
DIFFERENTIAL CONTRIBUTION OF BREEDING INSTITUTIONS TO BEAN GENETIC GAIN

Juliano Garcia Bertoldo, Pedro Patric Pinho Morais, Leandro Hellebrandt Kruger, Nicole Trevisani, Jefferson Luís Meirelles Coimbra, Altamir Frederico Guidolin and Haroldo Tavares Elias

SUMMARY

This study aimed to estimate the variance components and genetic gain of new lines or cultivars produced by different common bean breeding institutions included in the Value for Cultivation and Use (VCU) test in Santa Catarina State, Brazil. The data were obtained from VCU tests carried out from 2001 to 2007 in ten locations of the State of Santa Catarina. The variance components and best linear unbiased predictor (BLUP) were estimated by the restricted maximum likelihood procedure (REML). A greater contribution of non-genetic ef-

fects (σ_{ng}^2) on phenotypic variance (σ_f^2) was observed, compared to genetic effects (σ_g^2), for both grain yield and plant cycle. In general, the new lines or varieties from all institutions evaluated presented genetic gains for grain yield and plant cycle over the seven-year period, but with different magnitudes. The largest genetic gains (grain yield) were obtained by institutions A ($\Delta g = 19 \text{ kg} \cdot \text{ha}^{-1}$), B ($\Delta g = 133 \text{ kg} \cdot \text{ha}^{-1}$) and C ($\Delta g = 71 \text{ kg} \cdot \text{ha}^{-1}$). For plant cycle, only one institution did not obtain genetic gain (genotypes with gain close to zero).

Introduction

Bean is an important species for a large part of the world population. In Brazil this crop is cultivated in great part of the national territory, in almost all the seasons of the year. Several breeding institutions struggle to maintain or improve the current productivity and characteristics such as resistance to diseases and pests, higher content of oils, fiber and nutrients, etc. The promising lineages must be assessed in the final stages of the breeding program, before being recommended as a new cultivar.

In this sense, assays for cultivar evaluation are necessary, particularly the Value for Cul-

tivation and Use (VCU) Test for the assessment of promising lineages and registration of new cultivars in the National Registry of Cultivars (*Registro Nacional de Cultivares*; RNC), of the Ministry of Agriculture and Livestock (*Ministério da Agricultura e Pecuária*; MAPA). Before they can be registered in the RNC, cultivars must be submitted to VCU assays, which express the intrinsic value of the combination of the agronomic characteristics of cultivars with their properties for agricultural, industrial and commercial use and *in natura* consumption (Carvalho *et al.*, 2009). This procedure for the evaluation of lineages before registration and

recommendation is also used in other countries (Piepho and Mohring, 2006) besides Brazil.

Therefore, the evaluation of the set of genotypes used in the annual assays is fundamental to calculate the value of the genetic gain achieved in the breeding institutions that participate in the VCU assays. For such evaluation, the estimates of the components of phenotypic variance is one of the adequate procedures. The estimate of the variance components provides knowledge about the causes of variation, which leads to the prediction of gains with the selection of genetically superior plants (Coimbra *et al.*, 2009). Thus, estimates of

the genetic progress based on values achieved in the VCU assays or other assays have been evaluated in different species: bean (Matos *et al.*, 2007), sunflower (de La Vega *et al.*, 2007), rice (Bresseghele *et al.*, 1999; Atroch and Nunes, 2000), cotton (Carvalho *et al.*, 1997) and maize (Arias and Ramalho, 1998), among others. However, the estimates of the phenotypic variance components were not used in any of these studies.

Thus, the present work aimed at estimating the variance components and the genetic gain among and within the bean breeding institutions participating in the VCU assays for seven years, using the

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CONTRIBUCIÓN DIFERENCIAL DE INSTITUCIONES DE MEJORAMIENTO DE FRIJOL EN LA GANANCIA GENÉTICA

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RESUMEN

Este estudio tuvo como objetivo estimar los componentes de la varianza y la ganancia genética de nuevas líneas o variedades producidas por diferentes instituciones de mejoramiento genético del frijol incluídas en la prueba de valor de cultivo y uso (VCU), en el Estado de Santa Catarina, Brasil. Los datos fueron obtenidos a partir de ensayos VCU en el período comprendido entre 2001 y 2007, en diez localidades del Estado de Santa Catarina. Los componentes de varianza y el mejor predictor no sesgado lineal (BLUP) fueron estimados por el procedimiento de máxima verosimilitud restringida (REML). Se observó una contribución mayor de los efectos no-genéticos

(σ_{ng}^2) en la variación fenotípica (σ^2_p) en comparación con los efectos genéticos (σ_g^2) para la producción de granos y ciclo de la planta. En general, las nuevas líneas o variedades de todas las instituciones evaluadas presentaron ganancia genética para la producción de grano y el ciclo de la planta durante el período de siete años, pero con diferente magnitud. Las mayores ganancias genéticas para la producción de grano fueron obtenidas por las instituciones A ($\Delta g = 19 \text{kg}\cdot\text{ha}^{-1}$), B ($\Delta g = 133 \text{kg}\cdot\text{ha}^{-1}$) y C ($\Delta g = 71 \text{kg}\cdot\text{ha}^{-1}$). Para el carácter ciclo de la planta, solamente una institución no obtuvo ganancia genética (genotipos con ganancia cercana a cero).

CONTRIBUIÇÃO DIFERENCIAL DE INSTITUIÇÕES DE MELHORAMENTO DE FEIJÃO PARA O GANHO GENÉTICO

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RESUMO

Este estudo teve como objetivo estimar os componentes de variância e ganho genético de novas linhas ou cultivares desenvolvidas por diferentes instituições de melhoramento genético de feijão incluídos no ensaio de valor de cultivo e uso (VCU), no estado de Santa Catarina, Brasil. Os dados foram obtidos a partir dos ensaios de VCU do período de 2001 à 2007, em dez localidades do estado de Santa Catarina. Os componentes de variância e o melhor preditor linear imparcial (BLUP) foram estimados pelo procedimento de máxima verosimilhança restrita (REML). Foi observada maior contribuição dos efeitos não-genéticos (σ_{ng}^2) na variância fenotípica (σ^2_p),

em comparação com os efeitos genéticos (σ_g^2), tanto para produção de grãos e ciclo da planta. Em geral, as novas linhas ou variedades desenvolvidas por todas as instituições avaliadas apresentaram ganhos genéticos para produção de grãos e ciclo da planta ao longo do período de sete anos, mas com magnitude diferente. Os maiores ganhos genéticos foram obtidos pelas instituições A ($\Delta g = 19 \text{kg}\cdot\text{ha}^{-1}$), B ($\Delta g = 133 \text{kg}\cdot\text{ha}^{-1}$) e C ($\Delta g = 71 \text{kg}\cdot\text{ha}^{-1}$), para rendimento de grãos. Para o caráter ciclo da planta somente uma instituição não obteve ganho genético (genótipos com ganho próximo de zero).

method for estimating the phenotypic variance components.

Material and Methods

The present work used data from the Value for Cultivation and Use (VCU) Test, carried out annually in network by the Research Center for Family Agriculture of Chapecó and coordinated by the *Empresa de Pesquisa Agropecuária e Extensão Rural de Santa Catarina* (EPAGRI), with participation of other research institutions. A randomized block design was used, with four replications. The experimental unit comprised four lines with 4m of length, 0,45m spacing and useful area of 2,7m². The seeding rate consisted of 15

seeds per linear meter. Chemical control of pests and weeds and manual weeding were carried out, as needed, as soon as weeds appeared, to allow equal conditions.

The VCU assays were carried out from 2001 to 2007 in ten locations of the State of Santa Catarina (Águas de Chapecó, Campos Novos, Canoinhas, Chapecó, Ituporanga, Lages, Ponte Serrada, São Carlos, Urussanga and Xanxerê). For the purposes of this study, 49 genotypes of the black commercial group bean were used, including commercial varieties and lineages of different bean research institutions. The institutions names were coded in the genotype identification to avoid possible conflicts of in-

terest. The first institution (A) is EPAGRI, a state research company, (CHP970409, CHP9858, CHP9701, CHP971308, CHP970821, CHP9704, CHP9965, CHP9859, CHP9713, CHP9702, CHP9727, CHP9954, CHP9706, CHP9708, CHP9726, CHP9714, CHP970809, CHP9712, CHP9720, CHP01178, CHP9736, CHP970617, CHP9718 and CHP9955). The second institution (B) is the Brazilian Enterprise for Agricultural Research (EMBRAPA), a federal breeding company (AN9021332, BRS Campeiro, TB0202, TB9820, J56, Xamego, TB9713, Diamante Negro and SELCP9310635). The third institution (C) is the

Instituto Agrônômico do Paraná (IAPAR), a state research company (LP02130, IPR Graúna, IPR Uirapuru, LP9805, LP0151, LP98123 and Iapar44). The fourth institution (D) is FT Sementes, a private enterprise (FT Soberano, FT Bionobre, FT Nobre, FT 91370 e FT 84113); and the fifth institution (E) is the Technological University (UTF2810433, UTF4, Silvestre, UTF7, UTF53611313 and UTF5).

The following statistical model was used:

$$y_{ijkl} = \mu + \sigma^2 g_i + \sigma^2 l_j + \sigma^2 a_k + \sigma^2 gl_{ij} + \sigma^2 ga_{ik} + \sigma^2 la_{jk} + \sigma^2 gla_{ijk} + b_l + \sigma^2 \epsilon_{ijkl} \quad (1)$$

where μ : phenotypic effect, g_i : genotype random effect, l_j :

local random effect, a_k : year random effect, g_{ij} : random effect of the genotype \times location interaction, $g_{a_{ik}}$: random effect of the genotype \times year interaction, $l_{a_{jk}}$: random effect of the location \times year interaction, $g_{l_{ijk}}$: random effect of the genotype \times location \times year interaction, b_l : block effect, and e_{ijkl} : error.

To achieve the phenotypic or total variance components (σ^2_t), genotypic variance (σ^2_g) and the non-genetic variance, in this case, the local effect and all the possible interactions among genotype, location and year ($\sigma^2_{\text{location} + \sigma^2_{\text{year} \times \text{genotype}} + \sigma^2_{\text{location} \times \text{year} \times \text{genotype}} + \sigma^2_{\text{location} \times \text{genotype}} + \sigma^2_{\text{location} \times \text{year} \times \text{genotype}} = \sigma^2_p$), together with the best linear unbiased predictor (BLUP), the restricted maximum likelihood procedure (REML) was used, performed with the PROC MIXED command for experiments arranged in randomized block design (Littell *et al.*, 2006).

To estimate the institutional genetic progress in $\text{kg}\cdot\text{ha}^{-1}$ and days promoted over the seven years of the study, the following relation was used:

$$\Delta_{gi} = \left(\frac{\sigma^2_g}{\sigma^2_t} \right) \times (\mu_g) \quad (2)$$

where Δ_{gi} : institutional genetic progress, σ^2_g : genotypic variance, σ^2_t total variance, and μ_g : general phenotypic effect.

Results and Discussion

In the estimate of the variance components per institution, the results demonstrated higher contribution of non-genetic effects (σ^2_{ng}) for the phenotypic variance (σ^2_t), compared to the merely genetic effects (σ^2_g), both for the character grain yield and plant cycle (Table I). It can also be verified that, in general, the genotypic value was close among the institutions evaluated, low for the characters maximum grain yield $\% \sigma^2_g = 7$ and maximum plant cycle $\% \sigma^2_g = 1.4$. The general sum of the percentages of the genotypic variance components was $\sigma^2_g = 1.9\%$ and $\sigma^2_g =$

0,92% and of the non-genetic, $\sigma^2_{ng} = 98,1$; $\sigma^2_{ng} = 99,08$, for the character grain yield and plant cycle, respectively. Such values revealed the magnitude of the effect of the environment and the genotype \times environment interactions on the characters studied. However, the genotypic contributions were similar, but not the same, among the research companies or institutions, so that the institutions D ($\sigma^2_g = 0\%$) and E ($\sigma^2_g = 0,6\%$) developed genotypes with the lowest estimates of genotypic variance.

On the other hand, the institutions A ($\sigma^2_g = 0,8\%$), B ($\sigma^2_g = 5\%$) and C ($\sigma^2_g = 3\%$) achieved higher value in the estimate of genotypic variance (Table I). The results observed in the estimate of the variance components for the grain yield character and plant cycle within each institution (Table I) are significant for the breeding programs, since with the knowledge about the magnitude of the genotypic or environmental contributions, breeders can direct their program, intensifying or not the selection, predicting the genetic gains achieved with the selection and recommending genotypes for the regions of interest. In the present work, besides the relevant aspects mentioned, it was evident that the highest contribution was the disclosure of the genetic gains achieved in the bean breeding program between and within the breeding institutions studied, and knowledge about the main difficulties, such as the magnitude of the environmental effect.

To estimate the gain in yield unit ($\text{kg}\cdot\text{ha}^{-1}$) the relation Δ_{gi} (Eq. 2) was used. For example, in the institution B, for the grain yield character, the genetic value (σ^2_g) esti-

TABLE I
ESTIMATES OF THE VALUE OF THE GENOTYPIC (σ^2_g), NON-GENOTYPIC (σ^2_{ng}) AND TOTAL (σ^2_t) VARIANCES OBTAINED FROM THE EVALUATION OF 49 GENOTYPES OF BLACK BEAN USED IN THE VCU TEST FOR THE STATE OF SANTA CATARINA (2001-2007), COMPARING FIVE BEAN BREEDING INSTITUTIONS FOR GRAIN YIELD ($\text{kg}\cdot\text{ha}^{-1}$) AND PLANT CYCLE (DAYS)

Institutions	σ^2_g †	σ^2_{ng} ‡	σ^2_t §	e	σ^2_g (%)	σ^2_{ng} (%)
Variances for grain yield ($\text{kg}\cdot\text{ha}^{-1}$)						
A	8173.00	1019917.00	1028090.00	174408.00	0.8	99.2
B	58241.00	997698.00	1055939.00	171610.00	5.0	95.0
C	28617.00	948369.00	976986.00	200074.00	3.0	97.0
D	1	949340.00	949340.00	196019.00	0.0	100.0
E	8946.00	138330.00	1392576.00	149946.00	0.6	99.4
Total	103977.00	5298954.00	5402931.00	-	1.9	98.1
Variances for plant cycle (days)						
A	0.85	78.32	79.17	12.01	1.00	99.00
B	0.75	79.33	80.08	9.52	0.93	99.07
C	0.97	78.72	79.69	11.50	1.21	98.79
D	1.14	80.85	81.99	9.14	1.39	98.61
E	0.001	81.53	81.53	9.23	0.001	100.00
Total	3.72	398.76	402.48	-	0.92	99.08

† Sum of the genotypic variances (genotype (G)); ‡ sum of the non-genetic variances (year (A), location (L), interactions (A \times L, A \times G, L \times G, A \times L \times G)); § sum of the total variances ($\sigma^2_g + \sigma^2_{ng}$).

mated was 58,241 (Table I), the value of total effects (σ^2_t) was 1,055,939 and the general phenotypic effect (μ_g) was 2,423 $\text{kg}\cdot\text{ha}^{-1}$. Based on the Δ_{gi} relation the total genetic progress, in other words, the progress over the seven years (2001-2007), was estimated in $\text{kg}\cdot\text{ha}^{-1}$.

Therefore,

$$\Delta g_B = \left(\frac{58241}{1055939} \right) \times (2423) = 133 \text{kg}\cdot\text{ha}^{-1}$$

Using the same relation, the values of genetic progress were estimated for all the other institutions. Thus, the phenotypic effect (μ_i), genotypic variance (σ^2_g), total variance (σ^2_t) and the genetic gain (Δg) per institution is shown in Table II. For the character plant cycle, the genetic evolution over the seven years was similar, excepting the genotypes developed by institution E (Figure 1), whose values of genetic and non-ge-

TABLE II
VALUES OF PHENOTYPIC EFFECT (μ_i), GENOTYPIC VARIANCE (σ^2_g), TOTAL VARIANCE (σ^2_t) AND THE GENETIC GAIN (Δg) OBTAINED IN THE FIVE INSTITUTIONS FOR GRAIN YIELD ($\text{kg}\cdot\text{ha}^{-1}$) AND PLANT CYCLE (DAYS)

Institutions	Values			
	μ_i ($\text{kg}\cdot\text{ha}^{-1}$)	σ^2_g	σ^2_t	Δg ($\text{kg}\cdot\text{ha}^{-1}$)
A	2479	8173	1028090	19
B	2456	58241	1055939	133
C	2493	28617	976986	71
D	2221	0	949340	0
E	2102	8946	1392576	16
	M_i (days)	Σ^2_g	Σ^2_t	Δg (days)
A	89.06	0.75	80.08	0.83
B	89.06	0.85	79.17	0.95
C	89.06	0.97	79.69	1.08
D	89.06	1.14	81.99	1.23
E	89.06	0	81.53	0

A: Epagri, B: Embrapa, C: Iapar, D: Ft Sementes, and E: Technological University.

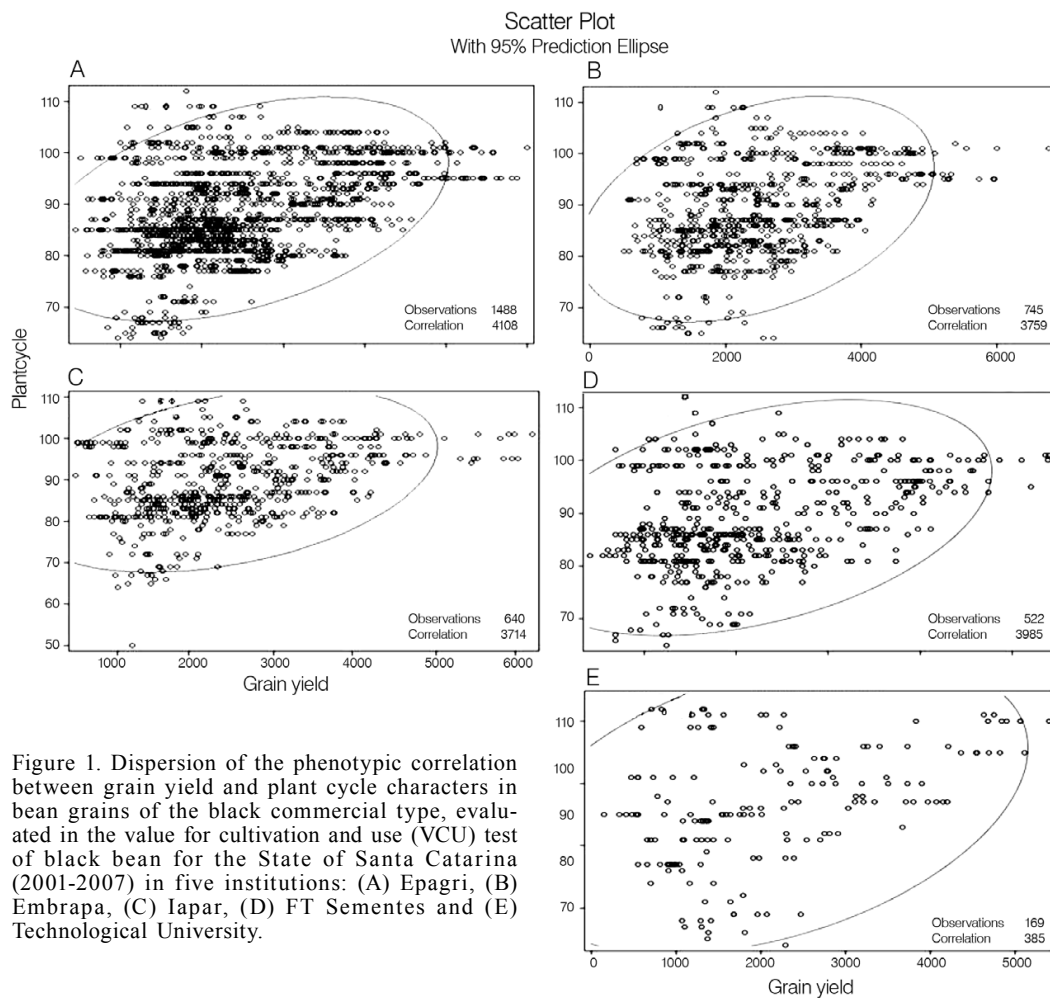


Figure 1. Dispersion of the phenotypic correlation between grain yield and plant cycle characters in bean grains of the black commercial type, evaluated in the value for cultivation and use (VCU) test of black bean for the State of Santa Catarina (2001-2007) in five institutions: (A) Epagri, (B) Embrapa, (C) Iapar, (D) FT Sementes and (E) Technological University.

netic effects for the general phenotypic effect of the institutional genotypes are in Table II.

Based on the results obtained, it is possible to affirm that all the institutions presented genetic gains for the grain yield character and plant cycle over the seven years, but in different magnitudes. Thus, in the estimate of the genetic gains promoted by the selection in the institutions evaluated, it can be observed that the highest gains were achieved in institutions A, B and C for the grain yield character. On the other hand, the gain was lower in institutions D (whose value was close to zero) and E. For the plant cycle character, in this case for precocity, all the institutions presented higher genetic gains when compared to institution E, which achieved small gains (close

to zero). It can also be verified that, in all the institutions, the highest contribution for the phenotypic effect was related to the environmental effect, while the genotypic effect had a lower value.

These results are in accordance with Laidig *et al.* (2008), who evaluated the variance components in 30 different crops in a VCU experiment in West Germany during 16 years, and concluded that the highest contribution for the phenotype was related to the environment. Besides, Rocha *et al.* (2009) verified, in the estimate of the phenotypes effects square of five locations of bean cultivation (Lages, Campos Novos, Ponte Serrada, Canoinhas and Xanxerê, all in Santa Catarina State), that differences among environments were higher, compared to geno-

type experimental factors and the genotype×environment interaction. Similarly, Rane *et al.* (2007), evaluating 25 wheat genotypes in 18 locations of India, observed strong influence of the environment on the phenotype value.

Thus, based on the results found, it can be inferred that breeding aiming at increasing the grain yield character or precocity or plant cycle extension requires a great effort from breeders, since there is a higher influence of the environment on both characters. Be-

sides, the institutions evaluated achieved, in a certain way, moderate genetic gains, related to the seven years evaluated.

Although all the institutions achieved genetic gains, the particular genotypes of each one of them were different for the characters grain yield and plant cycle (Table III). The results revealed significant differences by the t test ($P < 0.005$) among the genotypes developed by the five bean breeding institutions evaluated, for the characters grain yield and plant cycle (Table I). However, the differences observed among the phenotype effects of the genotypes of institutions A, B and C for the character grain yield were not statistically significant. Between C and A, $\mu_C - \mu_A = 14 \text{ kg} \cdot \text{ha}^{-1}$; for C and B, $\mu_C - \mu_B = 37,68 \text{ kg} \cdot \text{ha}^{-1}$; and between A and B, $\mu_A - \mu_B = 23,68 \text{ kg} \cdot \text{ha}^{-1}$. On the other hand, the mentioned institutions differed significantly in relation to institutions D and E (Table I), so that the minimum differences among the phenotype effects varied from $235,07 \text{ kg} \cdot \text{ha}^{-1}$ ($\mu_B - \mu_D$) to $353,52 \text{ kg} \cdot \text{ha}^{-1}$ ($\mu_B - \mu_E$). For the plant cycle character, the results differed from those

TABLE III
COMPARISON AMONG THE FIVE INSTITUTIONS THAT PARTICIPATED IN THE VCU TEST OF BLACK BEAN IN THE STATE OF SANTA CATARINA (2001-2007) FOR GRAIN YIELD AND PLANT CYCLE

Institutions	Differences among the phenotypes effects ($\mu_i - \mu_j$)	
	Grain yield ($\text{kg} \cdot \text{ha}^{-1}$)	Plant cycle (days)
C×A	14.00	0.77 *
C×B	37.68	0.58 *
C×D	272.75 *	0.62 *
C×E	391.20 *	3.12 *
A×B	23.68	-0.19
A×D	258.75 *	-0.14
A×E	377.20 *	2.35 *
B×D	235.07 *	0.04
B×E	353.52 *	2.54
D×E	118.45 *	2.49 *

* significant at 5% of error probability by the t test.

TABLE IV
COMPARISON OF THE GROUPS OF GENOTYPES
WITHIN INSTITUTIONS PARTICIPATING IN THE VCU
TEST OF BLACK BEAN IN THE STATE OF SANTA
CATARINA (2001-2007) FOR GRAIN YIELD AND
PLANT CYCLE

Institutions	Group of genotypes**	Character	
		Grain yield (kg·ha ⁻¹)	Plant cycle (days)
A	Superior	2658 *	90.97 *
	Inferior	2203 *	87.57 *
	General phenotypic effect	2479	88.97
B	Superior	2628 *	90.72 *
	Inferior	2246 *	86.02 *
	General phenotypic effect	2456	89.16
C	Superior	2612 *	91.90 *
	Inferior	2153 *	87.70 *
	General phenotypic effect	2493	89.74
D	Superior	2350 *	89.27 ns
	Inferior	1891 *	87.00 ns
	General phenotypic effect	2221	89.11
E	Superior	2443 *	88.72 *
	Inferior	1778 *	85.76 *
	General phenotypic effect	2102	86.62

* Significant at 5% of error probability. Superior group: genotypes with phenotypic effect above the general phenotypic effect; inferior group: genotypes with phenotypic effect below the general phenotypic effect, simultaneously.

found for the grain yield character (Table III), so that institution C differed significantly from all the institutions evaluated ($\mu_C - \mu_A = 1$ day; $\mu_C - \mu_B = 1$ day; $\mu_C - \mu_D = 1$ day; and $\mu_C - \mu_E = 3$ days); institution A did not differ from B and D, but differed from E ($\mu_A - \mu_E = 2$ days); institution B only differed from C, as already mentioned; institution D differed from C, but not from the others; and institution E differed from all other institutions, except B. Thus, statistically significant differences were evident among the institutions for the target characters of the study. In general, two main groups were formed related to the contributions for genetic gain: the first was formed by institutions A, B and C; and the second was formed by institutions D and E.

The differences observed among the institutions for the characters under study may result from the duration of the bean breeding program, as institutions A, B and C (group 1) are older

than D and E (group 2). Since the former had had more time in bean breeding, the number of genotypes achieved can be higher, and thus, the contribution for the genetic gain would also be higher. It can be highlighted that the institutions of group 2 cannot be considered non-effective in terms of genetic gain, but it is of lower magnitude. Besides, since the genotypes of institutions A, B and C present higher genetic component in relation to the other institutions, these institutions may be using better adapted parents, and the genotypes selected in the segregating populations may be more adapted to the environmental effects. Besides, the genetic variability present in the genotypes of the mentioned institutions may be broader, with a higher possibility of choosing potential parents for the crossings, which would result in more promising lineages and, thus, a more efficient selection. The results corroborate this premise,

since in the present work it was observed that the environmental effect is the main responsible for the change in the phenotypic value. Therefore, the genotypes that potentiated the effects of their interaction with the cultivation environment were the most promising. Consequently, the institutions presenting such genotypes achieved higher genetic gains. It should be pointed out that in the estimates of the genetic progress the pool of genotypes of each institution was considered; in other words, some genotypes are lineages in the first evaluation, intermediate, under final evaluation, or in pre-release. This difference among the levels of the genotypes may explain in part the discrepancy of the values achieved in the genetic gain (Δg) per institution. Institution A is an example of this, in which most lineages evaluated came from preliminary assays; in other words, some participated in the VCU for the first time. Besides, the objective of this work was not comparative, but elucidative.

In order to demonstrate the differences among the genotypes within institutions, the genotypes were grouped (Table IV) as follows: superior group (genotypes above the general phenotypic effect for the characters grain yield and plant cycle) and inferior group (genotypes below the general phenotypic effect for the characters grain yield and plant cycle, simultaneously). The results demonstrated that the groups were different by the t test ($P > 0.005$) for both characters in all the institutions, except for the plant cycle character in institution D, due to the differences between more productive and less productive genotypes in the same institution. It is important for breeders to identify the most responsive genotypes to selection or

environmental demands, so that superior genetic gain can be achieved with their recommendation. In this sense, the selection of superior genotypes should be based on the variance components in relation to the phenotypic effect components (Simeão *et al.*, 2002). For Bertoldo *et al.* (2009), knowledge about the variance components may contribute to breeding programs, identifying promising genotypes, among other aspects.

Therefore, genotypic values were predicted within each institution so as to reveal which potential genotypes contributed to the characters being evaluated. Out of the 49 genotypes evaluated, 18 presented predicted genotypic values above the general phenotypic effect (2430 kg·ha⁻¹) for the character grain yield; 10 from institution A; 5 from B; 4 from C and 3 from E (Table V). For the plant cycle character, out of the 49 genotypes evaluated, 11 were from institution A; 4 from B; 2 from C and 4 from D (Table VI). In other words, 20 genotypes presented predicted genotypic values above the general phenotypic effect (89,06 days). The genotypic value was not predicted for the institutions D (grain yield) and E (plant cycle) due to the lack of effective genotypic contributions for the characters analyzed.

The results obtained corroborate the existence of variability among the genotypes evaluated, since differences were revealed by the t test and by the prediction of the genotypic values. Besides, higher genetic gains can be achieved for grain yield, since the genotypic contribution was higher for this character, in comparison to the plant cycle character. Thus, the genotypes CHP970409 from institution A (6,71% of genetic gain), AN9021332 from institution B (5,21%), LP02130 from institution C (with

TABLE V
GENOTYPE PREDICTED VALUE THROUGH BLUP (g),
PREDICTION OF THE GENOTYPIC VALUES ($\mu+g$),
ACHIEVED GAIN (g%; kg·ha⁻¹) AND CONFIDENCE
INTERVALS (95%) FOR THE GRAIN YIELD CHARACTER
OF 49 BLACK BEAN GENOTYPES, SUBDIVIDED INTO
FIVE BEAN BREEDING INSTITUTIONS ($\mu= 2430\text{kg}\cdot\text{ha}^{-1}$)

Institutions	Genotypes	g	$\mu+g$	g%	Confidence intervals	
A	CHP970409	162.53	2585	6.71	2703	3174
	CHP9858	79.22	2502	3.27	2591	2976
	CHP9701	78.59	2501	3.24	2460	2802
	CHP971308	65.07	2488	2.69	2310	2985
	CHP970821	60.76	2484	2.51	2308	2983
	CHP9704	40.75	2464	1.68	2423	2765
	CHP9965	36.89	2460	1.52	2575	3046
	CHP9859	35.97	2459	1.48	2520	2904
	CHP9713	18.43	2441	0.76	2032	2463
	CHP9702	9.34	2432	0.39	2255	2726
	CHP9727	-7.38	2415	-0.3	1533	2348
	CHP9954	-7.28	2416	-0.3	2475	2859
	CHP9706	-8.52	2414	-0.35	1949	2614
	CHP9708	-25.25	2398	-1.04	1911	2576
	CHP9726	-25.31	2397	-1.04	1937	2371
	CHP9714	-30.94	2392	-1.28	1949	2382
	CHP970809	-31.79	2391	-1.31	2070	2746
	CHP9712	-40.54	2382	-1.67	1877	2552
	CHP9720	-49.06	2374	-2.02	1315	2084
	CHP01178	-52.87	2370	-2.18	1992	2658
CHP9736	-56.60	2366	-2.34	1975	2641	
CHP970617	-71.68	2351	-2.96	2144	2810	
CHP9718	-90.02	2333	-3.72	1864	2298	
CHP9955	-90.31	2332	-3.73	2095	2760	
B	AN9021332	126.42	2549	5.21	2169	2597
	BRS Campeiro	334.55	2757	13.8	2637	2924
	TB0202	232.19	2655	9.58	2365	3040
	TB9820	55.64	2478	2.3	2107	2772
	J56	40.08	2463	1.65	2247	2724
	Xamego	-98.56	2324	-4.07	2007	2510
	TB9713	-101.09	2322	-4.17	2311	2781
	Diamante Negro	-192.1	2231	-7.93	2074	2361
SELCP9310635	-397.14	2026	16.39	1552	2320	
C	LP02130	159.69	2582	6.59	2341	3007
	IPR Graúna	142.17	2565	5.87	2474	2760
	IPR Uirapuru	128.12	2551	5.29	2463	2750
	LP9805	21.35	2444	0.88	1926	2479
	LP0151	-115.26	2308	-4.76	2319	2790
	LP98123	-159.24	2264	-6.57	2081	2551
	Iapar44	-176.84	2246	-7.3	1664	2218
D	-	-	-	-	-	
E	UTF2810433	29.33	2452	1.21	2152	2817
	UTF4	94.33	2517	3.89	1743	2302
	Silvestre	-60.53	2362	1.21	1201	2053
	UTF7	-22.32	2400	-0.92	2070	2736
	UTF53611313	-40.80	2382	-1.68	1277	2092

6,59%) and UTF4 (3,89%) stood out for grain yield (Table V). For the character plant cycle, aiming at precocity, which is targeted in most breeding programs (Dalla Corte *et al.*, 2003; Machado *et al.*, 2008), the genotypes

CHP970809 from institution A (1,63%), BRS Campeiro from institution B (1,45%), Iapar44 from institution C (0,84%) and FT 84113 from institution D (0,09%) stand out for genetic gain. However, if the objective is to achieve a

TABLE VI
GENOTYPE PREDICTED VALUE THROUGH BLUP (g),
PREDICTION OF THE GENOTYPIC VALUES ($\mu+g$),
ACHIEVED GAIN (g%; kg·ha⁻¹) AND CONFIDENCE
INTERVALS (95%) FOR THE PLANT CYCLE CHARACTER
OF 49 BLACK BEAN GENOTYPES, SUBDIVIDED INTO
FIVE BEAN BREEDING INSTITUTIONS ($\mu= 89,06$ Days)

Institutions	Genotypes	g	$\mu+g$	g%	Confidence intervals	
A	CHP970409	1.20	90.26	1.34	88.48	95.02
	CHP9858	0.99	90.05	1.11	83.26	89.02
	CHP9701	0.82	89.88	0.92	87.94	94.48
	CHP971308	0.81	89.87	0.91	89.90	94.23
	CHP970821	0.72	89.78	0.81	82.84	88.61
	CHP9704	0.66	89.72	0.75	89.87	95.63
	CHP9965	0.45	89.51	0.51	87.43	90.89
	CHP9859	0.41	89.47	0.46	89.48	95.24
	CHP9713	0.38	89.44	0.43	89.39	95.16
	CHP9702	0.28	89.34	0.32	82.20	87.97
	CHP9727	0.18	89.24	0.20	82.01	87.77
	CHP9954	-0.01	89.05	-0.01	86.09	90.16
	CHP9706	-0.11	88.95	-0.13	86.77	90.23
	CHP9708	-0.17	88.89	-0.20	88.53	91.58
	CHP9726	-0.20	88.86	-0.22	86.73	90.19
	CHP9714	-0.23	88.83	-0.26	87.56	91.25
	CHP970809	-0.35	88.71	-0.39	88.26	91.32
	CHP9712	-0.40	88.66	-0.44	81.14	86.91
	CHP9720	-0.42	88.64	-0.47	87.24	90.92
	CHP01178	-0.49	88.57	-0.55	87.99	92.32
CHP9736	-0.91	88.15	-1.02	84.64	91.70	
CHP970617	-1.08	87.98	-1.21	86.33	90.01	
CHP9718	-1.10	87.96	-1.23	84.09	90.63	
CHP9955	-1.45	87.61	-1.63	85.80	89.49	
B	AN9021332	0.33	89.39	3.91	89.01	93.33
	BRS Campeiro	1.08	90.14	1.21	90.88	95.21
	TB0202	0.76	89.82	0.85	89.03	91.55
	TB9820	0.49	89.55	0.55	87.67	91.99
	J56	0.00	89.06	0.00	87.44	91.13
	Xamego	-0.28	88.78	-0.31	82.56	88.33
	TB9713	-0.40	88.66	-0.44	83.05	89.59
	Diamante Negro	-0.69	88.37	-0.78	81.89	87.66
SELCP9310635	-1.29	87.77	-1.45	86.46	88.99	
C	LP02130	1.58	104.84	5.91	91.10	95.43
	IPR Graúna	-0.02	89.03	4.91	82.98	88.74
	IPR Uirapuru	-1.18	77.30	2.91	87.39	89.92
	LP9805	0.57	89.63	0.64	89.24	91.77
	LP0151	-0.08	88.99	-0.09	86.16	90.96
	LP98123	-0.12	88.94	-0.13	89.79	94.12
	Iapar44	-0.75	88.31	-0.84	85.33	90.13
D	FT Soberano	1.16	100.65	1.91	89.06	91.59
	FT Bionobre	-1.38	75.30	0.91	83.68	88.48
	FT Nobre	0.16	89.22	0.18	88.08	90.61
	FT 91370	0.15	89.21	0.16	85.75	90.55
	FT 84113	-0.09	88.97	-0.09	85.52	90.32
E	-	-	-	-	-	

late cycle, the genotypes CHP970409 from institution A (1,34%), SELCP9310635 from B (3,91%), LP02130 and IPR Graúna from C (5,91% and 4,91%, respectively) and FT Soberano from institution D (1,91) are the most promis-

ing. According to Chiorato *et al.* (2008), the genotypes with high phenotype effects and wide variability should be selected, in grain yield, for considerable genetic gain.

In plant breeding, besides distinguishing the variances,

the differences among the phenotypes effects of the genotypes and knowledge about the relation among the breeding target characters are very important. Since the selection of superior genotypes aim at identifying several characters simultaneously, knowledge about the phenotypic correlations can help in the selection of a plant ideotype best suited to the demands of a modern and competitive agriculture (Coimbra *et al.*, 2000). Therefore, the phenotypic correlations were estimated within each institution (Figure 1). Thus, it can be said that the characters grain yield and plant cycle presented significant and positive correlations in all the evaluated institutions, with correlations of 0,41 (institution A), 0,37 (B), 0,37 (C), 0,39 (D) and 0,38 (E).

The dispersion of the phenotypic correlation (Figure 1) between the grain yield and plant cycle characters evidenced significance in the correlation between them. The dispersion matrix (Becker *et al.*, 1987) presents the relations among several variables, taken two at a time. The confidence ellipses (Moore and McCabe, 1989), on the other hand, are used as a graphic indicator of correlation. Consequently, when two variables are correlated, the confidence ellipse is circular and, as the correlation among the variables becomes stronger, the ellipse becomes more elongated (SAS, 1997). Therefore, based on the correlation matrix (Figure 1), it can be verified that the existence of positive and significant correlation between the two variables is not similar for all the genotypes evaluated. However, there is a general trend for most genotypes to be included in the correlation. Besides, it can be observed that the presence of ellipse corroborates the presence of positive and significant correlation between the two variables. In other

words, there is evidence that genotypes with longer plant cycle may allow higher increases in grain yield. Coimbra *et al.* (2000) verified that the primary and secondary components of the grain yield of black bean are not independent, concluding that taller plants and those with higher reproductive cycle influence negatively the number of grains per legume and positively the number of legumes per plant and the grain mass. One of the plausible explanations for the low genetic gain in the institutions is the fact that the ideotyped genotypes have a precocious cycle, since those with higher grain yield, in general, are those with a long cycle, due to the significant and positive relation between the characters, as verified in the phenotypic correlation.

Conclusions

1- In the estimate of the variance components, the results evidenced higher contribution of non-genetic effects (σ^2_{ng}) for the phenotypic variance (σ^2_f), compared to the solely genetic effects (σ^2_g), both for the character grain yield, and the character plant cycle.

2- All the evaluated institutions presented genetic gains for the grain yield and plant cycle characters over the seven years, but with different magnitudes.

3- The highest genetic gains were achieved in institutions A ($\Delta G = 19\text{kg}\cdot\text{ha}^{-1}$), B ($\Delta G = 133\text{kg}\cdot\text{ha}^{-1}$), and C ($\Delta G = 71\text{kg}\cdot\text{ha}^{-1}$) for the character grain yield.

4- For the character plant cycle, all the institutions presented higher genetic gains, excepting the institution E, which achieved small gains (close to zero).

5- The characters grain yield and plant cycle presented significant and positive correlation in all the institutions evaluated.

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