
GENETIC PROGRESS OF BLACK BEAN (*Phaseolus vulgaris* L.) OVER SEVEN YEARS

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SUMMARY

The present work aimed at estimating the components of the annual phenotypic variance in the Value for Cultivation and Use Testing (VCU) of bean during seven years in ten locations, in the Santa Catarina State, Brazil, and evaluating the potential and genetic progress for the grain yield and plant cycle characters of the assessed genotypes. The restricted maximum likelihood / best linear unbiased prediction (REML/BLUP) methodology was used. For such, the components of phenotypic variance, genotypic variance and non-genetic variance were obtained and, based on these data, the genetic progress and genotype potential (higher yield and long cycle) were estimated. The

results revealed that, for the evaluated characters, regardless of the year, the highest contributions to phenotypic variance derived from non-genetic effects. The analysis of the phenotypic correlation revealed a positive significant correlation (0.39) between the characters grain yield and plant cycle. The annual genetic progress in the set of genotypes evaluated was estimated in 12.87kg-ha⁻¹ for grain yield and 0.19 days for plant cycle. The low estimates for genetic progress may be mainly related to the high magnitude of the environmental effect, which was the component that contributed the most for the phenotypic formation of both characters.

The importance of common bean in Brazil is unquestionable. Since the beginning of its cultivation, it has been the main source of income for many families, and Brazil has become the world largest producer of bean. Bean also plays an important cultural role, since it is part of everyday meal of Brazilian people. Due to its significance, the cultivation of the species should receive new social and economic incentives.

To this end, based on breeding programs, a new cultivar should

meet the demand of both farmers and consumers, combining the best technological, nutritional and culinary qualities. For the effective success of a breeding program, new genotypes must be differentiated from those already existing, either by their higher grain yield or by changes in the agronomic characters or increased nutritional quality. Breeding programs should, in the first place, meet the demand of consumers and farmers, aggregating commercial and differentiated value to the new genotype. Thus, the main objectives of plant breeding are the im-

provement in production, nutritional qualities and other characteristics of commercial value (Moose and Mumm, 2008).

Different procedures can be used by breeders to verify the efficiency of breeding programs (Abreu *et al.*, 1994; Ribeiro *et al.*, 2003), particularly those based on i) number and area occupied by the recommended cultivars; ii) the comparison between recently recommended cultivars and the traditional varieties or 'landraces'; and iii) the use of the results obtained in experiments conducted for several years

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in different locations (Abreu *et al.*, 1994). In this sense, besides the processes described above, breeders can use the results from the evaluation of lineages in yield or competition assays (ER), or use the Value for Cultivation and Use Testing (VCU) to verify the breeding program progress. Both assays are essential in breeding programs, in the proposal and recording of new cultivars. In many countries, including Brazil, before recommending a new cultivar to the market, government authorities require the performance of a preliminary evaluation of the VCU (Piepho and Mohring, 2006).

Therefore, based on the annual evaluation of the variance components, which uses the average values of all the genotypes (set), environments and interactions between genotypes and environments, for all variables under study, there is more consistency in the assessment and comparison between years of VCU trials. Thus, it is possible to estimate the components of the annual phenotypic variation and predict the genetic potential of the genotypes introduced or removed, besides estimating the genetic progress, considering the set of genotypes evaluated for several years. The estimate of the variance components allows a better knowledge about the causes of variation and, thus, the prevision of the gains from the selection of genetically superior plants (Coimbra *et al.*, 2009). Methods that allow a prediction of the expected gains by phenotypic selection in segregating populations are therefore essential to optimize results (Bertoldo *et al.*, 2010). When using the variance components, the restricted maximum likelihood / best linear unbiased prediction (REML/BLUP) methodology may be the best option for inference in unbalanced data obtained with the use of genotypes from VCU. The prediction of genetic values using BLUP depends on the estimates of the variance components associated with the random effects of the model, and one of the preferred methodologies to estimate variance components is REML (Arnhold *et al.*, 2009). Mixed models based on the REML/BLUP statistical method are widely used in animal breeding. However, in plant breeding programs, their use has been restricted to date to perennial crops where unbalanced experiments are common (Fritsche-Neto *et al.*, 2010). To Chiorato *et al.* (2008) the use of mixed models by means of the REML and BLUP methods for the estimation of genetic parameters and prediction of genetic values, free of any environmental effects, can be an important method in the orientation of the common bean breeding programs.

The present work aimed at estimating the components of the phenotypic variance in VCU tests of black bean conducted in Santa Catarina State during

TABLE I
CHARACTERISTICS OF THE TEN LOCATIONS OF COMMON BEAN CULTIVATION IN SANTA CATARINA STATE

Location	Region	Mean annual temp. (°C)	Altitude (masl)	Growing season
Águas de Chapecó	West	20	291	Second
Campos Novos	Mid West	20	946	Main
Canoinhas	Northern Plateau	20	839	Main
Chapecó	West	20	670	Main
Ituporanga	Itajaí Valley	17	370	Second
Lages	Mountain Plains	16	904	Main
Ponte Serrada	West	16	1067	Main
São Carlos	West	20	264	Second
Urussanga	South	20	49	Second
Xanxerê	West	20	800	Main

Source: Governo de Santa Catarina (2009).

seven years in ten locations, and evaluating the genetic potential and progress of the genotypes evaluated for the grain yield and plant cycle characters, by the REML/BLUP methodology.

Material and Methods

For the purposes of this study, grain yield and plant cycle data of 56 black bean genotypes from Brazilian research institutions in the final stage of improvement were used, collected from annual VCU, and carried out in a network coordinated by the Empresa de Pesquisa Agropecuária e Extensão Rural de Santa Catarina (EPAGRI) - Centro de Pesquisa para Agricultura Familiar de Chapecó, over seven years (2001 to 2007). The study was conducted 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 (Table I).

The assays were conducted in a randomized experimental block design, with four replications. Seeding rate was 15 viable seeds per linear meter (250000 plants/ha). The experimental unit was composed of four lines of 4m of length, with spacing of 0.45m, and useful area of 2.7m². To provide equal conditions, the chemical control of pests and weeds and manual weeding were carried out when necessary, as soon as they appeared.

The following statistical model was used:

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

where μ : average, g_i : genotype random effect, l_j : location random effect, a_k : year random effect, gl_{ij} : genotype \times location interaction random effect, ga_{ik} : genotype \times year interaction random effect, la_{jk} : location \times year interaction random effect, gla_{ijk} : geno-

type \times location \times year interaction random effect, b_l : block effect, and ϵ_{ijkl} : error.

The entire statistical analysis was performed with SAS 9.1.3 (SAS, 2007). Based on the restricted maximum likelihood (REML) and best linear unbiased prediction (BLUP) procedures, performed with the PROC MIXED command for experiments under randomized block design (Littell *et al.*, 2006), the components of phenotypic or total variance (σ^2_{ϕ}), genotypic variance (σ^2_g) and non-genetic variance (σ^2_{ng}) were achieved, in other words, location effect and effect of all the possible interactions among genotype, location and year ($\sigma^2_{\text{location}} + \sigma^2_{\text{year} \times \text{genotype}} + \sigma^2_{\text{location} \times \text{year}} + \sigma^2_{\text{location} \times \text{genotype}} + \sigma^2_{\text{location} \times \text{year} \times \text{genotype}} = \sigma^2_p$), so that: $\sigma^2_{\phi} = \sigma^2_g + \sigma^2_{ng}$. Based on the estimate of the components of the total variance, the average BLUP's, genotypic values (σ^2_g) and the non-genetic values (σ^2_{ng}) were obtained and the total and annual genetic progress and potential genetics were estimated, so that:

average BLUP's = sum of the individual BLUP's of the genotypes per year; annual genotypic value $VG_g = \sigma^2_g / \text{year} (\%) \times \text{mean/year} (\text{kg} \cdot \text{ha}^{-1} \text{ or days})$; annual non-genetic value $VG_{ng} = \sigma^2_{ng} / \text{year} (\%) \times \text{mean/year} (\text{kg} \cdot \text{ha}^{-1} \text{ or days})$. The command PROC CORR procedure based on Moore and McCabe (1989) is used for the construction of the correlation dispersion ellipse and the correlations between characters.

Results and Discussion

Grain yield and plant cycl: the major contributor is the environment

The results revealed that in the composition of the total phenotypic variance for grain yield, regardless of the year, the largest contributions corresponded to the effects of location and interactions (varying between years from 90.70 to 99.70%). Namely, the character variance is

TABLE II

ESTIMATES OF THE VALUE OF THE GENOTYPIC (σ^2_g), NON-GENETIC (σ^2_{ng}), RESIDUAL (σ^2_e) AND TOTAL (σ^2_t) VARIANCES PER YEAR, COMPARING SEVEN AGRICULTURAL YEARS (2001-2007) FOR GRAIN YIELD (kg·ha⁻¹) AND PLANT CYCLE (DAYS) CHARACTERS, IN 56 GENOTYPES OF BLACK BEAN USED IN VCU TEST AT TEN LOCATIONS OF SANTA CATARINA STATE, BRAZIL

Year	Grain yield					
	$\dagger \sigma^2_g$	$\ddagger \sigma^2_{ng}$	$\text{§} \sigma^2_t$	% σ^2_g	% σ^2_{ng}	σ^2_e
2001	6.099	2.080.650	2.086.749	0.30	99.70	155.837
2002	43.354	1.417.538	1.460.892	2.96	97.04	122.676
2003	51.429	658.060	709.489	7.25	92.75	153.567
2004	25.325	980.113	1.005.438	2.52	97.48	133.878
2005	29.144	1.205.713	1.234.857	2.36	97.64	349.196
2006	26.305	972.214	998.519	2.63	97.37	198.884
2007	12.598	122.789	135.387	9.30	90.70	61.430
Total	194.254	7.437.077	7.631.331	-	-	-
Year	Plant cycle					
	$\dagger \sigma^2_g$	$\ddagger \sigma^2_{ng}$	$\text{§} \sigma^2_t$	% σ^2_g	% σ^2_{ng}	σ^2_e
2001	0.26	24.00	24.26	1.08	98.92	1.81
2002	0.75	60.59	61.34	1.22	98.78	12.51
2003	1.19	57.25	58.44	2.03	97.97	10.15
2004	0.79	72.37	73.16	1.07	98.93	15.64
2005	0.32	61.29	61.61	0.51	99.49	19.23
2006	2.45	49.77	52.22	4.69	95.31	5.01
2007	0.01	133.81	133.82	0.01	99.99	20.50
Total	5.77	459.08	464.85	-	-	-

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

mainly due to the non-genetic variance (Table II). A small genotypic contribution can be observed for the same character, which varied from 0.3 to 9.3%. Similar results were observed for the plant cycle character, so that the largest contributions are also due to the non-genetic variance (varying from 95.30 to 99.90%) and the smallest contribution is related to genotypic variance (0.01 to 4.69%) (Table II).

These results indicate that, for the characters of grain yield and plant cycle, most of the variations observed in the field are the result of environmental effects (such as years and locations), and a smaller part of the variation can be attributed to the genotype effect. The environment can be understood as the factors external to individuals, which challenge and influence them. Living organisms are constantly reacting and adapting to the environment and, in a broad sense, the environment is defined as all the intra- and extra-cellular factors that affect the phenotype expression (Brewbaker, 1969). Coimbra *et al.* (2009), evaluating 24 bean genotypes, observed that most of the variation among the marginal averages of 24 genotypes of the black group evaluated was attributed to the environmental variance, while the estimate of the genotypic contribution was smaller. Based on the evaluation of some characters segregating bean populations, including grain yield, Londero *et al.* (2006) concluded that this

character is greatly influenced by the environment, having a lower contribution of the genetic variance in the phenotypic expression. Similarly, while evaluating the phenotypic formation of the grain yield character in bean, Bertoldo *et al.* (2009) verified that the highest contribution was associated to the environment.

The higher contribution of the genotype for the characters evaluated in the present work, result in the following impacts on a breeding program: i) greater difficulty in conducting tests for genotype evaluation; ii) demand for a greater number of locations and years for the assessment of genotypes, since a genotype can be superior to another, according to the environmental effect (of year x and location y); and iii) lower genetic progress is achieved with the selection, and such genetic progress was obtained based on the differential of selection of individuals, intensity of selection and heritability estimate. A greater effect of the environment in relation to the genotype itself promotes biased heritability estimates and, consequently, a reduced expected gain with the selection process.

Characteristics of Santa Catarina VCU bean trials

According to the evaluation of the genotypes and locations where

the VCU assays were carried out in the Santa Catarina State (Table III), it can be observed that, every year, new genotypes were used in the assays and that the average grain yields varied in the different agricultural years. In total, 56 bean genotypes were evaluated, some of which were maintained, others were removed from the assays. Thus, considering the repetition of the same genotype in different years, the total number evaluated was 203 genotypes between 2001 and 2007, an average of 29 genotypes per year (Table III).

Even presenting a lower magnitude when compared to the environmental effect, the genotypic values can contribute to the general average, in lower degree. Thus, the change in the number and kinds of genotypes used may have influenced the average values of grain yield, where the exclusion of genotypes genetically superior or the inclusion of genotypes genetically inferior may have affected the average values. Ribeiro *et al.* (2003) verified that the value of grain yield varied as the genotypes were replaced. Thus, due to the inclusion of adapted cultivars, the value of the grain yield can be increased. However, this variation is more influenced by the environmental effects, which are higher than the genotypic value itself. On the other hand, since the genotypes are challenged by the environment, the presence of a genotype × environment (G×E) interaction must be considered and, in this case, genotypes with higher genetic contribution are able to provide higher yields.

During seven years the total genotypic value corresponded to 550.82kg·ha⁻¹, and to 78.68 kg·ha⁻¹ in average, while the total phenotypic value was 16.176kg·ha⁻¹, or 2310kg·ha⁻¹ on average for the seven years (Table III). The highest grain yield average was achieved in 2006 (3099kg·ha⁻¹) and the lowest in 2007 (1267kg·ha⁻¹). The individual contribution of the genotypes for the annual total variance revealed that, even with a higher genotype contribution as observed in 2007, it does not result in higher gains for the grain yield. In that year, even with a contribution of 9.3% or 117.83kg·ha⁻¹, the grain yield was lower. Opposite results can be observed for 2006; the highest grain yield for the seven years evaluated (3099kg·ha⁻¹) was obtained in the later year, with a small participation of the genotype in the phenotypic constitution (2.63% or 81.50kg·ha⁻¹).

The results obtained for 2006 and 2007, for example, corroborate those obtained from the decomposition of the phenotypic variance (Table II). Since the environmental variance constitute the largest contribution to the total variance, the genotypic effect represents a small part in the grain yield. For 2007, although the geno-

TABLE III
NUMBER OF GENOTYPES PER YEAR, GRAIN YIELD AND PLANT CYCLE, AVERAGE, PERCENTAGE OF THE GENOTYPIC VALUE AND GENOTYPIC VALUE EVALUATED IN THE VCU TEST OF BLACK BEAN FOR SANTA CATARINA STATE

Year	Grain yield				Average (kg·ha ⁻¹)	Genotypic value (%)	† Genotypic value (kg·ha ⁻¹)
	T	I	M	E			
2001	22	0	22	0	2546	0.30	7.64
2002	26	3	22	4	1924	2.96	56.95
2003	29	7	22	7	2243	7.25	162.62
2004	33	11	24	9	2501	2.52	63.02
2005	25	1	23	2	2596	2.36	61.26
2006	43	20	24	19	3099	2.63	81.50
2007	24	0	24	0	1267	9.30	117.83
Total	203	42	162	41	16176	27.32	550.82
General average	29				2310	3.90	78.68

Year	Plant cycle				Average (days)	Genotypic value (%)	† Genotypic value (days)
	T	I	M	E			
2001	22	0	22	0	97	1.08	1.04
2002	26	3	22	4	83	1.22	1.01
2003	29	7	22	7	90	2.03	1.82
2004	33	11	24	9	90	1.07	0.96
2005	25	1	23	2	94	0.51	0.47
2006	43	20	24	19	90	4.69	4.22
2007	24	0	24	0	81	0.01	0.008
Total	203	42	162	41	625	10.61	9.56
General average	29				89	1.5	1.4

T: number of genotypes evaluated in the year, I: number of new genotypes in relation to the previous year. M: number of genotypes maintained for evaluation in the following year, E: number of genotypes excluded from the evaluation in the following year, † estimate obtained with the genotypic value (%) multiplied by the average per year.

types contributed with 117.83kg·ha⁻¹, the average yield was the lowest of all the years (1267kg·ha⁻¹; Table III). This reveals that even when there is a significant genotypic contribution, the environmental effect continues to be the most influential in the total variance, although there is some influence from the genotype itself.

Similarly, for the plant cycle character there was a variation through the agricultural years, from 81 to 97 days (Table III). A small contribution of the genotype to this phenotype was also observed, so that the total genotypic value was 10.6% or 9.6 days in the seven years. The lowest average for plant cycle was obtained in 2007 (81 days) and, coincidentally, in the same year, the lowest genotypic contribution was also observed (0.01% or 0.01 days). However, this relation between higher/lower genotypic contribution and higher/lower cycle does not exist. It can be observed that in 2006, when the highest participation of the genotype was verified (4.69%), the average cycle (90 days) was not the highest. The differences between the years corroborated these results and revealed the inconsistency in the number of genotypes used in VCU tests, suggesting that the use of the set of

genotypes is more informative than genotypes evaluated separately, as is done in most cases (Table IV).

Based on the variance components estimated in the population under study and in the evaluation environments, it is also possible to predict the genetic potential of the genotypes used, which can be an interesting estimate for breeders. Thus, the potential genotypes can be considered as those that contribute positively or negatively to the phenotype, depending on breeders' interests, or those for which the predicted genotypic value is positive or negative. For example, if breeders are interested in an increased grain yield and precocity in the plant cycle, they must search for genotypes in which the contribution for the phenotypic variance is positive for grain yield and negative for plant cycle, thus providing a higher genetic gain.

Prediction of genetic potential based on BLUP and phenotypic correlation

In the present study the genetic potential was predicted by BLUP, revealing different groups of genotypes whose effects were positive and negative for the characters grain yield and plant cycle (Figure 1). Therefore, it is possible to separate the genotypes into four different groups: 1) positive contribution for grain yield and plant cycle (9 genotypes: CHP9701, CHP9706, CHP9965, CNFP8000, IPR Uirapuru, LP02130, TB0202, UTF28104 and Xamego); 2) negative contri-

TABLE IV
DIFFERENTIAL ANNUAL ESTIMATES FOR THE BLACK BEAN GENOTYPES EVALUATED IN THE VCU TEST FOR THE STATE OF SANTA CATARINA FOR GRAIN YIELD (kg·ha⁻¹) AND PLANT CYCLE (days).

Differential for grain yield / year	Differential number of genotypes	† Differential average yield	‡ Differential genotypic value (%)	§ Differential genotypic value (kg·ha ⁻¹)
2002/01	+4	-622	+2.66	49.31
2003/02	+3	+319	+4.29	105.67
2004/03	+4	+258	-4.73	-99.60
2005/04	-8	+95	-0.16	-1.76
2006/05	+18	+503	+0.27	0.24
2007/06	-19	-1832	+6.67	0.33
Total	-	-1279	9.00	110.92

Differential for plant cycle / year	Differential number of genotypes	† Differential average cycle (days)	‡ Differential genotypic value (%)	§ Differential genotypic value (days)
2002/01	+4	-14	+0.1	-0.06
2003/02	+3	+07	+0.8	+0.92
2004/03	+4	0	-0.9	-0.86
2005/04	-8	+04	-0.5	-0.49
2006/05	+18	-04	+4.2	+3.74
2007/06	-19	-09	-4.7	-4.21
Total	-	-16	-1.09	-0.96

† Estimated from the differences of the averages for the grain yield among the years, ‡ estimated from the differences of the genotypic values (%) among the years; § estimated from the differences of the genotypic values (days) among the years.

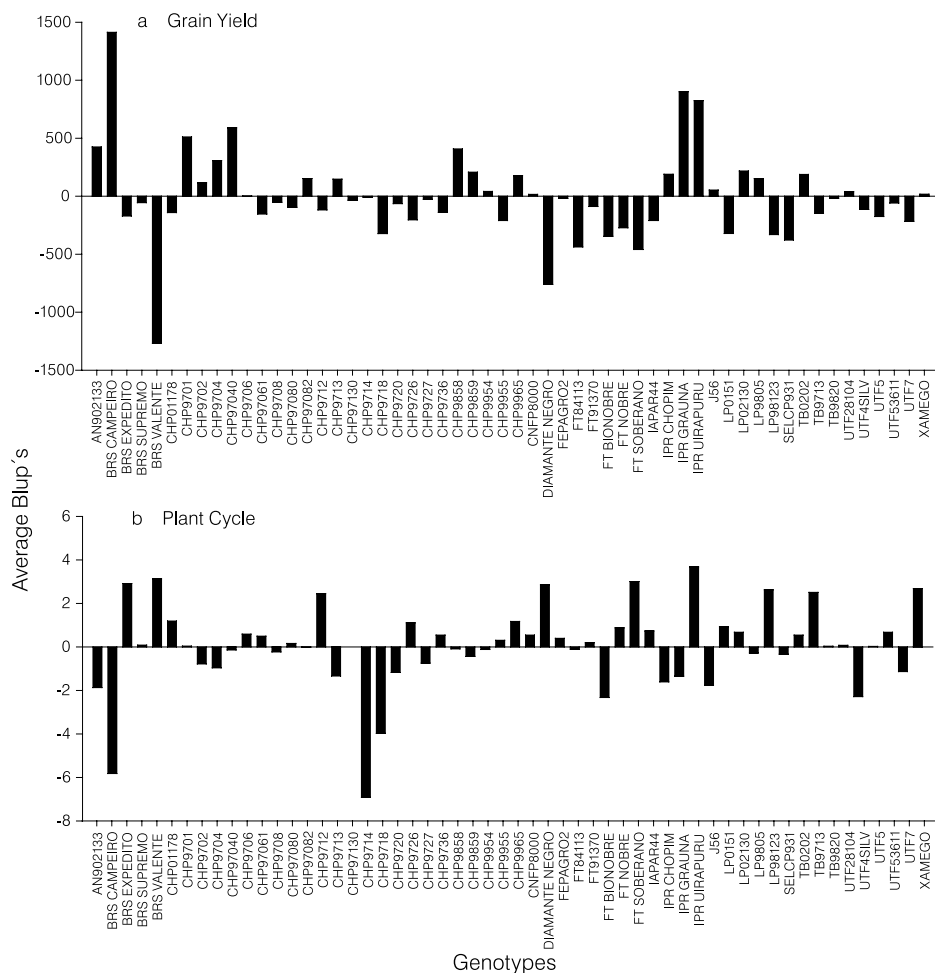


Figure 1. Values of the average genotypic effect for the character grain yield (a) and plant cycle (b) obtained from 56 black bean genotypes, when cultivated in ten environments, during seven years (2001 to 2007), predicted by the best linear unbiased prediction method (BLUP).

bution for grain yield and plant cycle (10 genotypes: CHP9708, CHP9714, CHP9718, CHP9720, CHP9727, FT84113, FT Bionobre, SELCP931, UTF4 Silvestre and UTF7); 3) positive contribution for grain yield and

negative for plant cycle (15 genotypes: AN902133, BRS Campeiro, CHP9702, CHP9704, CHP97040, CHP97082, CHP9713, CHP97130, CHP9714, CHP9718, CHP9720, CHP9726, CHP9727, CHP9736, CHP9858, CHP9859, CHP9954, CHP9955, CHP9965, CNFP8000, DIAMANTE NEGRO, FEPAGRO2, FT84113, FT91370, FT Bionobre, FT Nobre, FT Soberano, IAPAR44, IPR Chopim, IPR Graúna, IPR Uirapuru, J56, LP0151, LP02130, LP9805, LP98123, SELCP931, TB0202, TB8713, TB8820, UTF28104, UTF4 SILV, UTF5, UTF53611, UTF7, XAMEGO)

and LP9805); and 4) negative for grain yield and positive for plant cycle (22 genotypes: BRS Expedito, BRS Supremo, BRS Valente, CHP01178, CHP97061, CHP97080, CHP9712, CHP9726, CHP9736, CHP9955, Diamante Negro, FEPAGRO6, FT91370, FT Nobre, FT Soberano, IAPAR44, LP0151, LP98123, TB9713, TB9820, UTF5 and UTF53611).

The results also allow breeders to establish goals and select/recommend genotypes according to the objective of the program. If breeders seek increased grain yield with shorter plant cycle, they could use the genotypes in group 3. On the other hand, if they intend to achieve increased grain yield with longer plant cycle, the genotypes of the group 1 should be selected/recommended.

Besides, the phenotypic correlation analysis between the characters gives breeders a better understanding of the relations among the variables studied. In the present work, the general phenotypic correlation analysis revealed a significant positive linear correlation (0.39) between the characters grain yield and plant cycle (Table V). Based on the correlation estimate, it can be inferred that as plant cycle increases, grain yield increases. Therefore, the potential genotypes for grain yield improvement would belong to group A.

To demonstrate the presence of a positive and significant correlation between the characters studied, a dispersion ellipse of the correlations found was constructed (Figure 2). A positive and significant correlation was observed ($r=0.39$). According to Moore and McCabe (1989), confidence ellipses are used graphically as indicators of correlation. When two variables are correlated, the confidence ellipse is circular. As the correlation between the variables becomes stronger, the ellipse becomes elongated (Moore and McCabe, 1989; Herrera, 2005). The circular shape of the dispersion ellipse of the phenotypic correlation between grain yield and plant cycle also reveals a significant interaction between these characters.

The existence of different groups and the presence of correlation that explains about 16% of the common variation for the characters grain yield and plant cycle allow breeders to select genotypes of interest, combining different phenotypes independently. Genotypes with high yield and late cycle are an example of this, for cultivation in specific regions such as the mountain region of Santa Catarina. The correlation between characters indicates that the selection performed in a certain character may change in others, whose meaning may be or not of interest for breeding (Silva and Vieira, 2008). However, although the correlation between the two characters was sig-

TABLE V
PHENOTYPIC CORRELATION COEFFICIENT, GENERAL AND PER GROUP, BETWEEN THE CHARACTERS GRAIN YIELD AND PLANT CYCLE IN BEAN GRAINS OF THE BLACK COMMERCIAL GROUP EVALUATED IN THE VCU TEST OF BLACK BEAN FOR SANTA CATARINA STATE FROM (2001-2007)

	Variable	Grain yield (kg·ha ⁻¹)	Plant cycle (days)
General	grain yield (kg·ha ⁻¹)	1.00	0.39 *
	plant cycle (days)	0.39 *	1.00
Group A genotypes with yield above the overall average	Variable	Grain yield (kg·ha ⁻¹)	Plant cycle (days)
	grain yield (kg·ha ⁻¹)	1.00	0.38 *
	plant cycle (days)	0.38 *	1.00
Group B genotypes with grain yield values below the overall average	Variable	Grain yield (kg·ha ⁻¹)	Plant cycle (days)
	grain yield (kg·ha ⁻¹)	1.00	0.12 *
	plant cycle (days)	0.12 *	1.00

* significant by the t test at 5% probability.

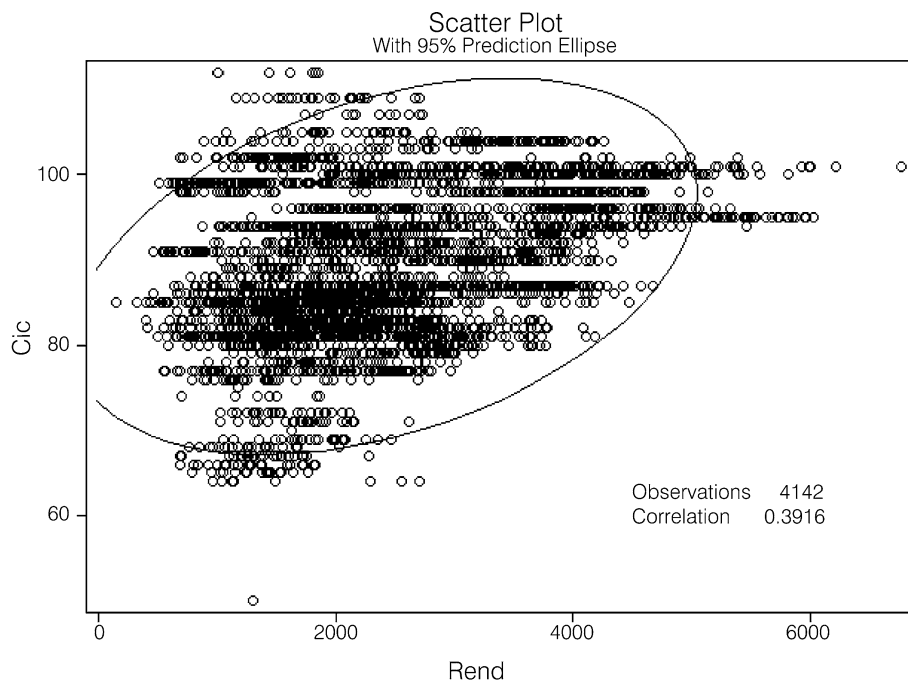


Figure 2. Dispersion of the phenotypic correlation for the characters grain yield and plant cycle in grains from the bean of the black commercial group evaluated in the VCU test of black bean for Santa Catarina State from 2001 to 2007.

nificant, not all the genotypes evaluated necessarily follow this correlation.

Genetic progress over seven years of bean breeding based on VCU trials

For breeders, a new genotype should be different from those currently recommended (already grown) and meet the demand of the market (consumers) and growers (farmers). Therefore, it is important to know the gain achieved with the selection or recommendation of genotypes for the location where the new genotype is intended to be cultivated, as the prediction of the variance components is important for breeders, in agronomic terms. Thus, the components of total, genotypic and non-genetic variance (σ^2_t , σ^2_g and σ^2_{ng} , respectively) were predicted, for the characters grain yield and plant cycle (Table VI).

The results revealed that out of a 100%, which is the value of the phenotypic or total variance (σ^2_t), 3.9 and 1.5% can be attributed to the genotypic variance (σ^2_g) for the characters grain yield and plant cycle, respectively. The other percentages (96.1% for grain yield and 98.5% for plant cycle) can be attributed to the non-genetic variance (σ^2_{ng}), namely, to the effect of the location and the interactions between the factors being evaluated. Specifically for grain yield, there is evidence in literature that the environment greatly affects this character (Falconer and Mackay, 1996; Allard, 1999). Although genetic control is not thoroughly understood, some au-

thors suggest that the plant cycle is controlled by a few major genes (Silva *et al.*, 2007) and the heritability of the character is relatively high (Ariell *et al.*, 1990; Barelli *et al.*, 1999). On the other hand, some authors have observed that the character plant cycle presents a continuous phenotypic distribution, which suggests that they are controlled by several pairs of genes that segregate independently, and each contributes to the phenotypic variance. In other words, each one can be classified as a quantitative character (Ribeiro *et al.*, 2004; Lima *et al.*, 2008) and the heritability for the character is low (Lopes *et al.*, 1995). Authors have different opinions, since any character is subject to the effect of the environment, the genotype and the interaction between the genotype and the environment. Therefore, the phenotypic constitution of an individual of a population may vary. In certain moments, there is loss of genetic variability among the genotypes and in other moments, gains. It may maximize or minimize the effect of the environment on the phenotype. Thus, for any character, all these factors affect the phenotypic expression.

Based on the estimate of the variance components, it was also possible to estimate the total genetic progress of the genotypes evaluated in the bean VCUs in Santa Catarina State (Table VI). The genetic progress is equivalent to the genotypic value, or the amount of the total phenotypic value can be attributed to genetic causes, which are those really sought by breeders. When the percentage total variance (σ^2_t)

for grain yield is 100%, the phenotypic value is 2310kg·ha⁻¹ and the percentage genotypic variance ($\sigma^2_{g\%}$) is 3.9%, it is possible to achieve the genotypic value of 90.09 ($\sigma^2_t \times \sigma^2_{g\%} = 2130 \times 3.9\% = 90.09 \text{kg} \cdot \text{ha}^{-1}$). For the plant cycle character, based on the same rationale, the genotypic value is estimated in 1.5 ($\sigma^2_t \times \sigma^2_{g\%} = 89 \times 1.5\% = 1.34$ days). Therefore, the total genetic progress (PG_t) achieved for the characters grain yield and plant cycle, from 203 genotypes evaluated during seven years in the VCU test in the state of Santa Catarina, was 90.09kg·ha⁻¹ and 1.34 days, respectively (PG_t = Vg). The annual genetic progress (PG_{t/a}) was estimated in 12.87kg·ha⁻¹ for grain yield and 0.19 days for plant cycle (PG_{t/a} = PG_t/years). The results obtained by the restricted maximum likelihood method (REML) are lower than those found by other authors, but are close to them: based on the methodology proposed by Vencovsky *et al.* (1986), Abreu *et al.* (1994) estimated an annual average gain of 1.9%; Ribeiro *et al.* (2003) verified an annual average gain for the grain yield of 0.88%, which corresponds to 18.07kg·ha⁻¹; and; Matos *et al.* (2007), who used the methodology proposed by Abreu *et al.* (1994), verified an annual average gain of 4.36%, which resulted in an annual productivity of 54.30kg·ha⁻¹.

According to Faria *et al.* (2007) the methods used to verify the genetic progress are: i) direct method ii) methods with multi-local assays, which are subdivided in original method, original method with weighting and methods which use a reference genotype; iii) regression method with original data; and iv) control as a correction factor. For most methods proposed, a genotype is used as control. In other words, it remains in the assays over the years, as proposed by Abreu *et al.* (1994). Eventually, a certain genotype remains as control over all the years tested and can be used as a reference to estimate the genetic gain (Faria *et al.* 2007). However, the selection of the control genotype is essential for the effectiveness of the method, since all the comparative inferences are carried out among all the genotypes of the assay/year vs the control. Córdova *et al.* (1996) emphasized that the selection of the reference genotype should be carefully made, since it must meet the expectations of farmers and breeders for performance, with a satisfactory grain production. Therefore, it is clear that the selection of the control genotype and the sensitivity of the method are challenging. In other methods, such as that proposed by Vencovsky *et al.* (1986), the annual genetic progress is obtained as the difference between the average productivity of the common genotypes in a certain year and in the previous year. Fernandes (1988) proposed the estimation of the genetic prog-

TABLE VI
PREDICTIONS OF THE TOTAL VARIANCE COMPONENTS FOR THE CHARACTERS GRAIN YIELD AND PLANT CYCLE ($\sigma^2g\%$, $\sigma^2ng\%$ e $\sigma^2t\%$), GENOTYPIC, NON-GENETIC AND PHENOTYPIC VALUES (VG, VNG AND VT), TOTAL AND ANNUAL GENETIC PROGRESS (PG_t AND $PG_{t/a}$) AND GENETIC GAIN EVALUATED IN THE VCU TEST OF BLACK BEAN CARRIED OUT IN THE STATE OF SANTA CATARINA IN SEVEN YEARS

Variance components	Character		Estimates
	Yield	Cycle	
Percentage genotypic variance	3.9	1.5	$(\sigma^2g\%)$
Percentage non-genetic variance	96.1	98.5	$(\sigma^2ng\%)$
Percentage total variance	100	100	$\sigma^2t\% = \sigma^2g\% + \sigma^2ng\%$
Phenotypic value	2310kg·ha ⁻¹	89 days	(V _t)
Genotypic value	90.90kg·ha ⁻¹	1.34 days	(V _g)
Non-genetic value	2.219kg·ha ⁻¹	87.66 days	(V _{ng})
Total genetic progress	90.09kg·ha ⁻¹	1.34 days	$PG_t = Vg$
Genetic progress per year ($PG_{t/a}$)	12.87kg·ha ⁻¹	0.19 days	$PG_{t/a} = PG_t/\text{years}$
* Total genetic progress	288.96kg·ha ⁻¹	-0.10 days	
* Genetic progress per year	41.28kg·ha ⁻¹	-0.014 days	

* Methodology of Vencovsky *et al.* (1986).

ress through the difference between the average productivity of the non-common genotypes of a certain year in relation to the previous year. None of the methods mentioned above uses the variance components for the estimation of the genetic progress.

Given the close results found for genetic progress with the different methods mentioned, it is important to highlight that, with the use of the method that employs a variety as control, the results depend on the performance of the control genotype. Thus, if it achieves low yields in a certain year, the progress will be higher. On the contrary, if the control presents a better performance compared to the evaluated genotypes, the genetic progress will be lower.

With the use of the REML/BLUP method, data related to all the genotypes are used and based on them the variance components are estimated. Thus, whether the genotype achieves a favorable or unfavorable performance in a certain year, the genetic progress is not directly related to the average of a single genotype, but to the set of genotypes evaluated in the year, which can add higher efficiency to the prediction of the genetic progress with the use of the variance components.

Final considerations

The results of the present study reveal that bean breeding programs must consider the large magnitude of the environmental effect on grain yield and plant cycle. The genotypes used in the VCU tests in Santa Catarina did not represent large genetic gains, although a certain genetic progress was achieved and potential genotypes were verified. However, the marked influence of the environment on the evaluated characters, as well as the low

variability between the genotypes for the characters studied, may explain the low gains. In order to guide new bean breeding programs, consideration must be given to the methods used. A possible strategy is the use of the G×E interaction, which could probably increase the technological, culinary and nutritional quality values of the new genotype and also meet farmers' specific demands. In other counties, it is common to take farmers' opinion into account and favor participative breeding, but this is unusual in Brazil. Some authors emphasize the participation of farmers in the selection process (Ceccarelli *et al.*, 2001; Almekinders and Elings, 2001) and the relevance of this participation in the selection of the lineage or lineages to be recommended. Still, with the breeding of varieties specific to certain regions and participative breeding, the rejection to new recommended varieties (generally with broad adaptability) may be reduced, thus further favoring the breeding programs.

Conclusions

In the composition of the total phenotypic variance for the characters grain yield and plant cycle, regardless of the year, the highest contributions is from non-genetic effects.

Grain yield presents a positive and significant correlation with the plant cycle character for the groups evaluated.

The potential genotypes for higher grain yield and long plant cycle are CHP9701, CHP9706, CHP9965, CNFP8000, IPR Uirapuru, LP02130, TB0202, UTF28104 and Xamego.

There is a low genetic progress in the set of genotypes of bean

from different breeding programs evaluated in Santa Catarina State for the characters grain yield and plant cycle.

The REML/BLUP method permitted to reach relevant inferences in the estimation of the genetic progress and potential.

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PROGRESO GENÉTICO DEL FRIJOL NEGRO (*Phaseolus vulgaris* L.) DURANTE SIETE AÑOS

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RESUMEN

El presente trabajo tuvo por objeto la estimación de los componentes de la variación fenotípica anual en la prueba de Valor de Cultivo y Uso (VCU) del frijol durante siete años en diez localidades del estado de Santa Catarina, Brasil, así como la evaluación del potencial y progreso genético para los caracteres rendimiento de grano y ciclo de vida de los genotipos ensayados. Se utilizó la metodología REML/BLUP (del inglés para máxima probabilidad restringida / mejor predicción lineal sin sesgo). Para ello, se obtuvieron los componentes de variación fenotípica, variación genotípica y variación no-genética y en base a estos datos se estimaron el progreso genético y potencial genotípico (mayor rendimiento y ciclo largo). Los resulta-

dos indican que, para los caracteres evaluados e independientemente del año, las mayores contribuciones a la variación genética provienen de efectos no genéticos. El análisis de correlación fenotípica reveló una correlación significativa y positiva (0,39) entre los caracteres rendimiento de grano y ciclo de vida. El progreso genético anual en el grupo de genotipos evaluados fue estimado en 12,87kg·ha⁻¹ para rendimiento de grano y 0,19 días para ciclo de vida de la planta. Las bajas estimaciones de progreso genético pueden ser relacionadas sobre todo al alto grado del efecto ambiental, que fue el componente con la mayor contribución a la formación fenotípica de ambos caracteres.

PROGRESSO GENÉTICO DO FEIJÃO PRETO (*Phaseolus vulgaris* L.) DURANTE SETE ANOS

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RESUMO

O presente trabalho teve por objeto a estimativa dos componentes da variação fenotípica anual na prova de Valor de Cultivo e Uso (VCU) do feijão durante sete anos em dez localidades do estado de Santa Catarina, Brasil, assim como a avaliação do potencial e progresso genético para os caracteres rendimento de grão e ciclo de vida dos genótipos ensaiados. Utilizou-se a metodologia REML/BLUP (do inglês para máxima probabilidade restringida / melhor predição linear sem sesgo). Para isto, se obtiveram os componentes de variação fenotípica, variação genotípica e variação não genética e com base a estes dados se estimaram o progresso genético e potencial genotípico (maior rendimento e ciclo longo). Os resultados indicam que, para os

caracteres avaliados e independentemente do ano, as maiores contribuições à variação genética provêm de efeitos não genéticos. A análise de correlação fenotípica revelou uma correlação significativa e positiva (0,39) entre os caracteres rendimento de grão e ciclo de vida. O progresso genético anual no grupo de genótipos avaliados foi estimado em 12,87kg·ha⁻¹ para rendimento de grão e 0,19 dias para ciclo de vida da planta. As baixas estimativas de progresso genético podem ser relacionadas sobre todo ao alto grau do efeito ambiental, que foi o componente com a maior contribuição na formação fenotípica de ambos os caracteres.