INNSPUB

International Journal of Biosciences | IJB |
ISSN: 2220-6655 (Print) 2222-5234 (Online)
http://www.innspub.net
Vol. 5, No. 10, p. 22-28, 2014

RESEARCH PAPER
OPEN ACCESS

Study of genetic variation and heredity-acceptance of morphological features of 15 peas genotypes

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Key words: Black-eyed pea, correlation, regression.

http://dx.doi.org/10.12692/ijb/5.10.22-28

Abstract

In order to study genetic variation, heredity-acceptance and relations between agricultural features, 15 genotypes of black-eyed pea were performed according to experimental complete accidental blocks plan with three replicates at Broujerd agricultural and natural resources research center. The result of variance analysis showed that genotypes are of significant difference regarding the features under study implying genetic variation among genotypes. The results from studying simple correlation of features showed that the correlation between single-bush yield and sheath number in the main stalk, sheath length, a hundred-seed weight, sheath weight, sheath number in bush, seed number in sheath, biologic yield, and harvest index was positive and significant and between single-bush yield and sheath width was negative and significant.

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Introduction

Bean with scientific name of *Phaseolous vulgaris* is diploid plant with (2n=22) chromosomes and with southern-and-central-regions origin of America Consistent. Seed legumes are among the main protein resources in dry and semi-dry regions and about two third of planted agricultural lands of Iran are located in these dry and semi-dry areas. Regarding human's increasing need for this valuable plant, the need for producing high-crops items with its suitable and high-quality yield, is felt more than before. For this purpose, to identify and evaluate features variation is of importance and also their effect on the plant's yield itself is necessary. In modifying plants, understanding the relations between features in indirect selecting the features not being easily measured or the features with low heredity-acceptance is so much important. When the number of independent variables effective on dependent variable becomes more, the extent of features dependency to one another becomes limited and in these conditions, correlations alone are not able to explain variables' relationships (Ariyo *et al.,* 1986).

By studying correlation and use of multi-variety statistical methods like decomposition to factors, causality analysis and step by step regression, it could be possible to identify the feature effective on seed yield and also the rest of relations effective on creating correlation between features. Beizaei *et al.* (2001), in examining phenotype and genotype correlation between bean's different features, reported the correlation between the features a hundred-seed weight, sheath number and seed number in sheath. Habibi *et al.* (2006), by examining 250 bean masses using the achieved results, observed that the greatest phenotype changes coefficient was achieved for a hundred-seed weight and the whole masses were divided into 2 great classes through cluster analysis. Bngar *et al.* (2003) evaluated 16 soya beans' genotypes. Yield regression showed that seed weight, bush height, and sheath number in bush were of positive and significant coefficients, whereas regression coefficient of minor-branch number in bush was negative. Benett and Adams (1997) recognized bean yield as a quantitative and complex feature that its elements are sheath number in bush, seed number in sheath and a hundred seed weight, and is severely affected by environment. There are a large number of these kinds of study in other plants. For example in a study, variation in deferent population of myrtle has been reported by Bajalan and Ghasemi Pirbalouti (2014). This feature, as was said, is of complicated heredity and low heredity capability. Therefore, the selection criterion for appropriate yield could be features with high heredity capability having high genotype correlation with yield. This plan's goals are as follows: 1) defines relations between yield and morphologic features relating to it, 2) examine and analyze features' correlation with one another, 3) recognize direct and indirect effects of different features with yield.

Materials and methods

This experiment was conducted according to complete accidental blocks plan (RCBD) with three replicates in agricultural year 2010-2011. Having defined soil characteristics, preparatory operations for land was done and plantation took place at date 2010. The first irrigation was done at May (2011). Each treatment consisted of four rows with four meters in length and 50-centimeters distance. In every row, 50 seeds were planted. Mean distance over row and between bushed was ten centimeters (with probability of seed mortalities, 10 extra seeds were planted in each row). The all maintenance operations (irrigation, weeding, fertilizing) were performed according to the district's usual procedure. In order to control weeds, the pesticides Trifluralin and for fighting against bug, at August (2011) the poisons Omite and Diazinon were used. The features under study in this experiment are: single-bush yield, bush height, knot number, sheath number in main stalk, sheath length, sheath weight, minor-stalks number, a hundred-seed, sheath number in bush, biologic yield, harvest index, mean seed-number in sheath, sheath width, seed length, seed width (morphological features) and the number of days until flowering (R5). Physiological ripeness (R9), germination (V0), appearance of the first three leaflets (V3) (phonological features) and protein percent (quality feature).

According to features type, measuring and evaluating them were performed in different developmental stages. Therefore, by considering marginal effects, from the middle two rows, available bushes in a square meter were removed and by choosing five bushes randomly, the intended features were measured and their mean was used in statistical calculations. The respective data first was examined regarding being normal and after verifying their normal condition, statistical analysis stages were done as following:

The data relating to each feature went through variance analysis and after verifying the difference between genotypes, mean comparison was performed through Dankan multi-range method (DMRT). The variance constituents and phenotype and genotype variation coefficients were defined. Simple correlation between features was competed using Pearson correlation.

To calculate general heredity of each feature, the following relationship was applied:

$$\boxed{H^2b.s = \frac{V_G}{V_G + V_E} = \frac{V_G}{V_P} \times 100} \qquad (1)$$

$$\boxed{V_E = Mse}$$

$$\boxed{VG = \frac{Mst - Mse}{r}} \qquad (2)$$

That is above formula, V_G, V_P and V_E are genotype, phenotype, and environmental variances, respectively. And also, r, Mse, and Mst constitute replication number, mean error squares and mean treatments squares, respectively. Step by step (stage) regression was used to define features justifying the greatest extent of yield variation.

In order to define the share of each feature in general variation, data-volume reduction and better interpretation of relationships through decomposition to main constituents (PCA) were applied using the features under study. Constituents' number with respect to logical justification and the number of characteristic roots greater than one were extracted and interpreted. And genotypes scatter diagram was drawn over the main constituents and also diagram for corresponding the results of decomposition to constituents and cluster analysis. In order to classify the genotypes under study, cluster analysis through Ward method and the distance measure by using standard variables were done. To perform statistical analysis, the software SAS 9, Minitab16, SPSS 19 and Excel 2010 were used.

Results and discussion

After examining normal condition of data distribution, analysis of variance was done. The results of simple variance for the features under study showed that difference between genotypes for the features seed width and seed number in sheath was significant at 5% level, and for the rest of features was significant at 1% level, that this thing implies great variation between these features, in genotypes under study.

Seed yield is a quantitative and complex feature being genetically controlled by great number of gens and is severely influenced by environment. For this reason, selecting suitable genotypes, based on yield, may not be of appropriate efficiency. Therefore, to identify the features holding high correlation with seed yield and high heredity-acceptance and, in addition, to measure them easily and with low price, are of importance to modifiers (Sing and Bhardwaj, 2007; Agram, 1996). Modifiers usually use these features as selection criteria to improve yield. The results of phenotype correlation of features showed that correlation between single-bush yield and sheath number in main stalk, sheath length, a hundred-seed weight, sheath weight, sheath number in bush, seed number in sheath, biologic yield and harvest index was positive and significant and between single-bush yield and sheath width was negative and significant. Zaman *et al.* (1989) reported positive and significant correlation between yield and sheath number in bush. The results achieved from decomposition to main constituents for whole genotypes of black-eyed pea including special values, relative and accumulative variance percentages for main constituents are present in table 1. The even constituents with special values more than one, in general explained 86% of whole variance. The results from step by step regression for black-eyed pea's genotypes are provided in table 2. By considering the features single-bush yield as dependent variable and other features as independent variables, six features were put in regression equation. Among these features, the biological yield feature was the first one being put in regression equation. According to R^2 value, this feature explains 42% of changes in single-bush yield. After that, the features harvest index, sheath width, a hundred-seed weight, sheath number in bush, and sheath weight were put in regression equation that in general explained 96% of yield changes. Generally, the results of step by step regression show that the features sheath width is of negative relation with yield, but the features biological yield of harvest index, sheath number in bush and sheath weight hold positive relationship with yield. So, they can be used to create modifying programs for yield increase.

Table 1. Special values, relative and accumulative variance percent and coefficients of special vectors relating to all characters.

Characters	1	2	3	4	5	6	7
yield	0.17	0.24	-0.39	0.13	0.08	-0.22	0.03
Plant height	0.33	0.21	0.15	-0.2	0.02	0.20	0.16
node	0.23	0.22	0.07	0.3	-0.25	0.16	-0.13
Main pod in stem	-0.07	0.38	0.09	-0.2	-0.22	-0.07	0.06
Length pod	-0.18	0.2/0	0.05	0.40	0.21	0.18	0.09
Ancillary stem	-0.33	0.13	-0.14	0.13	-0.13	0.20	-0.08
Weight of 100 seeds	0.23	-0.32	0.01	-0.01	-0.31	-0.02	-0.22
Weight pod	0.04	-0.31	-0.22	0.25	-0.14	0.22	0.23
Pod in shrub	-0.27	0.16	-0.22	-0.15	-0.17	-0.31	-0.27
Seed in pod	-0.27	0.05	-0.29	0.31	0.16	0.24	-0.11
Biological yield	0.0.1	0.29	-0.33	0.004	-0.004	0.24	-0.16
Harvest index	0.19	0.07	-0.11	0.2	-0.35	-0.46	0.15
Seed length	0.07	0.12	0.26	0.29	-0.09	0.02	-0.55
Seed diameter	0.36	-0.19	0.06	-0.12	-0.01	0.11	-0.02
Germination time	-0.14	0.13	0.04	-0.02	-0.41	0.39	0.33
Time to flowering	-0.1	0.25	0.37	0.24	-0.004	-0.14	0.04
Time to ripening	0.23	0.05	-0.05	-0.15	0.43	-0.26	0.25
Protein (%)	0.06	0.28	0.40	0.06	0.15	0.03	-0.06
Spatial amounts	4.85	3.5	3.06	2.51	1.71	1.44	1.08
Relative variance (%)	0.23	0.16	0.14	0.12	0.08	0.06	0.05
Accumulative variance (%)	0.23	0.39	0.54	0.66	0.74	0.81	0.86

Table 2. Step by step regression analysis of the feature yield (dependent variable) and other characters (independent variable).

Characters in model	step by step regression					
	First step	Second step	Third step	Fourth step	Fifth step	Sixth step
Fixed number	2.55	-19.18	69.37	100.19	-157.42	-158.61
Biological yield	0.33	0.33	0.34	0.35	0.33	0.27**
Harvest index		0.55	0.54	0.66	0.77	0.70**
Width pod			-14.1	-17.5	-17	-18.6**
Weight of 100 seeds				0.29	0.36	0.38**
Pod in shrub					12.4	13.1**
Weight pod						2.8*
S	5.79	4.11	2.61	3.03	2.55	1.94
R-Sq	42.58	72.33	81.16	87.95	92.31	96.03
R-S(adj)	38.16	68.89	76.02	83.13	88.04	93.03

Amini (1998), Acosta *et al.* (1997) in a regression model performed by them, expressed that 2 features of seed count and a hundred-seed weight had been put in the model that it signifies the importance of features and their effect on yield. For the purpose of characterizing variation and classify genotypes for the features under study, cluster analysis through Wad method was used and by dendrogram in distance of 7.41, genotypes were placed in three clusters (figure 1). In variance analysis between clusters, mean squares of clusters for the futures single-bush yield, sheath length, sheath weight, sheath number in bush, seed number in sheath, sheath width, harvest index, seed length, seed diameter, the time of becoming three leaflets and ripeness time did not become significant, however, for the features height, sheath number in main stalk, biological yield, germination time, flowering time and protein percent become significant at 5% level and the features knot number, minor-stalk number, a hundred-seed weight and seed width was significant at 1%. Cluster 1 regarding the feature minor-stalk number, cluster 2, regarding the features height, sheath number in main stalk, sheath length, sheath weight, biological yield, flowering time, and protein percent devoted more amount to themselves. Cluster 3, regarding a hundred-seed weight, and sheath width devoted more amounts to itself (table 3). The greatest distance is between clusters 2 and 3 that equal 5.62 that it indicates the individuals in these two clusters are of the most distance to each other. At the result, we can make use of the individuals in these clusters to achieve maximum variation. Scatter of 15 genotypes belonging to black-eyed pea, based on the two main constituents and its correspondence with cluster analysis has been shown in figure 2. The results from estimating general heredity-acceptance and variation coefficients showed that the highest general heredity-acceptance related to the feature sheath width with $h_{b.s}^2 = 5.98$ and the lowest general heredity-acceptance belonged to the feature seed number in sheath with $h_{b.s}^2 = 45.45$. Also, phenotype variation for all features was greater than genotype variation. High amount of heredity-acceptance for most features could be explained in this way that environment variance in this plan has been little.

Table 3. Clusters number, genotype number in each cluster, variance analysis, and mean comparison between clusters.

Characters	MS	Cluster 1	Cluster 2	Cluster 3
yield	69.16^{ns}	34.33 a	23.95 ab	22.09 b
Plant height	1773.28^{*}	72.08 b	114.5 a	90.79 b
node	46.67^{**}	9.57 b	16.4 a	14.64 a
Main pod in stem	13.23^{*}	4.08 b	8.15 a	3.85 b
Length pod	0.79^{ns}	9.15 a	10.48 a	9.28 a
Ancillary stem	3.77^{**}	4.48 a	2.66 b	3.01 b
Weight of 100 seeds	167.08^{**}	41.95 b	71.7 b	52.75 a
Weight pod	0.46^{ns}	2/2 a	2.54 a	2.52 a
Pod in shrub	2.52^{ns}	17.66 a	16.87 a	13.58 a
Seed in pod	0.55^{ns}	3.81 a	3.55 a	3.55 a
Biological yield	178.1^{*}	61.32 b	86.51a	58.07 b
Harvest index	73.05^{ns}	37.89 a	11/48a	42.22 a
Seed length	0.6^{ns}	12.2 a	12.65a	12.69 a
Seed diameter	0.78^{ns}	6.16 a	6.69 a	7.21 a
Germination time	0.07^{ns}	6.2 b	6. 36 ab	6.45 a
Time to flowering	54.11^{*}	53 b	58.5 a	58.5 a
Time to ripening	8.77^{ns}	120.85 a	120.16 a	117.5 a
Protein (%)	15.18^{*}	23.25 b	26.29 a	23.53 b

^{ns}, * and ** non-significant Significant at the level of 1 and 5%.

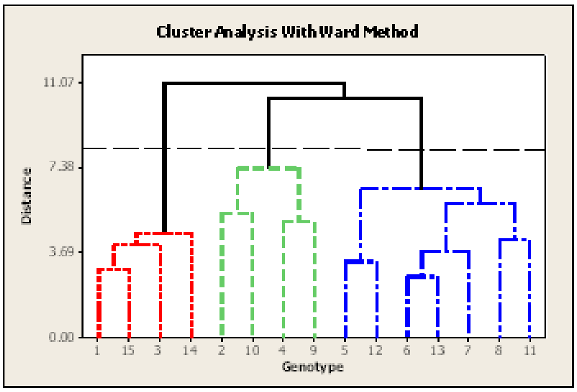

Fig. 1. Cluster analysis graph by Ward method for the genotypes under study.

Also, genetic difference among genotypes under study could be expressed as another reason for heredity-acceptance being high. Therefore the achieved results are not a reliable example for the rest of values and/or genotypes and it is only true for under study genotypes. Regarding table 3 it can be observed that the features having high genetic variance and, at the result, low environmental variance are of high heredity-acceptance. Phenotype variation coefficients for the whole features were greater than genetic variation coefficients.

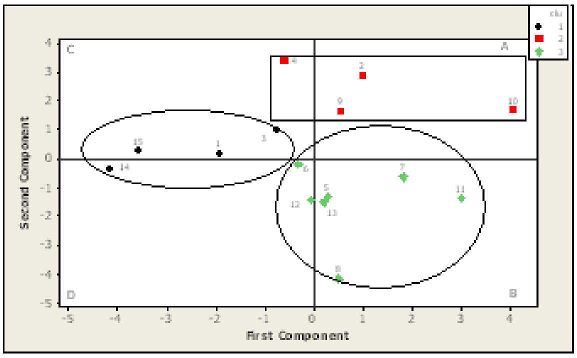

Fig. 2. The graph for correspondence between cluster analysis and decomposition into main constituents.

Acosta *et al.* (1997) in bean, Naroui *et al.* (2008) in lentil showed that generally phenotype variation coefficients are greater than genetic variation coefficients. The little difference observed between these coefficients for most features under study indicates low environmental effect on these features.

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