Genetic Diversity Assessment for Improvement of Nitrogen Fixation Ability and Seed Production in Iranian Common Bean Genotypes (*Phaseolus vulgaris* L.)

Ahmad Reza Golparvar

Department of Agronomy and Plant Breeding
Islamic Azad University- Khorasgan Branch, Isfahan, Iran, P.O.Box:81595-158
E-mail: agolparvar@khuisf.ac.ir

Abdollah Ghasemi Pirbalouti

Department of Agronomy and Plant Breeding, Islamic Azad University - ShahreKord Branch
ShahreKord, Iran

Abstract— **Common bean is one of the most important crops in majority regions of Iran. Existence of genetic diversity for biological nitrogen fixation and seed yield is very important for genetic improvement of this valuable crop. For this reason 64 common bean genotypes were cultivated in two separate randomized complete block design. Genotypes were inoculated with bacteria Rhizobium legominosarum biovar Phaseoli isolate L-109 only in one of the experiments. Second experiment was considered as check for the first. Standard deviation and analysis of variance revealed genetic diversity between common bean genotypes for all the traits. Factor analysis based on principal component analysis method and varimax rotation indicated that three important factors accounted for about 93.36 percent of the total variation among traits. The first factor assigned 50.58 percent of total variation between traits and was significantly related with biological nitrogen fixation, nodule number plant-1, total nitrogen of shoot, harvest index, 100-seed weight and pod number plant-1. This factor was titled as nitrogen fixation ability factor. Therefore, the traits related with this factor can be used for genetic improvement of nitrogen fixation ability in common bean genotypes. The second factor accounted for 31.72 percent of total variation and was correlated with traits seed yield, pod yield plant-1 and biological yield. This factor was considered as seed production factor and was proposed for increasing seed production in this crop. Result of factor analysis was confirmed using cluster analysis of variables.**

Keywords- Common bean, Rhizobium legominosarum biovar Phaseoli, Factor analysis, varimax rotation, cluster analysis

I. Introduction

Biological nitrogen fixation is one of the most important sources for production approximately 65% of nitrogen used in agriculture [9]. Indirect selection in early generations through traits correlated with seed yield and biological nitrogen fixation is important strategy in common bean breeding. In determining the potential of genetically different lines and cultivars, breeders have to observe many different characters that influence yield. Accurate evaluation of these characters is made more difficult by the genotype by environment interaction.

Guler et al. [5] determined the direct and indirect effects of various plant characters on yield and yield components using path analysis in common bean, faba bean, durum wheat, navy pea, chickpea, winter barley cultivars and small grains. Ghasemi et al. [2] emphasized on traits nodule number plant-1, nodule weight, pod number plant-1 and pod weight as the most important criteria for breeding biological nitrogen fixation in common bean cultivars.

Ulukan et al. [10] reported positive and significant relationships between biological yield with plant height, pod number plant-1 and grain number pod-1 in faba bean genotypes. The total coefficient of determination was found as 63.6% in the regression model for biological yield as dependent variable. Direct effects of plant height, pod number plant-1 and grain number pod-1 upon biological yield were positive. These traits determined as selection criteria for genetic improvement of biological yield.

Abdollahi et al. [1] recognized three factors in common bean cultivars that explained more than 90% of total variation exist among studied traits. These factors were entitled as biological yield, seed yield and nodule production, respectively. The traits related with these factors were proposed as indirect selection criteria for improvement of yield and nodule production in common bean genotypes.

In this research, genetic diversity for biological nitrogen fixation, seed yield and some metric traits were investigated to determine which characters are the best for genetic improvement of nitrogen fixation ability and seed production in common bean genotypes.

II. Materials And Methods

In this study, 64 common bean genotypes randomly selected from Tehran university collection were planted at the beginning of April 2009 at the Research field of Islamic Azad university in two separate randomized complete block design with four replications for each of experiment. In one of them seeds were inoculated with *Rhizobium legominosarum* biovar *phaseoli* isolate L-109 as check for another [2, 5]. In this way, trait biological nitrogen fixation is estimated using nitrogen-difference method proposed by Tamimi [8]. Isolate L-109 had been recognized as the

compatible isolate with Iranian common bean genotypes in this province at the basis of results given from previous study [2].

Measurements of investigated traits were done on five normal plants, which have been randomly chosen from the mid-row of each plot. The following measurements were achieved on; seed yield plant[-1], seed number pod[-1], pod number plant[-1], pod yield plant[-1], 100-seed weight, biological yield, harvest index, nodule number plant[-1] in 50% flowering, total nitrogen of shoot, and biological nitrogen fixation.

Biological nitrogen fixation was calculated as follows [8]: Biological nitrogen fixation = (N1-N0)/N1*100, Where; N_1 and N_0 consist of total nitrogen of shoot for each genotype in inoculation and non-inoculation conditions, respectively. Biological yield was considered as shoot dry weight and harvest index was estimated using formula:
Harvest index = Seed yield/Biological yield.

Correlation coefficients between traits were computed based on Pearson's method. Also, step-wise regression and path analysis were achieved for determination of the direct and indirect effects of the traits on biological nitrogen fixation and seed yield.

The principal factor analysis method was followed in the extraction of the factor loadings. Factors having eigen value higher than 1 selected for performing loading factors matrix. The varimax rotation method (an orthogonal rotation) was used in order to make each factor uniquely defined as a distinct cluster of intercorrelated variables. The factor loadings of the rotated matrix, the percentage variability explained by each factor and the communalities for each variable were determined. In order to better interpretation, loadings higher than 0.5 were considered as significant coefficients [7].

The array of communality and the amount of the variance of a variable accounted by the common factors together was estimated by the highest correlation coefficient in each array. The number of factors was estimated using the maximum likelihood method. Factor analysis was performed using SPSS16 software for all the traits of common bean genotypes. A cluster analysis based on ward's method was used for classification of variables and control the result of factor analysis.

III. Results And Discussion

Analysis of variance showed significant difference between genotypes for all the traits that indicate genetic variation for studied traits in common bean and possibility of selection for improvement these. Mean and standard deviation for the traits have been shown in table 1.

Correlation analyses showed that majority of the traits have positive and highly significant correlation with biological nitrogen fixation and seed yield traits. Regression and path analysis revealed efficacy of the studied traits as selection criteria for breeding biological nitrogen fixation and seed yield in common bean genotypes via indirect selection specifically from early generations.

Factor analysis indicated that only 3 first factors, which account for 93.36% of the total variance, are important (Table 1). Factor 1, which accounted for about 50.58% of the

variation, was strongly associated with biological nitrogen fixation, nodule number plant[-1], total nitrogen of shoot, harvest index, 100-seed weight and pod number plant[-1] (Table 1). This factor was regarded as nitrogen fixation ability factor. All variables except seed number pod[-1] and biological yield had positive loadings in factor 1. The sign of the loading indicates the direction of the relationship between the factor and the variable.

Factor 2, which accounted for about 31.72% of the variation, was named as seed production factor because it consisted of seed yield, pod yield plant[-1] and biological yield, which are associated with plant yield. The third factor was named number of seed plant[-1] factor. This factor accounted for 11.06% of the variation. This factor related with seed number pod[-1] and harvest index traits. Result obtained from cluster analysis (Fig 1) showed consistency between classifications of genotypes using two multivariate methods. The similar findings were obtained from other researches [1, 2, 3, 6].

Biplot display based on the plot of PC2 on PC1 classified the genotypes in four groups that one of them comprises genotypes having the most nitrogen fixation ability and seed production. These genotypes were selected as the suitable population for breeding programmes and improvement of important traits. Also, these genotypes will use in sustainable agriculture with decreasing application of chemical fertilizers by farmers [3, 4, 6, 7].

IV. Conclusion

In conclusion, principal component, factor and cluster analysis helps breeders to genetic improvement the important and complex traits such as nitrogen fixation ability and seed production via indirect selection for traits effective on these. In this study, traits biological nitrogen fixation, nodule number plant[-1], total nitrogen of shoot, harvest index, 100-seed weight and pod number plant[-1] were determined as the best selection criteria for breeding nitrogen fixation ability and the traits seed yield, pod yield plant[-1] and biological yield for seed production improvement.

References

[1] A. Abdollahi, M. Khoddambashi, and A.M. Rezaie, ''Factro analysis of phenological and morphological traits in common bean,'' Proc. 4th crop science Symp, Shahrekord University Press, Aug. 2009, pp. 169-174.

[2] A. Ghasemi Pirbalouti, I. Allahdadi, and Gh.R Akbari, ''Evaluation of yield and its components in common bean cultivars inoculated with Rhizobium legominosarum, Final report of research, Tehran University, 2005, pp:85, (In Persian).

[3] J.E. Barron, R.J. Pasini, D.W. Davis, D.D. Stuthman, and P.H. Graham, ''Response to selection for seed yield and nitrogen (N2) fixation in Common bean (Phaseolus vulgaris L.), Field Crops Research, vol. 62, 1999, pp. 119-128.

[4] I. Chirstiansen, and P.H. Graham, ''Variation in di-nitrogen fixation among Andean bean (Phaseolus vulgaris L.) genotypes grown at low and high levels phosphorus supply, Field Crops Research, vol. 73, 2002, pp. 133-143.

[5] M. Guler, M.S. Adak, and H. Ulukan, ''Determining relationships among yield and some yield components using path coefficient analysis in chickpea (Cicer arietinum L.), European Journal of Agronomy, vol. 14, 2001, pp. 161-166.

[6] S. Sheikh, S. Hussain, I.A. Qamar, and B. Roidar Khan, ''Breeding food and forage legumes for enhancement of nitrogen fixation, Quarterly Scienece Vision, vol. 6, 2000, pp. 49-57.

[7] W. Tadesse, and E. Bekele, '' Factor analysis of yield in grasspea (Lathyrus sativus L.), Lathyrus Lathyrism Newsletter, vol. 2, 2001, pp. 416-421.

[8] S.M. Tamimi, ''Genetics diversity and symbiotic effectiveness of rhizobia isolated from root nodules of common bean (Phaseolus vulgaris L.) grown in the soils of the Jordan valley, Applied Soil Ecology, vol. 19, 2002, pp. 183-190.

[9] J. Thomas, W. Hopper, and T.S. Ramasubramanian, ''Molecular biology tools to enhance biological nitrogen fixation by legumes, In O.P. Rupela, C. Johansen and D.F. Herridge (ed.) Extending Nitrogen Fixation Research to Farmers' Fields. ICRISAT, Patancheru, India, 1997, pp. 39-56

[10] H. Ulukan, M. Guler, and S. Keskin, ''A path coefficient analysis some yield and yield components in faba bean (Vicia faba L.) genotypes, Pakistan Journal of Biological Sciences, vol. 6, 2003, pp. 1951-1955.

TABLE I. MEAN, STANDARD DEVIATION, EIGEN VALUE, PERCENT OF VARIANCE, ROTATED FACTOR LOADINGS AND COMMUNALITY FOR ALL THE TRAITS OF IRANIAN COMMON BEAN GENOTYPES

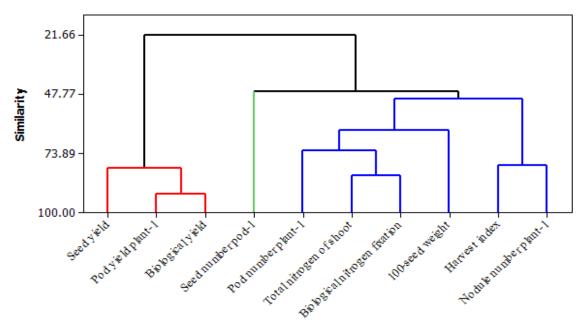| Traits	Factor 1	Factor 2	Factor 3	Communality	Mean	Standard deviation
Seed yield	0.476	**0.583**	0.434	0.860	0.23	0.06
Seed number pod^{-1}	-0.008	0.105	**0.911**	0.841	3.18	0.35
Pod number plant^{-1}	**0.695**	0.342	0.091	0.608	10.05	2.28
Pod yield plant^{-1} (gr)	0.210	**0.882**	0.065	0.827	16.47	5.40
100-seed weight (gr)	**0.442**	0.435	-0.102	0.396	37.32	6.14
Biological yield (gr)	-0.010	**0.974**	0.052	0.951	0.64	0.18
Harvest index (%)	**0.600**	-0.436	0.510	0.810	0.37	0.06
Nodule number plant^{-1}	**0.840**	-0.233	0.032	0.762	5.27	1.83
Total nitrogen of shoot (%)	**0.764**	0.219	0.142	0.652	9.03	0.83
Biological nitrogen fixation (%)	**0.758**	0.234	0.032	0.630	9.63	0.88
Eigen value	4.058	2.172	1.106			
Variance (%)	50.584	31.721	11.058			
Cumulative variance (%)	50.584	82.305	93.363			

Figure 1. Dendrogram of cluster analysis for classify variables based on ward's method