



RESEARCH PAPER

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Generation mean analysis to estimate genetic parameters for morphological traits in common bean (*Phaseolus vulgaris* L.)

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Article published on April 18, 2014

**Key words:** Three-parameter model, Hayman six parameters model, heritability, genetic advance, common bean.

**Abstract**

Six generation (P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub>) derived from two crosses ((A.1007 × DER.) and (GOLI × D81)) of common bean were grown in a randomized complete block design with three replication in 2010 at research field of Razi University, Kermanshah, Iran. Experiment was executed to estimate different genetic effects of five morphological traits (plant height, node number of main stem, node number of lateral branches, internode length and internode diameter) in common bean by using generation mean analysis. Results of analysis of variance showed that there was a genetic variation for traits. The results of generation mean analysis with three-parameter genetic model and also scaling tests (A, B, C and D) revealed inadequacy of the additive-dominance simple model to demonstrate the genetic mechanism controlling the traits. Hayman six parameters genetic model showed that dominance and epistasis effects were important in the inheritance of plant height, node number of main stem and node number of lateral branches, whereas only epistasis effect was important for internode length and internode diameter inheritance. Dominance effect had a more pronounced effect in genetic control of all characters. Furthermore, results of the study demonstrated existence of duplicate type of epistasis for most traits. Broad-sense heritability estimates were greater than narrow-sense heritability for all traits in both crosses. The genetic advance estimates were low for all the traits except for plant height in GOLI×D81083 cross.

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## Introduction

Common bean is the most important grain legume with yield potentials almost twice as chickpea legume (Broughton et al. 2003). The cultivated bean as an annual species with typical outcrossing rates less than 5% (Graham and Ranalli, 1997) is a morphologically diverse crop with large variation in growth (Singh *et al.*, 1991). To understand the gene action the knowledge of genetic variances, levels of dominance, and the importance of genetic effects is necessary (Wolf and Hallauer, 1977). Generation mean analysis is one of the genetic models which developed for the estimation of different genetic effects (Kearsey and Pooni, 2004). Generation mean analysis is a simple but useful technique for estimating gene effects for a polygenic trait, its greatest merit lying in the ability to estimate epistatic gene effects such as additive  $\times$  additive, dominance  $\times$  dominance and additive  $\times$  dominance effects (Singh and Singh, 1992). Besides gene effects, breeders would also like to know how much of the variation in a crop is genetic and to what extent this variation is heritable, because efficiency of selection mainly depends on additive genetic variance, influence of the environment and interaction between genotype and environment.

The evaluation of phenological and physiological traits of beans is a method studied to improve bean yields (Scully and Wallace, 1990; Scully *et al.*, 1991). Kornegay *et al.*, (1992) determined Growth habit and gene pool effects on inheritance of number of nodes on main stem and plant height in common bean. Karami *et al.*, (2011) carried out an experiment to determine gene action for some traits such as number of pods per plant of chickpea.

Heritability is an important parameter in breeding program. It indicates that how much of the phenotypic variability can be transmitted to the next generation (Falconer, 1981). The magnitude of such estimates also suggests the extent to which improvement is possible through selection. Nechifor *et al.* (2011) studied heritability for seed yield and its components and expected genetic advance.

Use of generation mean analysis in researches has some benefits such as :

1. Determine genotypic values of the individuals and consequently mean genotypic values of families and generations
2. Estimation the relative importance of average effects of the genes (additive effects), dominance deviations, and effects due to non-allelic genic interactions.
3. Use basic generations to provide powerful tests of the adequacy of a simple genetical model and in particular, complex effects such as epistasis, maternal effects, etc.

Many workers developed genetic model for the estimation of different genetic effects (Kunakew *et al.*, 2007; Checa *et al.*, 2006; Ojo *et al.*, 2006; Omoigui *et al.*, 2006; Kidambi *et al.*, 1997).

The aim of this study was to estimate the genetic parameters for morphological traits in common bean, using generation mean analysis, also broad sense heritability, narrow sense heritability and genetic advance for morphological traits in two crosses of common Bean estimates.

## Materials and methods

### *Plant materials and experimental Design*

Six different generations ( $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$ ) derived from two crosses involving (A.1007 ( $P_1$ )  $\times$  DER. ( $P_2$ )) and (GOLI ( $P_1$ )  $\times$  D81 ( $P_2$ )) were subjected to a field experiment. These six families are often referred to as the six basic generations.

A Randomized Complete Block Design (RCBD) with 3 replications was prepared at the research field of Razi University, Kermanshah, Iran in 2010. The plots of various generations had 3 rows. Each row was 3 m long with a between-row spacing of 50 cm and a within-row spacing of 10 cm. Before sowing, 50 Kg  $ha^{-1}$  N fertilizer was applied. The field was irrigated every five to seven days. Weeds were removed whenever appeared.

*Measurements*

The observations on plant height (PH), node number of main stem (NMS), node number of lateral branches (NAS) internode length (INL) and internode diameter (IND) were recorded. The number of analyzed plants per plot varied depending on the generations. Measurements were done according to the IPGRI (1982) descriptor list for *P. vulgaris* L.

*Statistical Manipulations*

Analysis of variance was done using MSTAT-C software. The three-parameter genetic model (Model 1, Mather and Jinks, 1982) was used for generation mean analysis. In addition, the individual scaling tests (A, B, C and D) of Mather (1949) and Hyman and Mather (1955) were employed to test their fitness to the additive-dominance model. In case of the inadequacy of the three-parameter genetic model and significance of scaling tests, six-parameter genetic model suggested by Hyman (1958) were used to estimate various genetic components.

Broad sense heritability ( $h_B^2$ ) and narrow sense heritability ( $h_N^2$ ) were calculated according to Warner (1952) and Allard (1960) formulas. The genetic advance ( $G_A$ ) was estimated according to Allard (1960), using  $G_A = k \times \sigma_p \times h_B^2$  formula, where  $k$  is 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  $F_2$  and  $h_B^2$ : broad sense heritability.

**Results and discussion**

*Analysis of variance*

The results of analysis of variance (Table 2) showed a significant difference among generations for all investigated traits, indicating the existence of genetic variation. Therefore, generation means for two crosses could be analyzed to estimate the genetic parameters for all traits.

**Table 1.** Characteristics of the cultivars used in this study

Cultivar	Characteristics					
	Introduced Place	Origin	Maturity time	Seed size	Growth type	Seed colour
A.1007	CIAT	Andian	Late	Large	indeterminate	Dark red
DER.	CIAT	Andian	Early	medium	determinate	Bright pink
GOLI	IRAN	Mesoamerican	Late	medium	indeterminate	Dark red
D81	CIAT	Andian	Early	Large	determinate	Red

CIAT: international center for tropical agriculture: A.1007: A.1007; DER.: DER.; D.81: D81

**Table 2.** Analysis of variance for all traits in common bean

SOV	df	Mean squares				
		PH	NMS	NAS	INL	IND
Replications	2	52.02	3.29	3.21	0.031	0.332
Generations	11	4016.27**	48.89**	47.8**	4.67**	0.305*
Error	22	68.71	2.48	1.50	0.40	0.103
C.V. (%)		7.58	11.23	9.55	8.20	6.63

\*\* , \*Significant at 0.01 and 0.05 levels of probability, respectively

Three-parameter genetic model

Three-parameter genetic model (Model 1, Mather and Jinks, 1982) and goodness of fit test of the model was estimated for traits (Table 3). To test the adequacy of the model, the residual error sum of squares was tested for goodness of fit, using a chi-square ( $\chi^2$ )

statistic. The results showed that chi-square ( $\chi^2$ ) statistic was significant in all cases. Also results depicted that the additive-dominance model was inadequate for all traits. Thus, it is difficult to estimate the genetic mechanism of these traits by this simple model.

**Table 3.** Estimated values of three-parameter genetic model for studied traits in two crosses of common bean

Cross	Parameter	Trait				
		PH	NMS	NAS	INL	IND
(DER.× A.1007)	[m] ±SE	100.43±1.26**	11.36±0.20**	10.45±0.21**	9.10±0.11**	4.65±0.06**
	[a] ±SE	-42.78±1.27**	-5.25±0.20**	-5.20±0.21**	0.57±0.12**	-0.18±0.06**
	[d] ±SE	7.68±1.94**	6.50±0.4**	6.48±0.38**	-3.40±0.13**	0.60±0.10**
	$\chi^2$	1547.62**	102.58**	68.04**	479.03**	13.79**
(GOLI× D81)	[m] ±SE	96.99±1.36**	12.40±0.48**	11.02±0.16**	7.96±0.09**	4.72±0.12**
	[a] ±SE	-42.83±1.35 <sup>ns</sup>	-5.08±0.48**	-4.87±0.16**	-0.16±0.09 <sup>ns</sup>	0.2±0.12**
	[d] ±SE	18.17±3.29 <sup>ns</sup>	3.75±1.03**	4.39±0.42**	-1.31±0.18**	-0.07±0.24**
	$\chi^2$	392.95**	32.54**	112.25**	99.15**	8.43**

\*\* , <sup>ns</sup> Significant at 0.01 level of probability and not significant, respectively

m: mean, [a] : additive and [d]: dominance gene effects

Individual scaling tests (A, B, C and D tests)

The individual scaling tests of Mather (1949) and Hyman and Mather (1955) were employed to test their fitness to the additive-dominance model. The results of scaling tests (Table 4) showed the A, B, C and D-scaling tests were significant for PH and INL in both crosses, while significant B and C-scaling test for NMS and NAS in A.1007 × DER. cross was recorded. In GOLI × D81 cross B-scaling test was significant for

NMS whereas B and D-scaling test were significant for NAS. For IND B-scaling test NAS significant. Thus in order to scaling tests results, significant differences for one or more tests in both crosses revealed. These significant tests indicate inadequacy of simple additive-dominance model, hence six parameters model was needed to explain the genetic variation. The scaling test also suggested the major role of epistasis for controlling studied traits.

**Table 4-** A, B, C and D scaling for the studied traits in two crosses of common bean

Cross	Parameter	Trait				
		PH	NMS	NAS	INL	IND
(DER.× A.1007)	A	81.76±5.53**	0.11±0.96 <sup>ns</sup>	-1.51±0.95 <sup>ns</sup>	5.42±0.41**	-0.06±0.23 <sup>ns</sup>
	B	172.82±4.98**	8.42±0.89**	5.30±0.88**	6.59±0.44**	1.35±0.22**
	C	202.69±10.64**	8.54±1.74**	4.94±1.83**	8.73±0.84**	0.76±0.44 <sup>ns</sup>
	D	-25.95±5.94**	0.001±0.94 <sup>ns</sup>	0.58±1 <sup>ns</sup>	-1.55±0.48**	0.23±0.24 <sup>ns</sup>
(GOLI× D81)	A	58.17±8.08**	2.17±2.74 <sup>ns</sup>	-0.29±1.07 <sup>ns</sup>	2.67±0.37**	0.25±0.53 <sup>ns</sup>
	B	148.53±7.60**	13.67±2.40**	10.23±1.01**	3.11±0.39**	-1.42±0.54**
	C	66.83±15.73**	5.80±5.41 <sup>ns</sup>	-0.34±2.19 <sup>ns</sup>	2.83±0.71**	0.15±1.10 <sup>ns</sup>
	D	-69.94±8.33**	-5.02±2.94 <sup>ns</sup>	-5.14±1.16**	-1.47±0.37**	0.66±0.58 <sup>ns</sup>

\*\* , <sup>ns</sup> Significant at 0.01 level of probability and not significant, respectively

*Hayman six parameters model*

Due to inadequacy of the three-parameter genetic model and significance of scaling tests, six parameters model suggested by hayman (1958) were used to estimate genetic components (Table 5). The results revealed that for PH in both cross, only additive component was not significant, therefore dominance effects and epistasis was important in the inheritance of this trait. For NMS in A.1007 × DER. cross, all components except [i] was significant, thus additive × additive genetic interaction effect was not important in the control of NMS in this cross, whereas in GOLI × D81 cross, dominance effect, additive × dominance and dominance × dominance interaction effects were important. Additive and dominance genetic effects

and additive × dominance interaction were important in the inheritance of NAS in DER.×A.1007 cross, while in GOLI×D81 cross, dominance effect and epistasis were important. For INL in DER.×A.1007 cross, only [l] component was significant, therefore in this cross dominance × dominance epistasis is important in the inheritance of this trait whereas in GOLI×D81 cross, the components [i] and [l] were significant indicating the role of additive × additive and genetic interaction effect in controlling of INL in current cross. For IND only additive × dominance [j] effect was significant in both cross. Thus additive × dominance epistasis is important in the inheritance of this trait.

**Table 5.** Estimated values of six-parameter genetic model for the studied traits in two crosses of common bean

Cross	Parameter	Trait				
		PH	NMS	NAS	INL	IND
(DER.×A.1007)	[m]	136.45±2.47**	15.86±0.38**	15.20±0.41**	0.82±0.14*	-5.19±0.10**
	[d]	-6.32±3.30 <sup>ns</sup>	1.40±0.56**	2.09±0.56**	-0.11±0.62 <sup>ns</sup>	0.12±0.09 <sup>ns</sup>
	[h]	56.07±12.05**	5.21±1.93**	5.79±2.03**	-1.23±2.19 <sup>ns</sup>	0.10±0.001 <sup>ns</sup>
	[i]	51.89±11.89**	-0.01±1.89 <sup>ns</sup>	-1.15±1.99 <sup>ns</sup>	0.67±2.16 <sup>ns</sup>	0.17±0.09 <sup>ns</sup>
	[j]	-45.53±3.60**	-4.15±0.60**	-3.40±0.60**	-0.14±0.69 <sup>ns</sup>	0.4±0.1**
	[l]	-306.5±16.97**	-8.52±2.84**	-2.64±2.88 <sup>ns</sup>	3.13±0.65**	0.33±0.26 <sup>ns</sup>
(GOLI×D81)	[m]	103.13±3.43**	14.38±1.23**	12.29±0.49**	7.43±0.15**	4.88±0.24**
	[d]	-1.25±4.73 <sup>ns</sup>	-0.33±1.60 <sup>ns</sup>	-0.07±0.64 <sup>ns</sup>	0±0.22 <sup>ns</sup>	0.47±0.32 <sup>ns</sup>
	[h]	125.59±17.10**	11.73±5.98*	13.25±2.38**	0.96±0.77 <sup>ns</sup>	-1.32±1.19 <sup>ns</sup>
	[i]	139.87±16.66**	10.03±5.87 <sup>ns</sup>	10.28±2.32**	2.94±0.75**	-1.32±1.16 <sup>ns</sup>
	[j]	-45.18±4.94**	-5.75±1.68**	-5.26±0.66**	-0.22±0.24 <sup>ns</sup>	0.83±0.34**
	[l]	-346.6±24.60**	-25.87±8.38**	-20.22±3.3**	-8.72±1.14**	2.48±1.68 <sup>ns</sup>

\*\* , \* , <sup>ns</sup> Significant at 0.01 and 0.05 levels of probability and not significant, respectively mean (m); additive genetic effect (d); dominance genetic effects (h); additive × additive genetic interaction effect (i); additive × dominance interaction effects (j); dominance × dominance interaction effects (l)

The results of the study revealed that [d] component was not significant for PH, INL and IND in both cross, indicating that selection in early generation will not be effective. In both crosses the contribution of dominance effect (h) was greater than additive effect (except IND in DER×A1007 cross). Therefore, dominance genes were the most important factors contributing to the genetic control of traits. A

negative estimate of dominance in some cases might be due to epistatic gene action in the cross combinations. Significance of (j) for PH, NMS, NAS and IND in both crosses, revealed that selection through selfing is not effective for improving these traits (Farshadfar et al., 2001; Sharifi, 2005), because among the digenic interactions, additive × dominance type is more fixable and more useful for plant

breeders, In addition, the opposite signs of [h] and [l] for all traits in both crosses except IND in

DER×A1007 cross, suggested duplicate type of epistasis (Sunil Kumar, 2005).

**Table 6.** Estimates of broad sense heritability ( $h_b^2$ ), narrow sense heritability ( $h_n^2$ ) and genetic advance (GA) in two crosses of common bean

Cross	Parameter	Trait				
		PH	NMS	NAS	INL	IND
DER.× A.1007	$h_b^2$	0.57	0.36	0.49	0.52	0.29
	$h_n^2$	0.47	0.13	0.45	0.41	0.25
	GA	13.21	1.30	1.90	0.97	0.27
GOLI×D8 1	$h_b^2$	0.48	0.55	0.57	0.21	0.32
	$h_n^2$	0.37	0.31	0.54	0.17	0.28
	GA	15.60	2.42	2.64	0.30	0.28

*Broad sense and narrow sense heritabilities*

According to the broad sense heritability ( $h_b^2$ ) and narrow sense heritability ( $h_n^2$ ) estimation (table 6) it can be seen that NAS, NMS and IND in DER.×A.1007 cross was shown

Moderate  $h_b^2$  (0.2-0.5) but PH and INL in this cross revealed high (greater than 0.5)  $h_b^2$  (Stanfield, 2002). In DER.×A.1007 cross moderate  $h_n^2$  was seen for PH, NAS, INL and IND but it was low for NMS. In contrast in GOLI×D81 cross, all traits (except INL which showed low  $h_n^2$ ) demonstrated moderate  $h_n^2$ . It can be seen that  $h_b^2$  estimates were greater than  $h_n^2$  for all traits in both crosses. Considering that  $h_b^2$  was not low for none cases, concluded that environmental effects constitute a minor portion of the total phenotypic variation for these characters. High estimates of  $h_b^2$  for PH and INL in DER.×A.1007 cross and NMS and NAS in GOLI×D81 cross indicated that selection based on mean values would be successful in improving these traits.

The genetic advance ( $G_A$ ) estimates (table 6) was low for node number of main stem, node number of lateral branches, INL and IND in both crosses, and also for PH in DER.×A.1007 cross, whereas it was moderate for PH in GOLI×D81 cross.

Moderate heritability coupled with high  $G_A$  were observed for PH in GOLI×D81 cross, suggesting that PH is mainly controlled by additive type of gene action in this cross. However moderate or high heritability coupled with low  $G_A$  was observed for all traits in both crosses except PH in GOLI×D81 cross, showing that these characters are controlled by non-additive genes (dominance and epistasis). Therefore judicious application of pure line selection may be effective for improving characters with moderate or high heritability and with low  $G_A$ .

**Acknowledgements**

The authors are grateful to Mr. H. R. Dori, staff of National Bean Research Station in Khomein town, for help in providing the plant materials.

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