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Evaluation of variations in chickpea *(Cicer arietinum* L.) yield and yield components by multivariate technique

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ABSTRACT

To estimate the extent of genetic diversity of 25 chickpea genotypes, an experiment was carried out based on randomized complete block design with four replications at Brojerd Agricultural Research Station during two seasons of 2012–2013 and 2013–2014. The first three principal components (PCs) explained 69.69% variation. Four groups of characters were distinguished in regard to first (PC1) and second (PC2) principal components. Factor analysis indicated that three main factors accounted 69.69% of the total variability. Three first factors accounted for 33.69%, 20.82% and 15.19% of total variability, respectively and the terms proposed for factors were 'phenological traits', 'morphological traits' and 'yield components'. Communalities indicated that studied traits were reliable and ranged from 0.537 (canopy height) to 0.881 (seed yield). Two-dimensional ordination biplot indicated positive correlation between seed yield, pods per plant, canopy width, harvest index and biological yield. Cluster analysis grouped 25 genotypes into two main groups and four clusters. At a distance of 5, the 11 traits examined formed into two clusters. These findings can be used in breeding strategies for future hybridization programs for yield improvement and are appropriate for classification of diversity among chickpea germplasm.

Introduction

Pulses, such as chickpea (*Cicer arietinum* L.), as dry seeds of leguminous, are an important sources of human regimen throughout the world [1]. The genetic diversity of genotypes makes them an important resource of genes for breeding programs, developing new farming systems, diversification of production and new quality products [2]. Information about genetic diversity helps the selection of parental genotypes from random populations. Accurate estimation of the levels and patterns of genetic diversity is useful to estimate the potential of heterotic combinations before attempting crosses and hence saving time and resources [3]. Such information can serve for introgression of desirable genes from wild germplasm to the high yielding germplasm resource [4], analysis of genetic variability in germplasm [5] and identification of different combinations for creating segregating progenies with greatest genetic variability [6].

Multivariate analysis techniques are series methods for study genotypes diversity such as principal component (PCA), cluster and factor analyses. These techniques can be utilized for identifying groups of genotypes that have beneficial traits for breeding and instructing the patterns of variation in genotype accession, to recognize relationships between genotypes [7]. The differences between factor and principal components analyses is that factor analysis finds the main factors, but principal components analysis summarizes the variability between original data [8].

Some researchers studied chickpea genotypes by multivariate analysis. Malik et al. [9] studied twenty chickpea genotypes and classified the genotypes in three clusters based on Euclidean dissimilarity. Malik et al. [10] studied genetic diversity of 113 *desi* chickpea genotypes by descriptive, cluster and principal component analyses and indicated the first four principal components accounted 71.99% of total variation. Pods per plant, secondary branches, biological yield, plant height, and seed yield displayed

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positive relation with PC1. Hundred seed weight, number of days to flowering and number of days to maturity indicated positive correlation with PC2. Farshadfar and Farshadfar [11] classified 360 chickpeas genotypes into four clasters and indicated the 63% of total variance explained by five first principal components. Ghorbani et al. [12] studied the relationships between seed yield and its components in 23 chickpea genotypes and indicated that five factors explained 81.65% of total variance by factor analysis. Talebi and Rokhzadi [13] studied 40 landrace of chickpea and indicated the first four principal components contributed 82.7% of total variability. Toker and Cagirgan [14] studied yield criteria in chickpea by phenotypic correlations and factor analysis and indicated factor 1 comprised of plant height, biological yield, seed yield and harvest index. Factor 2 consisted of branches and pods per plant. Factor 3 enclosed of only seed weight. These three factors explained 92.9% of total variation. Alipoor Yamchi et al. [15] studied 64 genotypes of Kabuli chickpea and indicated that four factors were explained 79% of total variation. The first and second factors were explained high percent of variation that including hundred seed weight, pod length, plant height, pod diameter, seed length, seed diameter, seed and pod weight, biological yield, grain yield and main branch diameter. The genotypes were classified in five clusters. The genotypes of third and fourth cluster had high yield and earliness in compare with the other clusters.

The present study was carried out to estimate the extent of genetic diversity in 25 chickpea genotypes by multivariate analysis, which will help to select prospective parents to develop transgressive segregates.

Objectives and methods

Field experiments

Twenty five chickpea (*Cicer arietinum* (L.)) genotypes (Table 1) were grown under dryland condition at Brojerd Agricultural Research Station (west of Iran) during two growing seasons of 2012–2013 and 2013–2014. The experiment was carried out based on a randomized complete block design (RCBD) with four replications, using 30 × 10 cm spacing and four-row plots of four m length. The size of plot was 1.2 × 4 m rows (4.8 m^2). Plants were fertilized with 35 kg ha^{-1} nitrogen from Urea and 70 kg phosphorus ha^{-1} from Super Phosphate Triple. All recommended agronomic practices were followed for raising good crop.

Some of traits including seed yield (SY), number of days to flowering (DF), number of days to maturity (DM), flowering period (FP), canopy height (CH), canopy width (CW), pods per plant (NPP), seeds per pod (NSP), hundred seed weight (HSW), biological yield (BY) and harvest index (HI) were measured in every years. Yield was recorded on basis of plot and then was converted to kg ha^{-1}.

Table 1
Name and origin of chickpea genotypes.

Entry number	Name/cross	Origin
1	215171	Iran
2	215296	Iran
3	215551	Iran
4	215618	Iran
5	215654	Iran
6	215664	Iran
7	215671	Iran
8	215686	Iran
9	215767	Iran
10	215843	Iran
11	215940	Iran
12	215941	Iran
13	215995	Iran
14	216001	Iran
15	216066	Iran
16	216084	Iran
17	216324	Iran
18	216325	Iran
19	216364	Iran
20	216368	Iran
21	215685–1	Iran
22	215685–2	Iran
23	Arman	Iran
24	AZad	Iran
24	Hashem	Iran

Statistical analysis

The following statistical model was adopted for experimental design:

$$Y_{ijkl} = \mu + E_i + R(E)_{j(i)} + G_k + GE_{ik} + e_{ijk}$$

Where, μ: general mean; E_i: effect of ith environment (i = 1, 2); $R(E)_{j(i)}$: effect of jth block within the ith environment (j = 1, 2, 3, 4); G_k: effect of kth genotype (I = 1, 2, … … …..25); GE_{ik}: effect of the interaction of the kth genotype with the ith environment; e_{ijk}: experimental error.

Principal component, factor and cluster analyses were executed on 25 genotypes of chickpea across both growing seasons by SPSS 17. The graphs were drawn also *via* SPSS 17 and Excel.

Results and analysis

Principal component analysis

Multivariate analysis of variance indicated significant differences between average vectors. Principal component analysis across two seasons is presented in Tables 2 and 3. PCA was carried out in order to describe and gain better understanding sources of variance among chickpea genotypes. Principal component analysis also lowers the number of traits responsible to the maximum percentage of total variation of the experimental data. Eleven principal components (PCs) axes are shown in Table 2 and Fig. 1. A trait with coefficient greater than 0.3, had large enough effect and was considered as an important trait. Traits having less than 0.2 coefficient value were considered to be no affect to the overall variation [16] The first three PCs explained 69.69% variation among the 25 genotypes. These results were supported by the finding of previous researchers, who studied chickpea genotypes by PCA [10,17,18] and reported that the first three PCs were the most important in reflecting the variation patterns among genotypes and the traits highly associated with these should be used in

Table 2
Principle component analysis of chickpea genotypes.

PCs	Eigenvalue	% of Variance	Cumulative %
1	4.003	36.390	36.390
2	2.131	19.369	55.759
3	1.532	13.932	69.690
4	.803	7.300	76.990
5	.615	5.593	82.583
6	.597	5.430	88.013
7	.448	4.072	92.085
8	.318	2.888	94.973
9	.286	2.596	97.569
10	.222	2.016	99.585
11	.046	.415	100.000

PCs: Principal components.

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