Genetic diversity analysis of White, Red and Chiti Bean under non stress condition

Shahab Khaghani[1*], Shohreh Khaghani[2], Mahdi Changizi[1] and Masoud Gomariyan[1]

1.Department of Genetic and Plant Breeding, College of Agriculture, Arak Branch, Islamic Azad University, Arak, Iran
2.Young Researchers and Elite Club, Arak Branch, Islamic Azad University, Arak, Iran.

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Abstract

Knowledge of genetic diversity and relationships between genotypes is mainly important for selection of parental genotypes. Moreover, assessing diversity across and within crop varieties is important to improve the description of collections in gene banks and in on-farm conservation practices. In order to evaluation and study of genetic diversity in the bean in normal condition, forty-five bean genotypes (15 genotypes of each white, red and chiti beans) were planted in a randomized group balanced block design with three replications under the non-stress condition and Twenty-four traits were recorded. The results showed that traits such as R7 (the number of days to stage podding), Bush type, 100 seed weight, bush height, height of internodes and steam diameter in white, red and chiti bean were significantly different (p<0.01). Furthermore, in the number of days to appearance of first three leaves let, pod/plant, seed/pod and seed/plant there were significant differences (p<0.05). According to simple correlation analysis of traits, the yield had a positive and significant correlation (p<0.01) with the length of the highest pod (r= 0.93). Moreover, in p<0.05 the correlations between steam diameter (r= 0.89), height of internodes (r= 0.85) and height of plant (r= 0.80) were significantly differences. Yield evaluation, that was carried out by stepwise regression analysis on the basis of yield traits, showed the number of pods/plant, seeds/pod, leaves/plant, and Length of the highest pod were the most important traits for population evaluation regarding yield. Also, the result of factor analysis showed that based on eigenvalues greater than one, seven factors was selected that these factors explained 80.66% of the total variation. Genotype number KS-41113, KS-41114, KS-31140, KS-31122, KS-41109, KS-31114, KS-41112, KS-41101, KS-41106 and KS-31104 were selected as the better choice.

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Introduction

High growth rate of population in developing countries has increased demands for food supplies. Food shortage and malnutrition problems have placed numerous stresses on the human health and environment (Aserse *et al*., 2012). During the recent decade, global food production has generally followed a positive growth rate, still on a per capita basis. Nonetheless, the number of constantly undernourished has further grown. The strange increase of hunger during the recent food crisis in 2007-2008 occurred in spite of a record cereal harvest in 2008 (Bongaarts, 2009; FAO, 2009). Number and percentage of the undernourished

person in the word were 870 million in 2012 (FAO, 2012). Moreover, most of the world's hungry people live in developing countries (FAO, 2009). There are many methods to overcome these problems include population control, sustainable agricultural development and increasing potential yield per plants. In numerous developing countries, the bean is consumed as the main source of protein in the human food and contains high levels of vitamin and minerals (FAO, 2009). The share of the bean consumption from total grain consumption in the world is estimated about fifty percent. As well as the common bean is a major food in Latin America and eastern Africa. It has an increasing produce rate in developed countries, where the population is concerned with healthier diets (Acosta-Gallegos *et al.*2007). Common bean (*Phaseolus vulgaris* L.) is certainly the most widely consumed grain legume in the world (Singh, 2001; Foschiani *et al.*, 2009) Furthermore, total agricultural lands in the world used for bean culture occupied around 29881721 hectares and Iran has developed 92000 hectares in bean production (FAO, 2014). This crop contains 20% to 25% protein that makes it a suitable choice for meat succession (Khaghani *et al.*, 2008). It is a morphologically diverse grain legume, with large obvious variations for traits related to growth habit, pigmentation, pods and seeds and others (Singh 2001, Coan *et al.* 2010, Chenl *et al.*, 2011). Knowledge of genetic diversity and relationships between genotypes is mainly important for selection of parental genotypes (Alistair *et al.*, 2009; Tantasawat *et al.*, 2010). Moreover, assessing diversity across and within crop varieties is important to improve the description of collections in gene banks and in on-farm conservation practices (Foschiani *et al.*, 2009). This diversity originates from natural evolution and has important impacts on biological sustainability. Moreover, some mathematical method used to compare the changes in seeds yield (Rosielle, and Hamblin, 1981; Khaghani *et al.*, 2008) and many methods have been used to identify crop lines that are productive in any

environments (Yadav and Bhatnagar, 2001; Reynold *et al.,* 2007).

As for multivariate methods, Franco *et al.* (1997) studied the performance of different clustering analyses. According to them founds, Ward's method is the best strategy when the sizes of the groups are similar and UPGMA is appropriate when the groups are of different sizes. Multivariate methods UPGMA and Principal Component Analysis have been used in other researches (Ortiz *et al.*, 1998; Huaman *et al.* 1999; Koutsos and Koutsika-Sotiriou 2001; Grenier *et al.,* 2001; Terzopoulos *et al.* 2003). In this study, genetic diversity of white red and chiti bean was compared.

Materials and Methods

In the present study forty-five genotypes of white, red and chiti bean (fifteen genotypes from each one) in Randomized group balanced block design with three replications under normal condition were tested (Table 1). The distances from plant to plant and from row to row were 30 centimetres and no fertilizers or any other soil additives were used.

Twenty-four traits include vegetative traits; generative traits and yield were studied. In order to study the variety of traits between the genotypes, a simple variance analysis was conducted on each trait. Moreover, several statistic tests such as stepwise regression, Principal Component Analysis (PCA, factors analysis, and cluster analysis and traits correlation were performed. Cluster analysis was applied to categorize different genotypes. Statistic calculations were done using SPSS 16, SAS 9.1 and Minitab 13.31 software packages. The p-value <0.05 considered as a significant and p<0.001 considered as a highly significant.

Results
Simple variance analysis of traits

Table 1
White, red and chiti genotypes

Row	White bean	Row	Red bean	Row	Chiti bean
1	KS-41111	16	KS-31114	31	KS-21111
2	KS-41112	17	KS-31140	32	KS-21108
3	KS-41113	18	KS-31112	33	KS-21110
4	KS-41114	19	KS-31108	34	KS-21104
5	KS-41115	20	KS-31101	35	KS-21103
6	KS-41116	21	KS-31106	36	KS-21109
7	KS-41117	22	KS-31107	37	KS-21102
8	KS-41110	23	KS-31122	38	KS-21101
9	KS-41101	24	KS-31105	39	KS-21106
10	KS-41103	25	KS-31104	40	KS-21114
11	KS-41109	26	KS-31109	41	KS-21113
12	KS-41108	27	KS-31110	42	KS-21105
13	KS-41106	28	KS-31116	43	KS-21682
14	KS-41105	29	KS-31103	44	KS-21107
15	KS-41102	30	KS-31111	45	KS-21112

The results showed that traits such as R7 (the number of days to stage podding), Bush type, 100 seed weight, bush height, the height of internodes and steam diameter in white, red and chiti bean were significantly different ($p<0.01$). Furthermore, in the number of days to the appearance of first three leaves let, pod/plant, seed/pod and seed/plant there were significant difference ($p<0.05$) (Table 2).

Comparison of means

Genotype grouping for different traits was conducted using multi-level Duncan test at $p<0.05$. The results showed that the most average belonged to red bean group (18.27 g/plant) and the least belonged to Chiti bean group (14.41 g/plant).

Stepwise regression on forty-five genotypes of bean

Yield evaluation, which was carried out by Stepwise regression on the basis of yield traits, showed the number of pods/plant, seeds/pod, leaves/plant, and Length of the highest pod to be the most important traits for population evaluation regarding yield. These traits consisted of 68% of the total variations. In this analysis seed yield was dependent variable and other traits were the independent variable. Results were shown in Table 3.

Simple correlation between traits in forty-five genotypes of bean

In the present study, Simple correlation of traits in forty-five genotypes of white, red and Chiti bean was calculated. According to these results, the yield had a positive and significant correlation ($p<0.01$) with the length of the highest pod ($r= 0.93$). Moreover, in $p<0.05$ the correlations between steam diameter ($r= 0.89$), height of internodes ($r= 0.85$) and Height of plant ($r= 0.80$) were significant.

Factor Analysis in forty-five genotypes of white, red and chiti bean

Table 2
The ANOVA Procedure of tested traits in forty-five genotypes of white, red and chiti bean

Traits	Mean Square					CV%
	Replication	Color	Color× Replication	Genotype inside Color	Error	
	df= 2	df= 2	df= 4	df= 42	df= 84	
(V1)¹	5.87	2.27	1.11**	0.38	0.29	6.52
(V2)¹	0.82	0.94	0.38*	0.25	0.2	4.40
(V3)¹	2.54	1.42*	0.17	0.42*	0.18	2.67
(V4)¹	11.25	7.82	2.47**	0.98**	0.46	3.14
(R5)¹	20.89	27.91	12.70	60.09**	5.13	5.36
(R6)¹	13.62	52.62	10.37*	61.67**	4.16	4.18
(R7)¹	14.68	96.82**	3.14	61.79**	4.81	4.15
(R8)¹	246.86	102.92	48.11**	132.21**	13.10	4.36
(R9)¹	114.62	57.65	45.66**	104.53**	11.05	3.70
bush type	0.95*	8.08**	0.07	0.88**	0.11	18.06
Pod/plant	172.66	286.75*	36.83**	25.94**	10.26	21.51
Seed/pod	1.89	5.06*	0.43*	0.87**	0.14	11.53
Seed/plant	3846.25*	6898.16*	544.46**	309.16**	123.53	22.39
100-seed weight	46.50	1340.59**	22.78	128.75**	9.98	9.20
Yield	571.74*	170.86	70.55**	32.11**	14.72	23.24
Height of plant	102.12	4783.82**	109.32*	545.19**	43.00	11.39
Height of internodes	0.02	17.81**	0.94	1.25**	0.50	13.35
Diameter of steam	1.52	13.14**	0.25	1.08**	0.19	7.23
Number of subphylum	1.57	3.94	1.39*	0.72**	0.39	13.82
Number of nodes	13.10	9.81	3.40	10.24**	2.35	14.09
Length of the highest pod	0.14	9.91	2.86**	3.26**	0.58	7.30
Leaf number/plant	282.10	1145.37	902.17	1327.08**	548.09	32.45
Dry weight of leaves/plant	12.22	27.03	7.43	10.26**	4.05	34.04
Dry weight of shoots/plant	869.41*	192.43	107.82	198.5*	65.01	26.70

**. Correlation is significant at the 0.01 level and *. Correlation is significant at the 0.05 level

Based on eigenvalues greater than one, factor selection was performed. These factors explained 80.66% of the total variation. From the all seven selected factors, the first that explained 29.47% of the total variance was labelled as flowering and maturating. Factor 2 labelled as 'yield' contained number of pod/plant, Seed number/pod, Seed number/plant and yield, which explains 19.90% of the total variation. The third factor accounted for 9.04% of the total variance. Next factor 7.85%, fifth factor 5.17%, sixth factor 4.87% and the last factor explained 4.33% of the variance (Table 4). As shown in Fig. I. genotype number 3, 4, 17, 23, 11, 16, 2, 9, 13 and 25 were selected as the better choice.

Cluster analysis of forty-five genotypes of white, red and chiti bean

In cluster analysis, the genotypes were classified into five groups and then dendrogram of cluster analysis was drawn. The result was shown in the Fig II.

Discussion

Practices against poverty and hungry can be performed in many ways including improving agricultural productivity, promoting better nutrition and improving access the food. Crop production efficiency depends on many factors. One of the most important factors is genotype diversity. Many studies are managed ex situ can increase considerably over time. Therefore, the chances of monitoring their diversity may be at risk. Genetic diversity of populations in situ can be improved, due to management practices they are subject to (Gomez *et al.* 2005) and in general as a concern of adaptation and evolution (Foschiani *et al.*, 2009).

According to Beebe *et al.*, (2008), bean lines that had greatest indices increased seed

Table 3
Stepwise regression on forty-five genotypes of bean

Variable	Estimate	std. error	R2	t	prob.
constant	-9.67	3.80	-	-2.54	0.015
Seeds/plant	0.207	0.027	0.388	7.51	0.000
Length of the highest pod	1.84	0.295	0.213	6.23	0.000
Seeds/pod	-1.72	0.625	0.051	2.76	0.009
Leaves/plant	0.033	0.015	0.031	2.23	0.031

Dependent Variable: yield

Table 4
Factor analysis in forty-five genotypes of white, red and chiti bean

	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5	Factor 6	Factor 7
R5	0.15	-0.03	0.13	0.00	0.12	0.07	-0.14
R7	0.18	-0.12	-0.15	-0.02	0.00	0.13	0.15
R6	0.12	0.03	0.12	0.00	0.08	-0.13	-0.06
R8	0.21	0.14	0.14	0.10	-0.17	0.20	-0.10
R9	0.18	-0.10	-0.07	0.02	-0.02	0.17	0.18
Number of pod/plant	0.02	0.19	-0.06	-0.05	0.15	0.18	0.00
Seed number/pod	0.03	0.32	0.05	0.25	0.23	0.03	0.09
Seed number/plant	-0.10	0.24	0.09	0.05	-0.16	-0.21	0.00
Yield	-0.05	0.53	0.03	-0.02	0.51	-0.13	0.10
Number of subphylum	0.12	0.03	0.16	0.11	0.02	0.02	-0.02
Number of nodes	0.12	0.13	0.16	0.05	-0.01	-0.04	0.00
Length of the highest pod	-0.01	-0.04	0.29	0.17	0.08	0.08	-0.12
Leaf number/plant	-0.05	0.04	0.27	0.11	-0.10	0.25	0.19
Height of internodes	0.12	0.02	0.11	-0.13	0.08	-0.12	-0.07
Diameter of steam	0.02	0.10	-0.00	0.30	-0.05	0.14	0.12
Height of plant	0.02	0.01	-0.04	-0.30	0.13	0.03	0.02
Dry weight of leaves/plant	0.03	-0.03	-0.07	-0.05	0.17	0.16	-0.13
Dry weight of shoots	0.07	0.03	0.11	-0.02	0.12	-0.10	0.02
bush type	0.03	0.06	-0.11	0.21	0.02	-0.50	0.01
V4	0.06	-0.13	0.03	0.06	0.05	0.38	0.23
V1	0.00	0.10	-0.22	0.14	0.02	-0.04	0.31
V2	0.01	0.11	-0.01	0.25	-0.23	0.12	0.32
V3	0.01	-0.01	-0.18	0.21	0.11	0.29	-0.63
Cumulative variance	29.47	49.37	58.42	66.27	71.45	76.33	80.66

Extraction Method: Principal Component Analysis.

yields in the favourable environment. In this study when a yield component such as pods/plants increased, a significant improve was observed in yield. Moreover, many correlations between the traits can be explained. Khaghani *et. al*. (2008) reported that in bean plants there were correlations between yield and other factors. The most correlation coefficient was observed in pod weight, pod/plant and seed/plant with yield. Furthermore, Panayotov *et al* (2009) have found that bean yield had a correlation with seed/plant, pod/plant, 100 seed weight and seed/pod. The positive correlation between yield with seed/plant, pod/plant and seed/pod in $p<0.05$ was discussed in the study carried out by Goncalves-Vidigal *et al* (2007).

Moreover, in $p<0.05$ seed length and 100 seed weight had a significant correlation with yield. On the other hand, in factor analysis, genotype selection can be conducted based on first and second factors. James *et al*., (2009) have found that progress in increasing the seed yield potential of common bean has been slow, but moderately efficacious that genotype introducing with high yield potential can be useful.

Conclusion

It is expected that the data existing here will enhance biological conservation and evolutionary process. Moreover, it can be account as the basis for selection of elite parents in undertaking breeding programs in future. Morphological traits are often used to quantify the genetic diversity in common bean genotypes
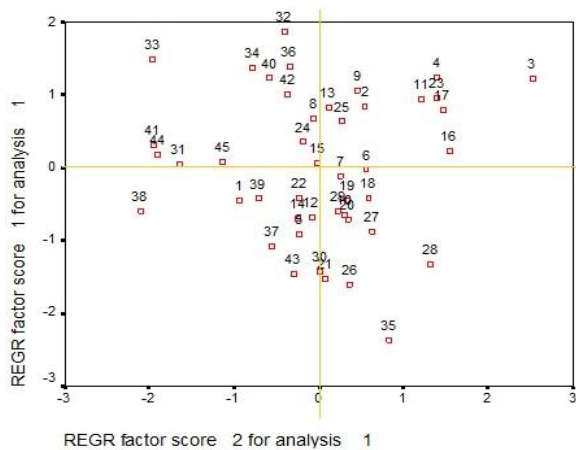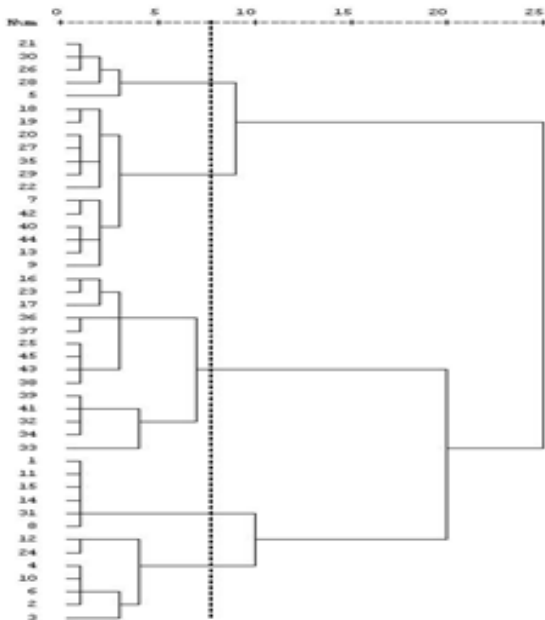

Fig. I. Selection of better genotypes

Fig. II. Dendrogram of cluster analysis

(Ceolin *et al.* 2007). Though the major limitation of morpho-agronomical characterization is that this kind of assessment often involves a high number of descriptors, many influenced by the nvironment, mainly those conditioned by many genes (Chiorato *et al.* 2007). Consequently, DNA markers are also used to determine the genetic diversity in common bean. In this study also genotypes with great yield potential were identified.

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شهاب خاقانی*۱ ، شهره خاقانی۱، مهدی چنگیزی۲ و مسعود گماریان۲

۱ باشگاه پژوهشگران جوان و نخبگان، واحد اراک، اراک، ایران

۲ دانشگاه آزاد اسلامی، واحد اراک، اراک، ایران

٭ عهده دارمکاتبات : sh-khaghani@iau-arak.ac.ir

چکیده فارسی

تنوع ژنتیکی و روابط بین ژنوتیپ ها دارای اهمیت بسیار زیادی برای انتخاب ژنوتیپ های والدینی است. علاوه بر این، ارزیابی تنوع در بین و درون گونه های زراعی برای بهبود توصیف کلکسیون های بانک ژن و حفاظت در رویشگاه های طبیعی مهم است. به منظور بررسی و مطالعه تنوع ژنتیکی در لوبیا در شرایط بدون تنش، چهل و پنج ژنوتیپ(پانزده ژنوتیپ از هر یک از لوبیاهای سفید، قرمز و چیتی) در یک طرح بلوک های متعادل گروهی با سه تکرار کشت شدند و بیست و چهار صفت ثبت گردید. نتایج نشان داد که صفات تعداد روز تا مرحله غلاف دهی، تیپ بوته، وزن صد دانه، ارتفاع بوته، طول میانگره و قطر سلقه در لوبیای سفید، قرمز و چیتی تفاوت بسیار معنی داری داشتند (p<0.01). همچنین در صفات تعداد روز تا ظهور اولین سه برگچه ای، تعداد غلاف در بوته، تعداد دانه در غلاف و تعداد دانه در بوته تفاوت معنی داری مشاهده گردید (p<0.05). همبستگی صفات نشان دلد عملکرد با صفت طول بلند ترین غلاف (0.93 = r) دارای همبستگی مثبت و بسیار معنی داری است، علاوه بر آن همبستگی عملکرد با صفات قطر ساقه (0.89 = r)، طول میانگره (0.85 = r) و ارتفاع بوته (0.80 = r) نیز معنی دار می باشد(p<0.01). مدل نهایی تجزیه رگرسیون گام به گام با درنظر گرفتن عملکرد بعنوان متغیر وابسته نشان داد که صفات تعداد غلاف در بوته، تعداد دانه در غلاف، تعداد برگ در بوته و طول بلندترین غلاف مهم ترین صفات برای ارزیابی عملکرد در جمعیت بودند. نتایج تجزیه به عامل ها نشان داد که بر اساس مقادیر ویژه بالای یک، هفت عامل مشخص شدند که این عامل ها ٪۸۰/۶۶ از کل تغییرات را توجیه می کنند. ژنوتیپ های KS-41106, KS-41101, KS-41112 KS-41114, KS-31140, KS-31122, KS-41109, KS-31114, KS-41113, و KS-31104 به عنوان ژنوتیپ های برتر در این شرایط انتخاب شدند.

کلمات کلیدی: تنوع ژنتیکی، لوبیا، تجزیه خوشه ای، تجزیه عامل ها، همبستگی