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

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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-41114, KS-41112, KS-41101, KS-41106 and KS-31104 were selected as the better choice.

Keywords: Genetic diversity; Bean; Cluster analysis; Factor analysis; Correlation


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 world 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, Chen 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; Terzopulos 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
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 1
White, red and chiti genotypes

<table>
<thead>
<tr>
<th>Row</th>
<th>White bean</th>
<th>Row</th>
<th>Red bean</th>
<th>Row</th>
<th>Chiti bean</th>
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<td>KS-31114</td>
<td>31</td>
<td>KS-21111</td>
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<tr>
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<td>KS-31140</td>
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<td>18</td>
<td>KS-31112</td>
<td>33</td>
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<td>KS-31108</td>
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</tr>
<tr>
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<td>KS-31101</td>
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<td>KS-31111</td>
<td>45</td>
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</tr>
</tbody>
</table>
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 to 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
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 (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 environment, 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.

References

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