysis showed that the first four principal components with eigenvalues greater than one (3.6569, 2.6899, 2.2396 and 1.0705) explain about 74.3% of the total variation among 49 chickpea genotypes (Table 5). Similar results for percentage of total variation explained by the first four PCs were reported by Temesgen et al. (2015).

The first principal component accounted for about 28.5% of the total variations. Traits such as days to flowering, harvest index, days to maturity, number of seed per pod, number of seeds per plant, number of pod per plant and hundred seed weight had high contribution to the total variation of the populations into clusters. Similarly, the high contribution of number of pod per plant, hundred seed weight and number of seed per pod in the first principal component were reported by Arora *et al*. (2018). The second component accounting for about 20.7% of the total variation predominantly illustrates variation in number of primary branch, biological yield, grain yield, number of pod per plant, number of seeds per plant and days to maturity. The third principal component accounted for 17.2% of the total variation and it was chiefly accounted by variation in number of secondary branch, grain yield, harvest index and hundred seed weight. The fourth principal component accounted for only 8.2% of the total variation and indicated with high variation in grain filling period, plant height and days to flowering. Generally, principal component analysis revealed that differentiation of the genotypes into different cluster was due to relatively high contribution of a number of character rather than smaller contribution of all characters. Thus trait such as days to flowering, days to maturity, number of pod per plant, hundred seed weight, number of seed per pod, harvest index and number of seed per plant in the first principal component contribute more for clustering.

Table 5. Eigenvectors, eigenvalues and percentage of total variance explained by the first four principal components (PC)

Trait	PC1	PC2	PC3	PC4
DF	-0.360	0.239	-0.235	-0.335
DM	-0.321	0.300	-0.209	0.085
GFP	0.184	-0.036	-0.061	0.687
PLHT	-0.260	0.176	-0.215	0.407
NPB	-0.048	0.446	0.225	-0.045
NSB	-0.064	0.206	0.466	-0.180
NPP	0.303	0.340	-0.229	-0.218

Table 5 Continuation

NSPP	**0.353**	**0.339**	**-0.250**	**-0.113**
NSP	0.342	0.060	-0.265	0.151
BY	-0.165	0.456	0.119	0.276
HSW	-0.327	-0.131	0.323	0.131
GY	0.218	0.343	0.406	0.167
HI	0.380	-0.042	0.339	-0.057
Eigenvalue	3.6569	2.6899	2.2396	1.0705
Proportion	28.1	20.7	17.2	8.2
Cumulative	28.1	48.8	66	74.3

DF =days to flowering, DM = days to maturity, GFP = grain filling period, PLHT= plant height, NPB = number of primary branches, NSB = number of secondary branches, NPP = number of pod per plant, NSPP = number of seed per plant, NSP = number of seed per pod, BY = biological yield, HSW = hundred seed weight, GY = grain yield, HI = harvest index.

CONCLUSIONS AND RECOMMENDATIONS

Generally this study showed that parents for different desirable traits can be easily chosen from clusters based on their merit. For example, genotype DZ-2012-CK-0290 can be chosen from cluster I for grain yield and number of primary branch; DZ-2012-CK-0242 for high biological yield from cluster II; DZ-2012-CK-0249 for maximum hundred seed weight (seed size) from cluster III; DZ-2012-CK-0309 for early flowering and maturity time from cluster III and DZ-2012-CK-0291 for number of seeds per pod, number of pods per plant, number of seeds per plant. These genotypes could be utilized in hybridization program for kabuli chickpea improvement.principal component analysis revealed that trait such as days to flowering, days to maturity, number of pod per plant, hundred seed weight, number of seed per pod, harvest index and number of seed per plant in the first and/or second principal component showed higher absolute values of eigenvectors.This indicated that these traits had higher contributions to thetotal variation of the genotypes into clusters and selection efforts based on these traits may be more effective.

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