Study on genetic variation and morpho-phenologic traits in Common bean (*Phaseolus vulgaris* L.)

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Abstract. In current research to assess the presence of variability for desired traits and amount of variation for different parameters, common bean (*Phaseolus vulgaris* L.) genotypes were sown in a randomized complete block design with three replications. The aim of this study was to determine the effects of some yield components on yield via path analysis, estimating genetic and phenotypic correlation coefficients and heritability in 9 common bean genotypes. Results showed that differences between genotypes in all the parameters, except for internode diameter (IND), number of seeds per pod (NSPP), seed diameter (SD), internodal length (INL) and hundred seed weight (HSW) were significant. The estimates of GCV were high for harvest index (123.98), number of nodes on the main stem (70.04), weight of pods per plant (54.13), grain yield per plant (50.33). Low broad sense heritabilities assign that if compared with number of nodes on the main stem, biological yield, weight of pods per plant, chlorophyll fluorescence, harvest index and straw weight, environmental effects on plant height, number of seeds per pod, internode diameter, pod length free tail, seed diameter, internodal length and hundred seed weight were found to be much higher. Grain yield per plant showed high significant positive genetic and phenotypic correlation with only weight of pods per plant. Path analysis indicated that the initial level of grain yield per plant, weight of pods per plant had the highest (1.313) direct effect on grain yield.

Key words: genotypic correlation, path analysis, genetic advance, heritability, common bea.

Introduction

Common bean (*Phaseolus vulgaris*) is grown and consumed principally in developing countries in Latin America, Africa, and Asia. It is a major source of dietary protein, which complements carbohydrate-rich sources such as rice, maize, and cassava (Faostat 2006). This plant is a true diploid with 11 chromosomes and a haploid complement of 588 (Bennett & Leitch 2005) to 637 Mbp (Arumuganathan & Earle 1991). Available evidence suggests that domestication centers (Mexico and the Andes) creates two groups of cultivars with different characteristics. The utilization of plant genetic resources is one key to improving agricultural productivity and sustainability. Use of genetic resources is as old as the history of agriculture. Hundreds of plants have been bred over many hundreds of years and thousands of varieties have been developed by natural and artificial selection (Sari et al. 2008, Zakizadeh et al. 2010, Zarei et al. 2012). The genetic uniformity of cultivars of a widely grown crop makes them uniformly susceptible to biotic or abiotic hazards. This genetic vulnerability may lead to complete crop loss. The main goal to be achieved by conservation of genetic resources is their present and future utilization for the benefit of mankind (Yawen et al. 2001). Evaluation and conservation of crop genetic resources have gone on for two hundred years (Brush & Meng 1998). Common bean are grown extensively in five major production areas; eastern and southern Africa, north and Central America, South America, eastern Asia and western and south-eastern Europe (Denis and Adams, 1978). The potential of a crop to respond favorably to breeding programs depends on the nature and magnitude of variability. Grain yield is a complex character and is the product of many yield components (Gravitus, 1959) and knowledge of existing genetic variations and the association between various yield traits and their heritability assumes importance (Dixit and Dubey, 1985). Heritability in the narrow and broad sense is important for the plant breeder since the effectiveness of selection depends on the additive portion of genetic variance in relation to total variance (Ghobadi et al. 2011, Geravandi et al. 2011, Zarei et al. 2012). This study deals with the determination the effects of some yield components on yield via path analysis, estimating genetic and phenotype correlation, coefficient and heritability, genetic advance, coefficient of variance genetic and phenotype, in 9 common bean genotypes.

Materials and Methods

Plant materials

In current research nine common bean genotypes from Greece and Iran including Adsrou 4, strazagorsky 5, Goli, Derakhshan, D-81083, Ks31159, Red Bean, White Bean and Beans Capsule were used. Their entry names and origins are presented in Table 1.

Table 1. Number, name and origin of the common bean (*Phaseolus vulgaris* L.) genotypes.

No.	Name	Origin
1	Adsrou 4	Greece Landrace
2	Strazagorsky 5	Greece Landrace
3	Goli	Iran
4	Derakhshan	Ciat
5	D-81083	Ciat
6	Ks31159	Ciat
7	Red Bean	Iran Lordegan Chahar Mahal Bakhtiari Landrace
8	White Bean	Iran Lordegan Chahar Mahal Bakhtiari Lan Drace
9	Beans Capsule	Iran Lordegan Chahar Mahal Bakhtiari Landrace

Field experimental and weather conditions

Genotypes were sown in the third week of May 2012 and May 2013 in Campus of Agriculture and Natural Resources, Razi University (longitude 48.9, latitude 34.21, and altitude 1319 m asl) in a randomized complete block design with three replications. The experimental plots consisted of 4 rows of 3 m length with 40 cm spaces and they were sown by hand. Weeds were removed by hand during the

growth period. Standard cultural practices were followed for raising the crop. Total precipitation in 2011/ 2012 was 296.5 mm, while it was 373.5 mm in 2012/2013.

Characters studied

The characters measured included biological yield pert plant (g) (BY), grain yield per plant (g) (GY), plant height (cm) (PH) (measured from the base of the plant to the tip of the plant at the time of physiological maturity), number of nodes on the main stem (NMS), weight of pods per plant (PW1), Pod length free tail (PFL), length seed (mm) (SL), seed diameter (SD), chlorophyll fluorescence (CHF), number of days to 50% flowering (DF-50%) (from the date of sowing to the date on which approximately 50% tillers produced flowers), number of days to 50% pods (DP-50%) (from the date of sowing to the date on which approximately 50% tillers produced pods), Pods width (PW2), Straw weight (StW), From these measurements, estimates of harvest index using Eq. 1 were also computed and analyzed.

$$HI = GY/BY \tag{1}$$

Genetic Parameters Estimates

Heritability in broad sense (H²) was estimated according to Falconer (1989) using eq. 2.

$$H^2 = \frac{\sigma^2 g}{\sigma^2 ph} \tag{2}$$

h^2: Heritability; $\sigma^2 g$: genotypic variance and σ^2 ph: phenotypic variance. Genotypic ($\sigma^2 g$) and phenotypic variances ($\sigma^2 ph$) were obtained from the analysis of variance table according to Comstock & Robinson (1952) using eq. 3 and eq. 4.

$$\sigma^2 g = \frac{ms1 - ms2}{r \times y} \tag{3}$$

$$\sigma^2 ph = \frac{ms1}{r \times y} \tag{4}$$

r: replication, y; year, MS1: Mean square for cultivar, MS2: Mean square for cultivar × season.

The mean values were used for genetic analyses to determine Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV), according to Singh & Chaudhury (1985) using eq. 5 and eq. 6.

$$GCV(\%) = \frac{\sqrt{\sigma^2 g}}{x} \times 100 \tag{5}$$

$$PCV(\%) = \frac{\sqrt{\sigma^2 ph}}{x} \times 100 \tag{6}$$

Where: genotypic variance $\sigma^2 g$, phenotypic variance ($\sigma^2 ph$), sample mean (x). Genetic advance (GA) was calculated with the method suggested by Allard (1960); Singh & Chaudhury (1985) using eq. 7.

$$GA = K.\sigma ph.h^2 \tag{7}$$

Genetic advance (GA), constant = 2.06 at 5% selection intensity (K), square root of phenotypic variance (σph). Heritability (H²).

GA as % of mean GAM= (GA/mean value) X 100 (8)

Phenotypic and genotypic correlations were approximation using the standard procedure suggested by Miller et al. (1958) and Kashiani & Saleh (2010) from the corresponding variance and covariance components using eq. 9 and eq. 10.

$$\text{Phenotypic correlation coefficient } rpxy = \frac{\sigma pxy}{\sqrt{\sigma^2 px \times \sigma^2 py}} \tag{9}$$

$$\text{Genotypic correlation coefficient } rgxy = \frac{\sigma gxy}{\sqrt{\sigma^2 gx \times \sigma^2 gy}} \tag{10}$$

Where, r pxy = phenotypic correlation coefficient between characters X and Y and r gxy= Genotypic correlation coefficients between characters X and Y.

Statistical Analysis

Analysis of variance, for all the characters evaluated using the computer software system of SAS (SAS Institute 2002).

Table 2. Statistical model for analysis of variance for combined data of two seasons.

Source of variation	df	MS	Expected MS
year (Y)	Y-1	-	-
Rep. within Year	Y(r-1)	-	-
Cultivars (G)	G-1	MS1	$\sigma^2 e + \sigma^2 gy + yr\sigma^2 g$
G × Y	(Y-1)(G-1)	MS2	$\sigma^2 e + r\sigma^2 gy$
Pooled error	y(r-1)(G-1)	MS3	$\sigma^2 e$

Results

Phenotypic variation: The results of analyses of variance over two years for the studied characteristics are presented in Table 3. Grain yield and some grain quality characteristics of the nine genotypes introduced from Greece and Iran landraces were assessed in two year study and a high significant variability among the common bean genotypes were determined with respect to the studied parameters (Table 4).

Table 3a. Analysis of variance for plant height (PH), internode diameter (IND), number of nodes on the main stem (NMS), Pods width (PW2), biological yield pert plant (BY), weight of pods per plant (PW1) and number of seeds per pod (NSPP) and of 9 common bean genotypes grown under field conditions. (* Significant at the 0.05 probability level)

Source of variation	PH	IND	NMS	PW2	BY	PW	NSPP
year (Y)	5104.16*	0.051	0.11	1.570**	70548.172	70548.172	5.36
Rep. within Year	105.314	0.01	5.38	0.026	152.52	152.52	0.615
Cultivars (G)	22362.18**	0.020	573.27**	0.121*	13929.3**	5245.25**	2.853
G × Y	882.86**	0.025**	2.80	.0096	873.215	574.87*	1.04**
Pooled error	254.740	.0041	4.51	10.92	903.51	184.41	0.266

Table 3b. Analysis of variance for chlorophyll fluorescence (CHF), Pod length free tail (PFL), grain yield per plant (GY), length seed (SL), seed diameter (SD), harvest index (HI) and internodal length (INL) of 9 common bean genotypes grown under field conditions. (* Significant at the 0.05 probability level)

Source of variation	CHF	PFL	GY	SL	SD	HI	INL
year (Y)	0.0044	6.38	9669.458**	0.992**	0.098**	732.909	3.81
Rep. within Year	0.0087	0.445	52.35	0.026	0.0011	28.46	1.182
Cultivars (G)	0.043**	16.079**	1972.092**	0.30*	0.011	7869.988*	7.15
G × Y	0.0032	2.525**	248.86**	0.037*	0.006**	167.034**	3.106
Pooled error	0.010	0.622	69.97	0.012	0.0011	51.038	1.52

Table 3c. Analysis of variance for hundred seed weight (HSW), days to 50% flowering (DF-50%), number of days to 50% pods (DP-50%) and Straw weight (StW) of 9 common bean genotypes grown under field conditions. (* Significant at the 0.05 probability level)

Source of variation	HSW	DF50%	DP50%	StW
year (Y)	849.422	196.46	3986.96*	28049.47
Rep. within Year	46.90	43.18	117.46	31.39
Cultivars (G)	177.85	1723.87*	2289.83**	9384.60**
G × Y	236.827**	287.129**	340.004**	509.581
Pooled error	42.19	38.01	46.15	764.32

Effects of cultivar (V) were found to be significant for all the parameters, except for internode diameter (IND), number of seeds per pod (NSPP), seed diameter (SD), internodal length (INL) and hundred seed weight (HSW).

Genetic variability: Genotypic variance, phenotypic variance, genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), broad sense heritability, genetic advance and genetic advance expressed as percentage of mean for 13 characters are presented in Table 4.

Estimates of Heritability: The results revealed considerable phenotypic and genotypic variances among the genotypes for the traits under consideration. In all traits a large portion of the phenotypic variance was accounted for by the genetic component and the contributions of genetic variance to phenotypic variance were more than 51% (Table 4). The estimates of GCV were high for harvest index (123.98), number of nodes on the main stem (70.04), weight of pods per plant (54.13), grain yield per plant (50.33). The remaining traits recorded moderate to low GCV estimates. The PCV values

Table 4a. Genetic parameters for some characteristics in common bean genotypes grown during two seasons 2011 /2012 and 2012 /2013 under field conditions.

Source of variance	Mean square								
	PH	IND	NMS	PW2	BY	PW	NSPP	CHF	PFL
$\sigma^2 g$	225.55	-0.0008	95.07	0	2176.014	778.39	0.302	0.006	2.25
$\sigma^2 ph$	372.69	0.0033	95.25	0.02	2327.08	874.20	0.47	0.0071	4.39
Heritability %	0.60	-0.242	0.99	0	0.93	0.89	0.63	0.929	0.51
GCV(%)	15.24	-4.56	70.04	0	40.24	54.13	15.05	11.44	14.15
PCV(%)	19.60	9.26	70.11	15.75	41.62	57.36	18.88	11.86	19.73
GA	23.85	-0.02	19.88	0	92.41	54.190	0.88	0.15	2.19
GAM	95.34	-3.22	142.8	0	79.73	105.14	24.10	21.12	20.62

Table 4b. Genetic parameters for some characteristics in common bean genotypes grown during two seasons 2011 /2012 and 2012 /2013 under field conditions.

Source of variance	Mean square								
	GY	SL	SD	HI	INL	HSW	DF50%	DP50%	StW
$\sigma^2 g$	287.20	0.043	0.0008	1283.82	0.67	-9.82	239.45	324.97	1479.16
$\sigma^2 ph$	328.68	0.049	0.0017	1311.65	1.19	29.64	287.30	381.63	1564.09
Heritability %	0.873	0.87	0.47	0.97	0.56	-0.33	0.83	0.85	0.94
GCV (%)	50.33	18.68	7.78	123.98	13.13	11.86	20.56	19.02	46.77
PCV(%)	53.84	19.96	11.24	125.31	17.46	20.59	22.52	20.62	48.100
GA	32.47	0.35	0.03	72.36	1.25	3.69	28.98	34.19	76.58
GAM	96.43	31.53	8.10	250.38	20	13.96	38.51	36.08	93.14

Table 5. Genotypic (Bold) and phenotypic correlations among different quantitative characters common bean.

	PH	NMS	PW	PFL	SL	DF50%	DP50%	BY	GY	PW2	StW	HI	CHF	NSPP
PH	1	0.97**	0.26	-0.64	-0.47	0.96**	0.97**	0.79*	0.25	-0.39	0.85**	-0.12	0.63	-0.49
NMS	**0.99**	1	0.30	-0.66	-0.50	0.97**	0.98**	0.85**	0.29	-0.37	0.91**	-0.13	0.52	-0.53
PW	**0.30**	**0.30**	1	-0.17	0.11	0.19	0.21	0.65	1**	-0.48	0.76*	0.19	0.70*	0.40
PFL	**-0.67***	**-0.70***	**-0.17**	1	0.54	-0.65	-0.62	-0.55	-0.19	0.8	-0.59	0.07	-0.07	0.57
SL	**-0.45**	**-0.54**	**0.18**	**0.54**	1	-0.52	-0.53	-0.33	0.11	0.23	-0.47	0.13	0.15	0.61
DF50%	**0.95****	**0.99****	**0.22**	**-0.68***	**-0.50**	1	0.99**	0.84**	0.18	-0.38	0.94**	-0.15	0.60	-0.46
DP50%	**0.97****	**0.98****	**0.17**	**0.63**	**-0.50**	**1.07****	1	0.87**	0.19	-0.35	0.94**	0.98**	0.58	-0.48
BY	**0.84****	**0.88****	**0.78****	**-0.50**	**-0.27**	**0.88****	**0.85****	1	0.63	-0.54	0.93**	0.03	0.84**	-0.11
GY	**0.29**	**0.28**	**1.17****	**-0.22**	**0.17**	**0.23**	**0.17**	**0.76***	1	-0.50	0.31	0.15	0.70*	0.43
PW2	**-0.38**	**-0.36**	**-0.55**	**0.85****	**0.33**	**-0.41**	**-0.31**	**-0.56**	**-0.66**	1	-0.42	-0.09	0.33	0.10
StW	**0.89****	**0.95****	**0.93****	**-0.52**	**-0.42**	**0.97****	**0.97****	**1.38****	**0.36**	**-0.38**	1	0.16	0.70*	-0.34
HI	**-0.13**	**-0.14**	**0.23**	**0.06**	**0.13**	**-0.13**	**0.98****	**-0.08**	**0.19**	**-0.14**	**0.07**	1	0.06	0.21
CHF	**0.63**	**0.54**	**0.55**	**0.25**	**0.22**	**0.56**	**0.55**	**0.70**	**0.55**	**0.22**	**0.6**	**0.09**	1	0.50
NSPP	**-0.48**	**-0.51**	**0.63**	**0.68***	**0.76***	**-0.45**	**-0.59**	**0.08**	**0.60**	**0.06**	**-0.18**	**0.25**	**0.37**	1

were higher than GCV values for all the traits which reflect the influence of environment on the expression of traits. The results of heritability indicated that a high heritability value was recorded for weight of pods per plant as yield components.

Estimates of expected genetic advance: The expected genetic advance values for 13 characters of the genotypes evaluated is presented in Table 4. Straw weight, harvest index, grain yield per plant, weight of pods per plant, biological yield pert plant and number of nodes on the main stem had high heritability accompanied with high genetic advance, while number of days to 50% flowering, number of days to 50% pods, length seed, and chlorophyll florescence had high heritability coupled with low genetic advance.

Genotypic and phenotypic correlations among characters: The phenotypic and genotypic correlations for traits are presented in Table 5. A positive association between grain yield and biological yield pert plant was obtained but there was no significant genetic correlation.

Discussion

In effort to determine the extent to which diversity in yield components are responsible for differences in yield among various cultivars, it must remember that overall variability depends on heritable and non-heritable components. While coefficients of variation measure the magnitude of variability present in a population, estimates of heritability and genetic advances are important preliminary steps in any breeding program as they provide information needed in designing the most effective breeding program and the relative practicability of selection (Sadeghi et al. 2011). The expected genetic advance values expressed as percentage of the genotypes mean for each character so that comparison could be made among various characters, which had different units of measurement. High heritability along with high genetic advance is an important factor for predicting the resultant effect for selecting the best individuals (Sadeghi et al. 2011). Weight of pods per plant gave the highest positive significant phenotypic and genotypic association with grain yield per plant implying that improving this character could result in high grain yield. The significant positive correlation of weight of pods per plant with yield per plant has been reported by Sabokdast et al. (2007), Santalla et al. (2004), Khshy (2012) and Dymvra et al. (1993).

The significant differences among common been genotypes in the investigation indicate the presence of genetic variability in the material used and provide a good opportunity for yield improvement. High ratios of the genotypic variance to phenotypic variance for number of nodes on the main stem, biological yield pert plant, weight of pods per plant, chlorophyll florescence, grain yield per plant, length seed, harvest index and straw weight indicate the existence of immense inherent variability that remains unaltered by environmental conditions among the genotypes, which in turn is more useful for exploitation in selection and hybridization programs. Although the genotypic coefficient of variation revealed the extent of genetic variability present in the genotypes for various traits, it does not provide full width to assess the variation that is heritable. Heritable variation is useful for permanent genetic improvement (Singh 2000). The largest use heritability of quantitative traits in genetic studies is to determine the predictive value of phenotypic reliable as a guide to crop improvement (Dabholkar 1992, Falconer & Mavkey 1996). The genotypic coefficient of variation along with heritability estimates provide reliable estimates of the amount of genetic advance to be expected through phenotypic selection (Burton 1952). High heritability estimates for number of nodes on the main stem, biological yield per plant, weight of pods per plant, chlorophyll florescent, grain yield per plant, length seed, harvest index, number of days to 50% flowering, number of days to 50% pods and Straw weight indicate a high response to selection in these traits. Heritability and genetic advance are important selection parameters. The estimate of genetic advance is more useful as a selection tool when considered jointly with heritability estimates (Johnson et al. 1955). High amount of genetic advance are suggests of additive gene action while low amounts are suggests of non-additive gene action (Singh and Narayanan, 1993). Thus the heritability estimates will be trustworthy if accompanied by high genetic advance. High estimates of heritability along with high genetic advance as percent of mean was observed for number of nodes on the main stem, weight of pods per plant, grain yield per plant, harvest index, straw weight and biological yield pert plant shows that these are simply inherited traits and most likely the heritability is due to additive gene effects and selection may be effective in early generations for these traits. However, length seed, number of days to 50% flowering and number of days to 50% pods had high heritability coupled with low genetic advance indicates non-additive gene effects.

According to the above discussion, number of nodes on the main stem, biological yield pert plant, weight of pods per plant, grain yield per plant, harvest index and Straw weight were shown to have high to moderate genotypic variance, high to moderate heritability and greater genetic gain. Selection can therefore be based on these characters and their phenotypic expression would be a good indicator of their genotypic potentiality. The remaining traits recorded lower scores in the three genetic parameters considered in this study and therefore offered less scope for selection as they were much more under the influence of the environment. An understanding of inter-character correlation is essential to successful selection of useful genotypes from the whole population but intensive selection for any characteristic might result in losses in others (Nienhuis & Singh 1988). The importance of genetic and phenotypic correlation and its use has been selection by a number of researchers (Chung & Goulden 1971, Denis & Adams 1978, Kelly & Adams 1987). The genotypic correlation coefficient measures the intensity of genetic relationship between treats and offers may provide important criteria for the selection process (Can & Yoshida 1999). A lot of genotypic correlation coefficients traits were significant than their corresponding phenotypic correlation coefficient values, this indicates that the traits are inherited. Significant correlation between grain yield per plant

and weight of pods per plant is achieved in two years. Therefore, selection for weight of pods per plant increase grain yield per plant. Correlation between variables was important to state that there is, and how this relationship is also important to know the relation.

Path analysis (data not shown) was carried out in this study. In the present study, the initial level of grain yield per plant, weight of pods per plant had the highest (1.313) direct effect on grain yield. The indirect effects of biological yield per plant through weight of pods per plant were high (0.85). As a result, it is better to not use the trait biological yield to enhance grain yield, previous studies have confirmed this result (Dursun 2007, Amini et al. 2002). Path analysis revealed that the secondary level straw weight has the most direct effect on biological weight (0.884) as well as the indirect effects of number of nodes on the main stem through straw weight had the highest (0.80) indirect effect through on biological weight Which is consistent with the results Akhshy (2012). Path analysis revealed that the tertiary level number of days to 50% pods has the most direct effect on straw weight (1.54). Therefore, the selection of number of days to 50% pods We attempt to increase the weight of straw, In addition to grain yield, for breeding purposes, fodder used.

The present study revealed that grain yield per plant had strong and positive genotypic correlation with weight of pods per plant. Path analysis indicated that the initial level of grain yield per plant, weight of pods per plant had the highest (1.313) direct effect on grain yield. So, it is concluded that these trait may be considered as the selection criteria for the improvement of grain common bean.

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