

INTERRELATIONSHIPS AND GENETIC ANALYSIS OF SEED YIELD AND MORPHOLOGICAL TRAITS IN MINI CORE COLLECTION OF IRANIAN LANDRACE, BREEDING LINES AND IMPROVED CHICKPEA (*Cicer arietinum* L.) CULTIVARS

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Mohammadi K. and R. Talebi (2015): *Interrelationships and genetic analysis of seed yield and morphological traits in mini core collection of Iranian landrace, breeding lines and improved chickpea (Cicer arietinum L.) cultivars*. - Genetika, Vol 47, No. 2, 383-393.

To determine the association between genetic parameters and morphological traits in chickpea (*Cicer arietinum* L.) genotypes, a field experiment was conducted with 49 different landrace, breeding lines and cultivated chickpea genotypes using a 7×7 lattice square design with 2 replications in the 2012-2013 growing season. Genetic parameters including genetic, environmental and phenotypic variances; coefficients of variation; heritability; correlation coefficients; factor analysis and path coefficients were estimated, and cluster analysis was performed. High heritability values observed in measured traits indicating that these traits are controlled mainly by additive genes and that selection of such traits may be effective for improving seed yield. Number of seeds per plant, 100-seed weight and plant biomass had a positive direct effect on seed yield. These traits also had positive and highly significant phenotypic correlations with seed yield. Using principal component (PC) analysis, the first three PCs with eigenvalues more than 1 contributed 70.94% of the variability among accessions. The germplasm were grouped into 3 clusters. Each cluster had some specific characteristics of its own and the cluster I was clearly separated from cluster II and III. Overall the results, it can be concluded that seed yield in chickpea can be improved by selecting an ideotype having greater number of seeds per plant, 100-seed weight and plant biomass.

Key words: chickpea, cluster analysis, heritability, variance components

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is one of the most important grain-legume crops in the world, with the Asia region contributing most to the production, 7.67 million tonnes (Mt) of the 10.38 Mt of the world chickpea production (TALEBI and ROKHZADI, 2013). Chickpea (*Cicer arietinum* L.) is a winter grain legume crop and plays a vital role in the economy of the farming

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communities of the rainfed areas. The major chickpea producing countries in Asia are India, Turkey, Pakistan, and Iran. The region in the present day located between South-eastern Turkey and north-west of Iran and the adjoining areas of Syria has been proposed to be the Vavilovian center of origin for the cultivated chickpea (*Cicer arietinum* L.) (VAN DER MAESEN, 1987; TALEBI *et al.*, 2008). The productivity of chickpea in Iran is low and instable, which may be attributed to the evolution of cultivars with narrow genetic base making them vulnerable to biotic stresses. Cultivar with narrow genetic base emerged due to the extensive use of few and closely related germplasm lines in crop improvement program. Diverse genetic backgrounds of parental lines provide the allelic variation necessary to create favorable new gene combinations. The increasing demand for protein-rich raw materials for forage or intermediary products for human nutrition have led to a greater interest in this crop as a protein source (TALEBI *et al.*, 2007). The genetic diversity among and within landraces makes them a valuable resource as potential donors of genes for breeding purposes, diversification of production, developing new farming systems and new quality products (Jing *et al.*, 2010). Today it is realized that the use of genetically different varieties is an effective strategy in order to minimized genetic vulnerability (FATEHI *et al.*, 2011). Depending on their geographical regions, landraces had specific genetic background that can be used in genetic research program (HARLAN, 1975). In addition, landraces are important genetic resources that improve gene pools of modern cultivars by introducing new alleles (NEVO and PAYNE, 1987). Strategies to increase yield of chickpea would be improved by an understanding of how morpho-agronomic characters interact with one another in affecting yield (BOARD *et al.*, 1999; SADEGHI *et al.*, 2011). Towards a clear understanding of the type of plant traits, correlation, path coefficient and factor analysis are logical steps. Therefore, to fill this knowledge gap, the present investigation was undertaken to ascertain the most important yield-related morphological traits of different germplasm accessions of chickpea and to find out their heritability based on phenotypic and genotypic variation, which could be useful in future breeding programs of chickpea.

MATERIALS AND METHODS

Forty nine chickpea genotypes available in the Iranian National Plant Genetic Bank were evaluated for yield and important morphological traits during 2012-2013. Genotypes include: 16 improved breeding lines were obtained from the International Center for Agricultural Research in the Dry Areas (ICARDA), Aleppo, Syria (Table 1), 28 Iranian landrace chickpea (*Cicer arietinum* L.) accessions from different geographical location of Iran provided by Seed and Plant Improvement Institute, Karaj, Iran, and five improved cultivars (ILC263, Arman, Hashem, ILC3279 and Pirooz) that used in most of chickpea cultivation area of Iran. The experiment was conducted in a 7×7 lattice square design with 2 replications. Plots consisted of three rows, 3 m in length, with 30 cm row spacing and 10 cm between plants. Data on seed yield and other traits were taken and recorded from the two middle rows in each plot.

To determine the relationships between examined traits and seed yield per plant, correlation coefficients were calculated using the STATISTICA program. The path coefficient analysis was performed by examining seed yield per plant as a dependent variable. Phenotypic correlations were determined and factor analysis was performed using STATISTICA software. Nei's genetic distance (NEI, 1973) was determined among the genotypes and used for grouping of the genotypes by UNJ (Un-weighted Neighbor Joining) cluster method (PERRIER *et al.*, 2003). The fit of dendrograms obtained were checked by bootstrapping using 100 replications.

Table 1. List of chickpea accessions used in this study

No.	Genotypes	Source	No.	Genotype	Source
1	Flip00-17C	ICARDA	26	Landrace17	Iran-Esfahan
2	ICCV92311	ICARDA	27	Landrace18	Iran-Jiroft
3	Flip94-30C	ICARDA	28	Landrace19	Iran-Torbat
4	ICCV96325	ICARDA	29	Landrace20	Iran-Karaj
5	ICCV03111	ICARDA	30	Landrace21	Iran-Karaj
6	ILC 263	ICARDA	31	Flipo 03-153c	ICARDA
7	Landrace1	Iran	32	Flipo 03-45c	ICARDA
8	Arman	Iran	33	Flipo 00-14c	ICARDA
9	SEL 93TH	Iran	34	Flipo 03-152c	ICARDA
10	Hashem	Iran	35	Flipo 96-154c	ICARDA
11	Landrace2	Iran-Kerman	36	Flipo 03-38c	ICARDA
12	Landrace3	Iran-Torbat	37	Flipo 03-19c	ICARDA
13	Landrace4	Iran-Karaj	38	Flipo 02-59c	ICARDA
14	Landrace5	Iran-Esfahan	39	Flipo 03-147c	ICARDA
15	Landrace6	Iran-Esfahan	40	ILC 3279	ICARDA
16	Landrace7	Iran-Ardabil	41	Flipo 02-58c	ICARDA
17	Landrace8	Iran-Jiroft	42	Kaka	Iran-Kordestan
18	Landrace9	Iran-Torbat	43	Pirooz	Iran
19	Landrace10	Iran-Ardabil	44	ICC V2	ICARDA
20	Landrace11	Iran-Esfahan	45	C421	Landrace-Cyprus
21	Landrace12	Iran-Shiraz	46	C419	Landrace-Cyprus
22	Landrace13	Iran-Torbat	47	C426	Landrace-Cyprus
23	Landrace14	Iran-Esfahan	48	C412	Landrace-Cyprus
24	Landrace15	Iran-Khoe	49	C425	Landrace-Cyprus
25	Landrace16	Iran-Karaj			

NTSYS ver 2.02 (ROHLF, 1998) and DARwin ver 5.0 (PERRIER and JACQUEMOUD-COLLET, 2006) were used for clustering. Total genetic, phenotypic, and environmental variances, plus broad-sense heritability were calculated following SINGH and CHAUDHARY (1979). Variance components were estimated using expectations as below:

$$EV = MSE$$

$$GV = (MSG - MSE) / r$$

$$PV = (EV + GV) / r$$

where EV, GV and PV are variance components for error, genotype and phenotype, respectively, and MSE and MSG are the observed values of the mean squares for error and genotype, respectively. Broad sense heritability estimates were calculated on entry basis using the following relationship:

$$h^2 = GV / PV$$

The genotypic coefficient of variation (GCV), environmental coefficient of variation (ECV) and phenotypic coefficient of variation (PCV) were calculated using the formulas:

$$GCV = \sqrt{GV / \bar{U}} \times 100$$

$$ECV = \sqrt{EV / \bar{U}} \times 100$$

$$PCV = \sqrt{PV / \bar{U}} \times 100$$

where \bar{U} is the mean value of the particular trait of interest.

RESULTS AND DISCUSSION

Variance analysis and means comparison

Analysis of variance on the studied traits presented in the Table 1, revealed significant differences among genotypes for all the measured characters. The variability between genotypes was high for all traits ($P < 0.01$), indicated that differences existed between the accessions for yield and other yield related traits. The experimental coefficient of variation (CV) varied from 2.5 to 9.5. In general, CV value lower than 20% is considered to be good, indicating the accuracy of conducted experiments. For each of the traits evaluated, descriptive statistics, including mean, minimum, maximum and LSD values are summarized in Table 3. Among traits, grain yield (kg/ha) ranged from 213.89 to 2566.67 with a mean value of 1172.35 kg/ha. High differences between the maximum and minimum mean values were found for all other traits. The high range of variation observed plant biomass, number of seeds per plant, 100-seed weight and plant yield. This considerable variability provides a good opportunity for improving traits of interest in chickpea breeding programs.

Table 2. Mean squares for 8 agronomic traits in 49 chickpea accessions evaluated at Sanandaj, north-west of Iran in 2012-2013.

S.O.V	df	Mean of Square							
		PH	NPB	NSB	SP	SW	BIO	Y	HI
Replicate (R)	1	14.1	6.12	5.2	11.1	10.1	211.7	125.1	218.3
Genotype	48	1125.3**	16.06**	785.7**	258.6**	847.8**	25698.1**	98598.6**	3569.7**
Col × Rep	12	54.1	8.91	4.2	23.1	14.1	258.7	498.1	24.3
Row × Rep	12	114.1	5.96	3.8	44.2	28.3	81458.7**	2598.5	568.3*
Error	24	24.1	1.2	7.4	15.7	19.25	215.9	698.2	55.3
CV (%)		2.5	4.7	6.9	9.5	5.8	4.3	7.5	1.9

PH=plant height; NPB=number of primary branches; NSB=number of secondary branches; SP=number of seeds/plant; SW=100 seed weight; BIO=plant biomass; Y=grain yield (kg/ha); HI=harvest index. *, ** significant at $P = 0.05$ and 0.01 , respectively.

For each of the traits evaluated, descriptive statistics, including phenotypic and genotypic and environmental coefficients of variation (PCV, GCV and ECV) and broad sense heritability are summarized in Table 4. Across the traits studied, PCV ranged from 10.33% for number of primary branches to 58.73% for harvest index. The GCV values were the lowest (<20%) for plant biomass and highest (99.79%) for number of secondary branches. In contrast, h^2 estimates were comparatively high all the measured traits (Table 4). These results indicated that measured traits in this study can be used for improving seed yield in chickpea. Due to higher heritability estimates, great benefits from selection might be expected for all the traits studied. The present results are in accordance with those previously reported by TALEBI and ROKHZADI (2013) and ZALI *et al.* (2011). The higher values of heritability for most of studied traits indicate that these characters can be used as genetic parameters for improvement and selection of high yielding genotypes.

Table 3. Mean of different morphological traits evaluated in 49 chickpea accessions

Genotype Number	PH	NPB	NSB	HI	Yield	BIO	SW	SP
1	41.67	5.33	3.00	22.14	1520.56	6867.78	26.98	16.11
2	26.67	6.00	3.67	23.96	528.89	2205.00	12.13	12.44
3	24.67	5.33	3.33	17.88	213.89	1178.33	16.81	3.56
4	29.33	5.67	3.00	37.05	898.33	2411.11	16.97	15.11
5	36.67	5.00	2.67	39.15	1403.89	3601.11	26.34	15.24
6	34.67	3.33	6.00	41.46	2278.89	5522.22	25.25	25.78
7	36.33	3.00	5.00	38.22	1606.11	4203.89	13.53	34.44
8	43.67	2.00	3.67	35.29	2566.67	7276.11	22.48	32.73
9	35.67	2.33	5.00	36.75	1158.89	3157.78	26.81	12.33
10	45.33	2.67	2.67	9.10	307.22	3321.11	22.49	3.80
11	31.33	2.33	3.00	16.31	1217.35	7641.67	24.26	14.36
12	33.33	2.00	5.33	35.51	1462.22	4075.56	18.81	22.02
13	38.00	1.67	4.33	31.43	1462.22	4662.78	22.87	18.24
14	27.00	1.67	4.00	27.67	1018.89	3675.00	16.53	17.58
15	28.33	2.33	2.00	16.33	490.00	2971.11	20.03	6.91
16	41.33	2.33	5.00	16.79	1228.89	7509.44	15.26	23.23
17	39.33	2.00	4.33	8.64	365.56	4238.89	21.94	4.80
18	35.00	2.33	2.00	27.87	797.22	2842.78	19.66	11.56
19	38.00	2.00	1.00	16.40	906.11	5537.78	16.52	15.67
20	28.67	1.33	2.00	40.21	1003.33	2492.78	36.86	7.78
21	40.33	2.33	5.00	22.34	1337.78	5985.00	20.93	18.33
22	34.33	2.33	3.00	26.37	1376.67	5218.89	16.80	23.44
23	37.33	2.67	4.33	17.20	898.33	5222.78	24.61	10.47
24	37.33	1.67	3.33	24.09	933.33	3881.11	17.68	15.11
25	44.33	2.67	4.67	20.69	672.78	3262.78	26.10	7.36
26	37.33	1.67	5.33	22.55	1120.00	4900.00	12.70	25.11
27	38.33	2.00	2.00	8.13	692.22	8337.78	20.61	9.36
28	32.33	2.33	3.00	48.01	1858.89	4130.00	18.44	28.89
29	35.67	1.33	4.67	18.20	902.22	4962.22	27.03	9.58
30	42.67	2.67	5.00	20.78	1287.22	6210.56	20.51	17.91
31	47.67	2.33	3.00	26.30	1174.44	4468.33	24.71	13.58
32	43.33	2.67	4.00	18.51	1042.22	5557.22	18.44	16.11
33	31.67	2.33	6.00	15.22	1081.11	7178.89	36.78	8.36
34	37.00	2.00	3.00	26.48	1333.89	5001.11	31.16	12.11
35	37.67	2.67	3.67	23.25	1473.89	6370.00	34.69	12.13
36	37.33	2.00	3.33	29.35	2177.78	7412.22	28.65	21.68
37	41.33	2.33	4.00	17.63	878.89	4970.00	29.90	8.44
38	36.00	2.67	5.00	20.41	886.67	4297.22	26.33	9.59
39	35.67	2.00	2.67	20.18	878.89	4371.11	28.82	8.90
40	32.67	2.33	4.00	31.48	1193.89	3791.67	23.13	14.80

41	35.67	2.00	2.67	31.44	964.44	3099.44	29.75	9.26
42	32.67	2.00	4.67	29.99	925.56	3083.89	24.93	10.61
43	45.67	2.33	2.67	16.30	828.33	5090.56	23.05	10.31
44	34.33	2.33	5.33	30.06	1256.11	4184.44	30.19	11.89
45	37.33	2.33	4.00	39.21	1423.33	3717.78	12.82	32.21
46	27.67	2.67	4.33	37.64	1135.56	3006.11	17.75	18.24
47	35.00	2.00	4.00	31.68	945.00	2971.11	22.00	12.24
48	36.00	1.67	3.33	24.82	1065.56	4308.89	31.08	9.80
49	38.00	2.00	2.33	35.14	2057.22	5938.33	23.21	25.47
Maximum	47.67	6.00	6.00	48.01	2566.67	8337.78	36.86	34.44
Minimum	24.67	1.33	1.00	8.13	213.89	1178.33	12.13	3.56
Mean	36.15	2.55	3.77	26.25	1172.35	4643.41	23.03	15.43
LSD	4.39	1.18	1.94	6.2	299.7	882.8	5.6	3.42

Table 4. Genetic parameters for different agronomic traits in 49 chickpea genotypes

	GV	EV	PV	GCV	PCV	ECV	h_i^2
Plant Height	550.6	24.1	287.3	38.9	28.1	81.24	1.91
Number of primary branches	7.43	1.2	4.31	17.05	10.33	68.55	1.72
Number of secondary branches	375.65	7.4	191.5	99.79	71.2	14.12	1.96
Harvest Index	1757.2	55.3	906.25	81.79	58.73	14.83	1.93
Yield	48950.2	698.2	24824.2	64.57	45.93	76.81	1.97
Biomass	12499.9	215.9	6357.9	16.4	11.7	20	1.96
100-Seed weight	414.2	19.25	216.72	42.33	30.67	91.1	1.91
Number of seeds per plant	121.55	15.7	68.62	27.89	21.07	10.04	1.77

Correlation coefficient analysis

Seed yield is a complex trait that receives the interactive effects of many other plant traits, which are in turn influenced by their genetic structures and the environment where the plant is grown. Thus the direct evaluation and improvement of seed yield itself may be misleading due to the influence of the environmental component. Therefore, it is essential to analyze the data for the relative contribution of various components to yield performance. The simple correlation is an important tool for this purpose. The correlation coefficients between seed yield and measured morphological traits are presented in Table 5. The seed yield had highly significant positive correlation with number of seeds per plant and harvest index, suggesting that these traits may be important yield predictors and perhaps it is the most important for yield improvement in chickpea. In some cases, compensation of characters related to yield was indicated by the presence of negative correlations among these characters with seed yield. Number of primary branches had significant negative correlation with yield (Table 5). Between the traits, strong positive correlation were observed between number of seeds per plant and harvest index (0.64**), plant biomass with plant height (0.43*), while negative significant correlations were observed between number of seeds per plant with 100-seed weight (-0.44*), harvest index with plant height (-0.33*). These results suggest that any positive increase in such

traits will improve the seed yield of chickpea, and are in agreement with the findings of TOKER (2004), OBAIDULLAH *et al.* (2006), FARSHADFAR *et al.* (2008) and ZALI *et al.* (2009).

Table 5. Correlation coefficients between different agronomic traits in chickpea genotypes

	PH	NPB	NSB	HI	Yield	BIO	SW	SP
PH	1							
NPB	-0.22	1.00						
NSB	-0.02	-0.06	1.00					
HI	-0.33*	0.06	0.14	1.00				
Yield	0.09	-0.13	0.24	0.64**	1.00			
BIO	0.43*	-0.25	0.11	-0.28*	0.49**	1.00		
SW	0.09	-0.23	0.01	-0.03	0.11	0.18	1.00	
SP	0.05	-0.06	0.25	0.61**	0.80**	0.32*	-0.44*	1.00

Path coefficient analysis

Sometimes, correlation coefficient gives misleading results because the correlation between two variables may be due to a third factor. It's therefore necessary to analyze the cause and effect relationship between dependent and independent variables to entangle the nature of relationships between the variables (SIDRAMAPPA *et al.*, 2008; TALEBI and KARAMI, 2011). The results of the path coefficient analysis are shown in Table 6. This path analysis demonstrate the influence of seed yield component on yield as well as the process that determined the magnitude of these seed yield components, thereby providing a more complete view of how drought stress and irrigated conditions affect seed yield formation in chickpea. Number of seeds per plant had the greatest direct effect on seed yield (p.c. = 0.619). Also its indirect effect on seed yield more positive through harvest index and plant biomass, but negative and low through 100-seed weight (-0.273). The main reason for strong direct effect of number of seed per plant index was due to the strong positive correlation (0.80**) of this character with seed yield (Table 6). Harvest index, plant biomass and and 100-seed weight were other characters that showed considerable positive direct effects of seed yield. These results suggested that the selection for high yield chickpea genotypes may be improved by increasing the number of seeds per plant, 100-seed weight and with plant that able to produce higher branches consequently higher biomass and seed numbers. These finding are in agreement with TALEBI *et al.* (2007), TALEBI and KARAMI (2011) and ALI *et al.* (2009).

Table 6. The direct and indirect contribution (Underline indicates direct effect) of various morphological characters to seed yield in chickpea

	1	2	3	4	5	6	7	Correlation with yield
1) Plant Height	(0.015)	-0.004	-0.001	-0.006	0.006	0.001	-	0.09
2) No. Primary branches	-0.012	(0.052)	-0.004	0.003	-0.014	-0.012	-0.004	-0.13
3) No. secondary branches	-	0	(-0.005)	-0.001	-0.001	-0.001	-0.002	0.24
4) Harvest index	-0.123	0.022	0.051	(0.37)	-0.104	-0.012	0.225	0.64**
5) Biomass	0.146	-0.086	0.037	-0.096	(0.34)	0.061	0.109	0.49**
6) 100-seed weight	0.03	-0.076	0.003	-0.011	0.061	(0.342)	-0.151	0.11
No. seeds per plant	0.03	-0.038	0.154	0.377	0.198	-0.273	(0.619)	0.80**

Principal component analysis

Principal component analysis can determine which of the characters most strongly contributes to the PC. The analyses reduced the original 8 characters in the experiment to 3 PCs. The first 3 PCs with eigenvalues >1 explained 70.94 % of the variation among the 49 accessions (Table 7). Other PCs had eigenvalues <1 and have not been interpreted. PC1, which is the most important component, explained 32.23% of the total variation and was positively related to harvest index, number of seeds per plant and seed yield; PC2 accounted for 24.04% of the total variation and the characters with the greatest weight on this component were plant height and plant biomass. PC3 accounted for 14.67% of the total variation and mainly related to 100-seed weight.

Table 7. Factor analysis of 8 characters on three principal factors in chickpea genotypes

Variables	PC 1	PC 2	PC 3
PH	-0.06	0.72	-0.36
NPB	0.16	-0.53	-0.30
NSB	-0.38	0.02	0.14
HI	0.68	-0.55	0.35
Yield	0.94	0.11	0.15
BIO	-0.41	0.76	-0.19
SW	0.12	0.45	0.82
SP	0.93	-0.14	-0.30
Eigen Value	2.57	1.92	1.17
% variance explained	32.23	24.04	14.67
% of cumulative	32.23	56.27	70.94

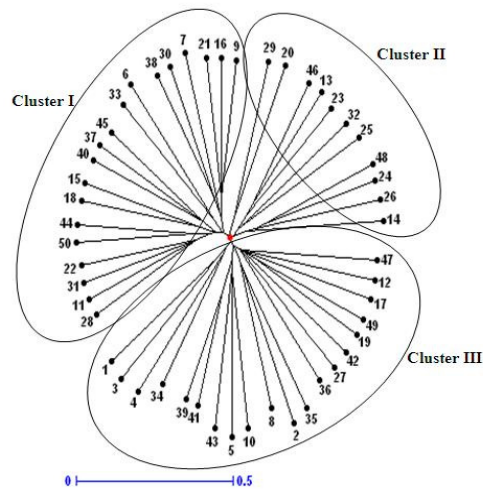


Figure 1. Dendrogram of the chickpea accessions based on the dissimilarity matrix developed using morphological markers.

Cluster analysis

Forty nine chickpea accessions were grouped into three clusters (Fig 1). Cluster I included 18 genotypes, which ten of them were landrace genotypes that originated from different zones of Iran and showed moderately 100-seed weight and consequently moderate high yield. Cluster II, contained eleven genotypes which all of them were landrace genotypes. Genotypes belonged to this cluster were small seed size and had lower seed yield in compare to genotypes in other two clusters. Cluster III, contained 20 genotypes. Genotypes grouped in this cluster were different improved cultivars and breeding lines and had higher seed yield in compare to other genotypes (Fig 1).

CONCLUSIONS

The description of agronomically important and useful characteristics is an important prerequisite for effective and efficient utilization of germplasm collections in breeding programs. A small mini core collection of landrace, breeding line and improved chickpea cultivars has been assembled and we have shown that there is a high level of morphological diversity for most of the traits observed, which may be useful for future breeding endeavors. The exploitation of crosses between genetically distant parents (e.g., recombinants parents from the local accessions and the introduced genotypes) and those from diverse local sources may produce higher heterosis, better genetic recombination and segregation in their progenies and result in varieties with broad genetic base (CHAHAL and GOSAL 2002). Based on the three analyses using in this research among all traits, the number of seeds and 100-seed weight appeared to be the best criteria for selection. In general, based on correlation, path and factor analyses, the results of the present study suggested that a chickpea cultivar, for increased yield should have maximum number of seeds and higher seed size. Thus, identify these traits as selection criteria in further studies in chickpea breeding program may be useful for breeders to introduce suitable chickpea cultivars. Thus, there is an opportunity to bring about improvement of the crop yield through direct and indirect selection as well as improving of these characters through hybridization using the germplasm collections in Iran.

Received September 20th, 2014

Accepted December 25th, 2014

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**MEĐUSOBNI ODNOS GENETIČKE ANALIZE PRINOSA SEMENA I
MORFOLOŠKIH OSOBINA MINI KOLEKCIJE IRANSKIH SORATA,
SAMOPLODNIH LINIJA I POBOLJŠANIH GENOTIPOVA LEBLEBIJE
(*Cicer arietinum* L.)**

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Izvod

Vršena su ispitivanja asocijacije genetičkih parametara i morfoloških osobina 2012/2013 sezone gajenja kod 46.različitih sorata, smooplodnih linija i gajenih genoipova leblebije (*Cicer arietinum* L.). Vršena je analiza genetičke varjanse, varijanse fenotipa i uslova sredine, koeficijent variranja, naslednost, koeficijent korelacije, određivanje pat koeficijenta kao i konstrukcija dendograma (klaster analiza). Visoke vrednosti naslednosti ispitivanih osobina pokazuju da su te osobine velikim delom pod kontrolom aditivnih gena i da selekcija na te osobine može da bude efektivna u povećanju prinosa zrna. Germplazma je grupisana u tri grupe (klastera). Svaka grupa (klaster) ima sopstvene specifične karakteristike a klaster I se jasno razdvaj od klastera II i III. Zaključeno je da se prinos leblebije može povećati selekcijom idiotipa koji imaju veći broj zrna po biljci, veću težinu 100 zrna i veću biomasu..

Primljeno 20. IX. 2014.

Odobreno 25. XII. 2014.