

**GENETIC VARIABILITY, HERITABILITY AND EXPECTED GENETIC  
ADVANCE AS INDICES FOR YIELD AND YIELD COMPONENTS  
SELECTION IN COMMON BEAN (*PHASEOLUS VULGARIS* L.)**

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**Abstract**

*The present study was conducted at the University of Agronomic Sciences and Veterinary Medicine Bucharest, during the 2009 growing season and were evaluated four hybrid population: (Ami x SEA13)F<sub>2</sub>, (Starter x SEA13)F<sub>2</sub>, BC<sub>1</sub>-1(F<sub>1</sub> x Ami), BC<sub>2</sub>-2(F<sub>1</sub> x Starter). The aims of this work were to estimate the variance components, phenotypic and genotypic coefficients, heritability for seed yield and its components (pods number per plant, seeds number per pod, 1000-seed weight, seed yield per plant) and expected genetic advance as indices for yield selection in common bean. The highest proportion of genetic variance presented a number of seed per pod in both crosses (crosses 1  $V_g = 40\%$ ; crosses 2  $V_g = 50\%$ ). Amongst the yield characters, a very small difference between GCV% and PCV% was observed for the character seeds number per pod in both crosses and both generations. Large difference between GCV% and PCV% was observed for the number of seed characters per plant, 1000-seeds weight and seed yield per plant. This indicated the role of environmental influence on this characters. Moderate heritability coupled with high genetic advance were observed for pod number per plant, seed number per pod and seed yield per plant in both generations and both crosses.*

**INTRODUCTION**

Yield is the principal factor for determining improvement of a crop. Like other legumes, seed yield in common bean (*Phaseolus vulgaris* L.) is a quantitative character and influenced by a number of yield contributing traits. The selection of desirable types should therefore be based on yield as well as on other yield components. Information on mutual association between yield and yield components is necessary for efficient utilization of the genetic stock in crop improvement program of this crop.

Seed yield in common beans is a complex trait with three components: number of pods per plant, number of seeds per pod, and mean seed weight [8]. Heritability, or the degree of genetic control associated to some interest trait, is one of the most important parameters within the breeding context. Heritability indicates how much of the phenotypic variability has a genetic origin, and gives objective information for the genetic selection process [6]. For any planned breeding programs aimed to

improve grain yield potentials of crops, it is necessary to obtain adequate information on the magnitude and type of genetic variability and their corresponding heritability. This is because selection of superior genotypes is proportional to the amount of genetic variability present and the extent to which the characters are inherited. Heritability for example, is used to indicate the relative degree to which a character is transmitted from parent to offspring. The magnitude of such estimates also suggests the extent to which improvement is possible through selection. The present study was undertaken to estimate the variance components, heritability for seed yield and its components and expected genetic advance.

## MATERIAL AND METHODS

This research work was carried out at University of Agronomic Sciences and Veterinary Medicine Bucharest during the 2009 growing season. We included in this study two hybrid combinations for each population: F2-1 = Ami x SEA 13, F2-2 = Starter x SEA 13; BC1-1 = F1-1 x Ami; BC1-2 = F1-2 x Starter. The initial breeding material (F1, F2, BC1), using three parents: SEA 13, Ami, Starter, was achieved with cyclical and backcross hybridations in the 2007-2008 period under greenhouse conditions. The genotypes for crosses were selected based on variability for growth habit, maturity, seed size and resistance to drought (Table1). The populations F2, BC1, were studied in the field in 2009 year. Sowing was done manually in the bean breeding field. The experimental design was random blocks, in three replications. Each single row was 4 m long, spaced 65 cm apart and with 6 cm between plants within row. It represented single plant selection. Number of pods per plant, number of seeds per pod, 100-seeds weight and seed yield per plant were determined.

### Statistical analysis

Phenotypic variance ( $V_P$ ), genotypic variance ( $V_G$ ), and environmental variance ( $V_E$ ) were determined by formulas proposed by Brewbaker [3]. Broad sense heritability ( $H_{bs}$ ) was calculated using the formula proposed by Mahmud și Kramer [7]. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PGV) were estimated by the formula suggested by Burton [4]:  $GCV = \frac{\sigma^2_g}{\bar{X}} \times 100$ ;  $PCV = \frac{\sigma^2_p}{\bar{X}} \times 100$ , were  $\sigma^2_g$ ,  $\sigma^2_p$  are standard deviation of the genotypic and phenotypic variances and  $\bar{X}$  is the mean performance of each trait. The genetic advance (GA) was calculated according to Allard's [1], and was estimated from the following formula:  $GA = K \times \sigma_p \times h^2_b$ , were K-the selection differential in standard units in the present study and it was 2.06 at 5% level of selection;  $\sigma_p$  - standard deviation of the phenotypic variance of F2;  $h^2_b$ —heritability in broad sense. Genetic advance expressed as percentage of mean (GA%) was measured by the following formula:  $GA\% = \frac{GA}{\bar{X}} \times 100$ .

*Table 1*

**Characteristics of parents used in crosses: origin country, growth habit (GH), seed size (SS), seed color (SC), maturity (M) and other features**

<b>Cultivars</b>	<b>Origin*</b>	<b>GH**</b>	<b>SS***</b>	<b>SC</b>	<b>M</b>	<b>Features</b>
SEA 13	Colombia CIAT	III	Small	Cream	80	Drought resistance
AMI	Romania NARDI Fundulea	III	Medium	White	76	Low maturity Rust resistance
STARTER	Romania NARDI Fundulea	II	Small	White	82	<i>Xanthomonas</i> sp. resistance

*\*ICTA-International Centre of Tropical Agriculture, NARDI - National Agricultural Research and Development Institute; \*\*\*Size according with Singh et al.(1991a) weight of 100 seeds in grams (Small – 100 seeds <25 g; Medium – 100 seeds ≥ 25 g to ≤ 40 g; Large – 100 seeds > 40 g); II - indeterminate upright bush; III - indeterminate semi-viney prostrate.*

**RESULTS AND DISCUSSION**

**Means and variances**

The mean values as well as phenotypic, genotypic and environmental variances of the characters studied are presented in Table 2. Analysis of main values for the characters pod number per plant, seed number per pods, 1000-seeds weight and seed yield per plant, highlights that a wide variability between genitors used in hybridization exists for these traits. Analysis of genotypic and environmental variances resulted in differential contribution of genotypes in hereditary character, expressed by weighting different genotypic variance in the phenotypic variance, from a cross to another. Also resulted importance of environmental variance in phenotypic expression of characters analyzed. The highest proportion of genetic variance in phenotypic variance presented seed number per pod, environment having less influence in the expression of this character, unless phenotypic expression of the other characters studied. Characters are influenced differently by environmental conditions. Its variations caused substantial changes in expression of the characters “pod number per plant”, “1000-seeds weight” and therefore “seed yield per plant” and changes were less pronounced for “seed number per pods”.

**Coefficients of variation**

The comparison of characters as regards to the extent of genetic variation could be better judged by the estimation of genotypic coefficient of variation (GCV) in relation to their respective phenotypic coefficient of variation (PCV). Amongst the yield characters very small difference between GCV and PCV was observed for the character like seed number per pod in both crosses and both generations (Table 3).

It indicates that the observed variations for the trait were mostly due to genetic factors. However, the environment played a little role on the expression of this trait.

Table 2

Mean ( $\bar{X}$ ), phenotypic and genotypic variance ( $V_P, V_G$ ), genotypic variance express as percentage of phenotypic variance ( $V_G \%$ ), environmental variance ( $V_E$ ), environmental variance ( $V_E$ ) express as percentage of phenotypic variance ( $V_E \%$ ) in two crosses of common bean - F2, BC1

Crosses	Genetic parameters	Traits			
		Pods per plant	Seeds per pod	1000-seeds weight (g)	Seed yield per plant (g)
Ami x SEA 13	$\bar{X}_{F2}$	21.90	4.39	230.8	19.55
	$\bar{X}_{BC1}$	21.15	4.34	250.3	22.67
	$V_P$	2.73	0.05	42.25	4.92
	$V_G$	1.00	0.02	16.35	1.59
	$V_G \%$	36.63	40.00	38.69	32.30
	$V_E$	1.73	0.03	25.90	3.33
	$V_E \%$	63.37	60.00	61.31	67.70
Starter x SEA 13	$\bar{X}_{F2}$	23.26	4.53	249.8	20.16
	$\bar{X}_{BC1}$	20.33	4.45	261.0	29.16
	$V_P$	3.06	0.08	64.92	4.33
	$V_G$	1.26	<b>0.04</b>	28.30	1.05
	$V_G \%$	41.17	50.00	43.59	24.25
	$V_E$	1.80	0.04	36.62	3.28
	$V_E \%$	58.83	50.00	56.41	75.75

On the other hand, large difference between GCV and PCV was observed for the characters pod number per plant, 1000-seeds weight and seed yield per plant. This indicated the role of environmental influence over this characters (Table 3).

In this experiment, high GCV was observed in character like seed yield per plant. The high GCV for this trait indicated further selection could improve the genotypes.

#### Heritability and genetic advance

Johnson et al. [5] reported that effectiveness of selection depends not only on heritability but also on genetic advance. Moderate heritability coupled with high genetic advance were observed for pod number per plant, seed number per pod and seed yield per plant in both generations and both crosses (Table 4). Similar results were reported by Asifa et al. [2], indicating that these traits are mainly controlled by additive type of genes. However, moderate heritability coupled with low genetic advance was observed for 1000-seeds weight in both generations, both crosses (Table 4). Thus this character is controlled by non-additive genes (dominance and epistasis). Our results agreed with those of Singh and Singh [9]. Therefore, judicious application of pure line selection may be effective for improving the characters with moderate or high heritability and with low genetic advance.

Table 3

**Estimates to genotypic and phenotypic coefficients of variation  
(GCV - %, PGV - %) in two crosses of common bean F2, BC1**

Crosses	Genetic parameters	Traits			
		No. pods per plant	No. seeds per pod	1000-seeds weight (g)	Seed yield per plant (g)
Ami x SEA 13	GCV – F2	4.56	3.18	1.75	6.44
	PCV – F2	7.53	5.01	2.81	11.35
	RD%	39.44	36.52	37.72	43.25
	GCV – BC1	4.72	3.22	1.61	5.55
	PCV – BC1	7.47	5.06	2.59	9.74
	RD%	36.81	36.36	37.83	43.01
Starter x SEA 13	GCV – F2	4.81	4.41	2.12	5.05
	PCV – F2	7.52	6.40	3.22	10.31
	RD%	36.03	31.09	34.16	51.01
	GCV - BC1	5.50	4.49	2.03	3.49
	PCV – BC1	8.55	6.29	3.08	7.13
	RD%	35.67	28.61	34.09	51.05

RD %: Relative difference between PCV% and GCV% =  $[100 (PCV-GCV)] / PCV$

Table 4

**Estimates of heritability in broad sense (H-bs), genetic advance (GA) and  
genetic advance express as percentage (GA %) mean of four quantitative  
characters in two crosses of common bean F2, BC1**

Crosses	Genetic parameters	No. pods per plant	No. seeds per pod	1000-seeds weight (g)	Seed yield per plant (g)
Ami x SEA 13	H-bs	0.36	0.40	0.38	0.32
	GA – F2	1.22	0.18	5.09	1.46
	GA % - F2	<b>5.57</b>	<b>4.10</b>	<b>2.20</b>	<b>7.46</b>
	GA - BC1	1.17	0.16	4.73	1.36
	GA % - BC1	<b>5.53</b>	<b>3.61</b>	<b>1.89</b>	<b>6.00</b>
Starter x SEA 13	H-bs	0.41	0.50	0.43	0.34
	GA - F2	1.48	0.23	7.14	1.03
	GA % - F2	<b>6.36</b>	<b>5.07</b>	<b>2.85</b>	<b>5.10</b>
	GA – BC1	1.36	0.27	6.39	0.99
	GA % - BC1	<b>6.69</b>	<b>6.07</b>	<b>2.45</b>	<b>3.40</b>

## CONCLUSIONS

1. The genetic parameters discussed here are functions of environmental variability, so estimates may differ in other environment. Based on the moderate heritability and high genetic advance shown by the different characters, especially, pod number per plant and seed number per pod, it could conclude that the determinant genetic effects of the phenotypic expression of these characters are fundamentally of the additive type. For this reason, a high response should be achievable after several selection cycles.

2. Seed yield can be improved in both crosses by selecting ideotypes having more number of pods per plant coupled with number of seeds per pod.

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