# Estimates of genetic parameters in common bean genotypes

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### ABSTRACT

Sixteen common bean genotypes, commercial varieties and advanced lines, were assessed at the Nucleus of Agrarian Sciences at the Federal University of Mato Grosso do Sul, Dourados campus, in the 'dry' harvest 2000/2001. Genetic and phenotypic parameters in control of morpho-physiological traits and yield components were estimated. These parameters were estimated at plant level. Variance estimates between and within genotypes and at plot level were obtained in randomized complete block experiments. Three replicates of each genotype were available for the calculations. The populations under study had wide genetic variability for all the traits studied whereas the main stem length was the most promising trait for selection and days to maturity was the least promising. The plot level analysis showed greater precision than plant level analysis.

KEY WORDS: Phaseolus vulgaris; genetic variability; assessment methods.

#### INTRODUCTION

One of the stages in common bean genetic breeding programs, mainly in the introduction of germplasm for later selection, or use in hybridization programs, consists of their characterization and assessment to establish the available genetic variability. The strategy adopted in this process consists of using a series of descriptors that individualize phenotypically each accession and the estimation of genetic parameters that measure or quantify the variability in the population for each trait assessed (Hidalgo, 1991).

Knowledge of the phenotypic variability existing in a population and how much this is due to genetic differences is fundamentally important, according to Ramalho et al. (2000) because it permits understanding of the genetic control of the trait and the potential of the population for selection. For Santos et al. (1985) the determination of the genetic control of the traits is an initial stage of more suitable procedures.

Estimating genetic parameters such as variances, heritability, coefficient of genotypic determination, the coefficient of genetic variation, the b ratio (CVg/ CVe ratio), and correlation of a population allows inference on the available genetic variability. A breeder can define the best selection strategy to obtain superior genotypes based on the estimates for the important traits.

Estimates of genetic parameters in common bean plant cropping have been obtained by various authors (Ramalho et al., 1986; Santos et al., 1985, 1986; Santos and Vencovsky, 1986; Pereira Filho et al., 1987; Pinho et al., 1991; Teixeira et al., 1995; Aguiar et al., 2000; Coelho et al., 2002).

In the face of these considerations, the present study aimed to estimate the parameter of genetic variability of common bean genotypes for various traits and compare assessment methodologies.

#### MATERIAL AND METHODS

The experiment was carried out in the experimental area of the Agrarian Science Nucleus at the Federal University of Mato Grosso do Sul (UFMS) in the 'dry' harvest in the 2000/2001 growing season. This area is located on the geographic coordinates 22° 12'16" latitude south and 54° 48'20" longitude west, altitude 452 meters. The climate is classified as Wet Mesothermic, according to the Köppen international system with 1500mm mean annual precipitation. The soil is classified as Purple distrofferic latosol, with clay texture.

Tables 1 and 2 show rainfall and the monthly mean temperatures during the experiment.

Table 3 shows the genotypes used in the experiment that included advanced lines and commercial varieties. A randomized complete block experimental design was adopted with three replications for each treatment. The experimental plot consisted of two 1.50m lines of plants spaced at 0.50m. The soil was prepared with two gradings, one plowing and the other leveling. The sowing drills were fertilized with commercial formula chemical fertilizer 4-20-20 at 300 kg.ha-1. A sowing density of 12 plants per linear meter was used. The experiment was sown on 24.03.01. Disease and pest control, weeding and complementary irrigation were performed to keep plant growth and development. Cover fertilizer was applied 25 days after seedling emergence using 40 kg.ha<sup>-1</sup> N in the form of sulfate ammonia. The plants were harvested and threshed on 28 May 2001.

In the plant level analysis, the 24 plants in the three plots of each treatment were assessed individually for the traits: days to emergence (DE), days to flowering (FL), insertion height of the first inflorescence (AI), length of main stem at flowering (CP1), number of nodes on the main stem at flowering (NOS1), days to maturity (MAT), height of insertion of the first pod (AV), main stem length at maturity (CP2), number of nodes on the main stem at maturity (NOS2), number of pods per plant (VAG), number of seeds per pod (SEM) and grain yield per plant (PRD1).

In the plot level analysis, the mean of eight plants from each plot was considered and the weight of 100 seeds (PCS) and grain yield in kg.ha-1 were assessed in addition to the characteristics mentioned previously. The traits FL, CP1 NOS1 and AI were assessed at the R6 phenological stage of the plant and MAT, CP2, NOS and AV at the R9 phenological stage. In the SEM trait analysis, three pods per plant were assessed totaling 24 per plot and 72 per treatment.

For the plant level analysis, a completely randomized design was used. Analyses of variance were performed and the genetic parameters estimates were obtained for between and within genotype variances. A random model in which all effects were assessed as random was used according to the following expression (Cruz, 2001):  $Y_{ij} = \mu + g_i + \varepsilon_{ij}$ , where:

 $Y_{ij}$  = observed value of the j-eth plant in the i-eth treatment;

 $\mu$  = general experimental mean

 $g_i = effect of genotype i$ 

 $\varepsilon_{ii}$  = random error associated with observation  $Y_{ii}$ 

The analysis of variance and F test for the completely randomized design is shown in Table 4. The variance components and the genetic and phenotypic parameters were estimated using the GENES computer program (Cruz, 2001).

The parameters below were estimated for each characteristic using the following expressions (Cruz, 2001):

a) Phenotypic variance:  $(s_F^2) = \frac{MSG}{k}$ 

Table 1. Rainfall in ten-day periods, from March 2001 to June 2001 in Dourados. Dourados - MS 2002.

		Rainfall	mm	
Months	1° ten-day	2° ten-day	3° ten-day	total
March	20.0	29.8	83.6	133.4
April	17.0		56.4	73.4
May		13.7	72.4	86.1
June	30.9	26.6	9.8	67.3

**Table 2.** Monthly mean maximum, mean and minimum temperatures (oC) in the period March 2001 to Jun<sup>e</sup> 2001 in Dourados. Dourados-MS 2001.

14	a la station de la second	Temperature (°C)	
Months	minimum	mean	maximum
March	20.2	25.8	31.7
April	18.0	24.8	30.3
May	12.5	18.3	24.1
June	11.6	17.4	23.2

b) Mean environmental variance:  $(s_E^2) = \frac{MSR}{k}$ 

c) Mean genotypic variance: 
$$(\hat{\sigma}_{G}^{2}) = \frac{MSG - MSR}{k}$$

d)Genotypic determination coefficient:  $R^2 = \frac{\sigma^2_G}{\sigma^2_F}$ 

e)Coefficient of genetic variation: (CVg)  $\frac{\sqrt{\sigma_{G}^{2}}}{m} x100$ 

f) b quotient (CVg/CVe ratio) :  $\sqrt{\frac{\sigma_G^2}{\sigma_G^2}}$ 

With: k = 
$$\frac{N - \left(\frac{1}{N}\sum_{i=1}^{g} r_i\right)}{g - 1}$$
 and N =  $\sum_{i=1}^{g} r_i$ 

where  $r_i$  is the maximum number of replications of the i-eth genotype.

A randomized complete block design was used in the analysis of variance of traits evaluated at plot level. The following statistical model was used (Cruz, 2001):  $Y_{ij} = \mu + g_i + b_j + \varepsilon_{ij}$ 

where:

 $Y_{ij}$ : value observed of the j-eth block in the i-eth genotype;

 $\mu$  : general mean of the experiment;

 $g_i$ : effect of genotype i;

b<sub>i</sub> : effect of block j;

 $\varepsilon_{ii}$ : random error association to observation  $Y_{ii}$ .

The analysis of variance model, the mean squares, the the expected mean squares plus the F test are shown in Table 5.

The parameters below were estimated for each characteristic, using the following expressions (Cruz, 2001):

G

a) Phenotypic variance: 
$$(s_F^2) = \frac{MS}{b}$$

Table 3. Genotypes used in the experiment.

 Table 4. Analysis of variance for the completely randomized design.

SV	DF	SS	MS	E(MS)	F
(Genotypes) E G	g - 1	SSG	MSG	$\sigma^2 + k\sigma_g^2$	MSG/MSR
(Residual) D G	n - g	SSR	MSR	$\sigma^2$	
Total	n - 1	SSTo			

 $CV = (100\sqrt{MSR})/m$ ; EG: between genotypes; DG: within genotypes.

b) Mean environmental variance:  $(s_E^2) = \frac{MSR}{b}$ 

c) Mean genotypic variance:  $\begin{pmatrix} & 2 \\ \sigma & g \end{pmatrix} = \frac{MSG - MSR}{b}$ 

g)Genotypic determination coefficient:  $R^2 = \frac{\sigma^2_G}{\sigma^2_F}$ 

h)Coefficient of genetic variation: (CVg) =  $\frac{\sqrt{\sigma_{G}^{2}}}{m} x100$ 

i) b quotient (CVg/CVe ratio) : 
$$\sqrt{\frac{\sigma_c}{\sigma}}$$

All the components of variance and the genetic and phenotypic parameters were estimated using the computer software GENES (Cruz, 2001).

#### **RESULTS AND DISCUSSION**

Tables 6, 7, 8 and 9 show the summary of analyses of

variance and the estimation of the genetic parameters. The data in Tables 6 and 7 refer to the individual analysis at plant level and show the existence of wide genetic variability in the population since the differences observed were significant statistically (p < 0.01) for all the traits. The genotypic determination coefficient indicated that the genetic variance component corresponded to over 70% of the total phenotypic variability of all traits.

The high genetic variability among genotypes indicated that selection is likely to result in genotype improvement According to Coimbra et al. (1998) estimation of  $\sigma_G^2$ ,  $\sigma_F^2$ ,  $\sigma_E^2$  and  $R^2$  are influenced by the number of replications and environments by genetic differences among the parents and by the type of assessment (individual or family).

The assessment at plot level gave greater participation to the genetic components of variation in the phenotypic expression of the traits than the individual assessment consequently resulting in lower coefficient values of experimental variation (Tables 8 and 9).

The coefficient of genotypic determination  $(R^2)$ , because it includes all the genetic influences in the

Table 5. Analysis of variance for the randomized complete block design (random model).

SV	DF	SS	MS	E(MS)	F
Blocks	b-1	SSB	MSB	$\sigma^2 + g\sigma_b^2$	
Genotypes	g-1	SSG	MSG	$\sigma^2 + b\sigma^2_{g}$	MSG/MSR
Residual	(b-1)(g-1)	SSR	MSR	$\sigma^2$	
Total	gb-1	SSTo		14 16 18 - 19 19	

Mean = m; CV% =  $(100 \sqrt{MSR})/m$ 

**Table 6.** Summary of the analyses of variance and genetic parameter estimates for structural and physiological traits of common bean genotypes. ('dry' harvest 2000/2001). Dourados-MS 2002 (plant level analysis).

SV	DE	FL	AI	$CP^1$	NÓS <sup>1</sup>	MAT
	- 11 - 52		MS	Nogel T		
Genotype(GI = 15)	11 651/	263.141/	12.711/	1008.131/	33.481/	159.691/
Residual( $GI = 368$ )	3 39	9.64	2.16	207.03	1.70	10.52
Mean	6.86	36.98	8.80	70.47	17.35	68.49
CV (%)	26.96	8.36	16.61	18.95	7.51	4.75
	Service a		Genetics			
			Parameter			
R <sup>2</sup>	70 90	96.33	82.97	97.93	94.92	93.40
CVg (%)	8 59	8.75	7.48	26.61	6.63	3.63
h(CVg/CVe)	0.31	1.04	0.45	1.40	0.88	0.76

DE: days to emergence; FL: days to flowering; AI: height of insertion of the 1st inflorescence (CM); CP1: length of main stem at flowering (cm); NOS1 - number of nodes on the main stem at flowering; MATt - days to maturity; Genetic parameters: R<sup>2</sup>: genotypic determination coefficient.  $CV_g$ : coefficient of genetic variation. b ratio:  $CV_g/CV_e$  ratio; (<sup>1</sup>) significant at 1% probability by the F test.

expression of the phenotype and not only the additive effects, cannot be taken as a precise indicator of expected genetic gain by selection, but it does give indexes of expected performance in a given population in trait selection. The estimates of genotypic determination coefficient (R<sup>2</sup>) were high (over 70%) for all the traits and the highest in the two methodologies were those observed for the traits PRD, PCS, CP1, CP2 and FL (over 95%). The lowest estimates of coefficient of genotypic determination were for the traits DE and AI. According to Yokomizo and Vello (2000) the high genetic determination coefficient for a certain trait indicates greater heredity for this trait, less environmental influence and lower genotype x environment interaction.

When assessment at plot level was adopted (Tables 8 and 9) the estimates of genotypic determination for all the traits were superior to those obtained by assessment at plant level (Tables 6 and 7) suggesting that this methodology exerts better control on the environmental influence and consequently increases the proportion of the genetic variance in the phenotypic expression of the trait.

As in the genotypic determination, the genetic variation coefficient  $(CV_g)$  permits inference to be made on the genetic variability in the different traits. High  $CV_g$  values indicate that the population is promising for selection for the trait under study. The highest  $CV_g$  values (over 25%) were obtained for CP1, VAG and PRD1and2 and the lowest (under 10%) for DE, AI, FL, NOS and MAT. MAT had the

lowest coefficients of genetic variation. The values obtained by assessment at plot level were slightly superior to those obtained by the individual assessment of the plants. The  $CV_g$  values obtained for the traits assessed are in line generally with those obtained at CIAT (CIAT, 1983).

The b ratio  $(CV_g/CV_c \text{ ratio})$  that indicates a very favorable situation for selection when b = 1 varied for all the traits depending on the analysis used. (Vencovsky, 1978) It was always superior to 1 indicating therefore a favorable situation for selection when this was made considering the mean per plot, which was ascertained due to the lower CV<sub>c</sub> obtained by this method that reduced the influence of the environment in the phenotypic expression of the traits. Good b ratio values were generally obtained for the main stem length (CP1 and CP2) (over 1) in both methodologies that, associated to the wide genetic variability (high R<sup>2</sup> and CV<sub>g</sub> estimates) existing in the population, made it favorable for obtaining expressive genetic gains in the selection of this trait.

The b ratio indicates that progress from selection is not expected for the VAG and PRD1 and PRD2 traits, in spite of the presence of genetic variability in the population. This is because these traits are greatly influenced by environmental effects. The adoption of assessment methodology that reduces the interference of the environment increases the b value, making the situation more favorable to selection. The traits for which the population showed itself lesser promising for selection because of the low CV<sub>g</sub> values are DE, FL and MAT that were also the traits with

**Table 7.** Summary of the analyses of variance and genetic parameter estimates for structural and physiological traits of common bean genotypes. ('dry' harvest 2000/2001). Dourados-MS 2002 (plant level analysis).

SV	AV	$CP^2$	NÓS <sup>2</sup>	VAG	SEM	PRD <sup>1</sup>
			MS		1000 1 1000 1	
Genotype(GL=15)	23.581/	9925.1111/	36.011/	130.161/	5.081/	385 711/
Residual(G= 368)	2.32	257.60	2.32	8.04	0.41	5.83
Mean	7.89	101.93	19.02	8.19	4.42	6.67
CV (%)	19.73	15.78	8.03	36.69	14.50	36.79
			Genetics	Freed and	-19BL-0	00115
10.0 .000 .000 . 20 .000			Parameter			
$\mathbb{R}^2$	90.12	97.40	93.54	93.81	91 93	03.18
CVg (%)	12.16	19.74	6.24	28.38	9 9 9 9	27 77
b (CVg/CVe)	0.61	1.25	0.77	0.79	0.68	0.75

AV: height of insertion of the 1st pod (cm); CP1: length of main stem at flowering (cm); NOS1 - number of nodes on the main stem at flowering; VAG: number of pods per plant; SEM: number of seeds per plant; PRD1: yield per plant (grams); Genetic parameters:  $R^2$ : genotypic determination coefficient.  $CV_g$ : coefficient of genetic variation. b ratio:  $CV_g/CV_e$  ratio <sup>1</sup>/ significant at 1% probability by the F test.

SV	DE	FL	AI	$CP^1$	NÓS <sup>1</sup>	MAT	AV
State and the second				MS			-
Blocks (GL=2)	$1.30^{2/}$	3.301/	$0.75^{2/}$	$4.07^{1/}$	0.1111/	5.961/	0.531/
Genotypes(GL=15)	1.381/	33.851/	1.651/	1223.281/	4.001/	17.321/	2.691/
Residual(GL=30)	0.29	0.64	0.33	21.39	0.18	1.49	0.44
Mean	6.86	37.98	8.80	70.47	17.38	68.44	7.89
CV(%)	7.95	2.16	6.53	6.09	2.45	1.78	8.61
		a service as the		Genetics			
				Parameter			
R <sup>2</sup>	78.50	98.09	79.86	98.25	95.44	91.38	83.64
CVg (%)	8.77	8.97	7.51	26.35	6.49	3.35	11.25
b (CVg/CVe)	1.10	4.13	1.14	4.32	2.64	1.87	1.30

**Table 8.** Summary of the analysis of variance and genetic parameter estimates of structural and physiological common bean traits ('dry' harvest 2000/2001). Dourados-MS 2002 ( plot level analysis).

DE: days to emergence; FL: days to flowering; AI: height of insertion of the 1st inflorescence (cm); CP1: length of main stem at flowering (cm); NOS1 - number of nodes on the main stem at flowering; MATt - days to maturity; AV: insertion height of the 1st pod; Genetic parameters:  $R^2$ : genotypic determination coefficient.  $CV_g$ : coefficient of genetic variation. b ratio:  $CV_g/CV_g$  ratio (<sup>1</sup>) significant at 1% probability by the F test.

Table 9. Summary of the analyses of variance and genetic parameter estimates for common bean structural traits and yield ('dry' harvest 2000/2001). Dourados-MS 2002 ( plot level analysis).

SV	CP <sup>2</sup>	NÓS <sup>2</sup>	VAG	SEM	PRD <sup>1</sup>	PRD <sup>2</sup>	PCS
Blocks(GL=2)	23.21 <sup>1/</sup>	0.671/	1.14 <sup>1/</sup>	MS 0.06 <sup>1/</sup>	0.60 <sup>1/</sup>	38305.59 <sup>1/</sup>	0.02 <sup>1/</sup>
Genotypes(GL=15)	1235.03"	4.26	0.64	1.04	0.31	094546.90"	29.60"
Mean	101.93	19.02	8.19	4.42	6.67	1533.19	0.10
CV(%)	5.22	2.28	10.06	7.76	8.64	8.53	1.71
			1.24	Genetics Parameter			
R <sup>2</sup>	97.70	95.55	96.04	88.85	97.32	97.41	99.63
CVg (%)	19.67	6.12	28.64	12.66	30.09 3.48	30.24	16.45

CP2: length of main stem at maturity (cm); NOS: number of nodes on the main stem at maturity; VAG: number of pods per plant; SEM: number of seeds per plant; PRD1: yield per plant (grams); PRD2: grain yield in kg.ha-1; PCS: weight of 100 seeds; Genetic parameters: R<sup>2</sup>: genotypic determination coefficient.  $CV_g$ : coefficient of genetic variation. b ratio:  $CV_g/CV_e$  ratio (<sup>1</sup>) significant at 1% probability by the F test.

the lowest b values in the assessment at plant level, especially the days to maturity trait (MAT).

The coefficient of variation in the experiments was low for all analyzed traits in the plot level analysis, suggesting high reliability for those experiments. When the individual plant level analysis was used, traits such as AI, AV, VAG CP2 and PRD1 presented high CV<sub>e</sub> values, showing low precision of this methodology in assessing these characteristics.

#### CONCLUSIONS

The results of the present study permitted the following conclusions:

The population under study has wide genetic variability for all the traits assessed;

Selection for main stem length (CP1 and CP2) will result in greater progress than selection for early or late maturity; At plot level analysis controlled the residual variance better and was more precise that plant level analysis.

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# RESUMO

Estimativas de parâmetros genéticos em genótipos de feijoeiro comum

Dezesseis genótipos de feijoeiro comum, entre variedades comerciais e linhagens avançadas, foram avaliadas no Núcleo de Ciências Agrárias da Universidade Federal de Mato Grosso do Sul, Campus de Dourados, na safra "da seca" do ano agrícola 2000/2001. Parâmetros genéticos e fenotípicos foram estimados para os caracteres morfofisiológicos e os componentes de produtividade. Os parâmetros foram estimados por planta, obtendo-se as estimativas das variâncias entre e dentro de genótipos, e por parcela, no delineamento experimental blocos casualizados, com três repetições para cada genótipo. As populações em estudo mostraram possuir ampla variabilidade genética para todos os caracteres estudados, sendo o comprimento da haste principal o caráter mais promissor para seleção e dias para maturação o menos promissor. A avaliação por parcela mostrou maior precisão do que a avaliação por planta.

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