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Agronomic Performance and Genetic Variability among Common Bean Genotypes in Savanna/Pantanal Ecotone

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ABSTRACT

In order to evaluate the agronomic performance and estimate the genetic variability of 24 common bean genotypes grown in the Savanna-Pantanal ecotone and see, which characters can be used for selection of superior genotypes. Treatments consisted of 24 common bean genotypes (CNFC 10429, CNFC 10408, CNFC 10467, CNFC 10470, CNFC 10762, CNFP 10104, CNFP 10793, CNFP 10794, BJ4, CNFRJ 10556, VR3 VC3 e VC6, IAPAR 81, BRS Campeiro, BRS 7762 Supremo, BRS Esplendor, BRS Valente, BRS Pitanga, BRS Radiante, BRS Requinte, BRS Pontal, BRS 9435 Cometa e BRS Estilo). The following traits were evaluated: Early flowering, early maturity, height of the first pod, number of pods per plant, number of grains per pod, weight of 100 grains and grain yield. The following parameters were estimated: environmental, phenotypic and genotypic variances, experimental and genotypic coefficient of variation, genotypic coefficient of determination, b quotient, environmental, phenotypic and genetic correlations. The CNFP 10794 genotype had the best agronomic performance in the Savanna-Pantanal ecotone region. The population presents genetic variability and potential for selection of all traits. Based on genetic parameters estimates, the characters number of grains per pod and weight of hundred grains can be used in direct selection for more productive genotypes.

Key words: Agronomic traits, correlations, genetic parameters, *Phaseolus vulgaris*

INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) growing is traditionally performed in three periods of the year: The "first period", the "second period" and the "autumn/winter harvest", also called the "third period". Considering the three annual harvests, the grain production of common bean obtained in 2013 was 2.8 million tons, in an area of 3.11 million ha, being the average yield estimated in 900.32 kg ha^{-1} (CONAB., 2014).

This crop is grown almost all states of Brazil, in several soil and climatic conditions and at different times and cropping system. Due to climatic instability and the heterogeneity of soils there is great difficulty to perform successfully the genetic improvement of bean. Knowledge of the existence of phenotypic variability in a population grown in a given location and how much of this variability is due to genetic differences is fundamentally important in breeding programs (Cruz *et al*., 2004). This allows knowing the genetic control of the character and the potential of the population for selection. The study of the genetic control and heritage of agronomic traits through estimates of genetic parameters in a population allows inferences about its genetic variability and what can be expected in gain with the selection. Knowing the correlations among traits of interest for selection allows the breeder to know the degree of association among economically important traits, given that the selection of specific trait changes the behavior of the other. The estimates obtained are used by the breeder to define appropriate strategies for achieving superior genotypes based on the most important traits (Correa *et al*., 2003).

In order to establish information that can contribute to genetic breeding of common bean, the study aimed to evaluate the agronomic performance and estimate the genetic variability of 24 common bean genotypes grown in Savanna-Pantanal ecotone and verify which traits can be used to superior genotypes selection.

MATERIALS AND METHODS

Characterization and location of the study area: The experiment was conducted in the municipality of Aquidauana-MS, region belonging to transition zone between the Savanna and the Pantanal, comprising the geographic coordinates 20°20 S and 55°48 W, in an altitude of 207 m.

The region climate is, according to the classification described by Köppen-Geiger, is Aw (Savanna Tropical) with average annual rainfall of 1200 mm and maximum and minimum temperatures of 33 and 19°C, respectively. The soil of the area is Ultisol Dystrophic of sandy texture, whose chemical characteristics are described in Table 1.

Statistical design and analysis: The experimental design was a randomized complete block with three replications. The experimental unit consisted of four rows of plants with 5.0 m length, spaced 0.50 m apart, considering the useful area just the two central rows of each plot which were processed the evaluations.

Treatments consisted by 24 common bean genotypes, constituted by lines CNFC 10429, CNFC 10408, CNFC 10467, CNFC 10470, CNFC 10762, CNFP 10104, CNFP 10793, CNFP 10794, BJ4, CNFRJ 10556, VR3 VC3 and VC6 and by commercial cultivars IAPAR 81, BRS Campeiro, BRS 7762 Supremo, BRS Esplendor, BRS Valente, BRS Pitanga, BRS Radiante, BRS Requinte, BRS Pontal, BRS 9435 Cometa and BRS Estilo. All genotypes are prostrate or semi-prostrate, coming from Embrapa Arroz e Feijão.

The preparation of the area consisted of two consecutive heavy disking from two harrow leveling. Sowing was performed manually on 04/16/2010 in mechanically open grooves with a depth of 5 cm and at a sowing density of 15 seeds per meter. The chemical fertilizer, in formula 4-20-20, was manually distributed and incorporated into the soil of the grooves at a dose corresponding to 300 kg ha^{-1}.

At sete Days After Emergence (DAE) was performed thinning of seedlings, leaving eight seedlings per meter. Hand weeding was done from 15 DAE which minimized the competitive effect of *Ipomoea* sp. and *Beldroega* sp., the main weed species at the place of the trial. It was not applied insecticides and/or fungicides in the leaves of the plants. It was carried out topdress nitrogen fertilization in line on V4 stage with 60 kg ha^{-1} N, distributed in a continuous fillet, using urea as nitrogen source.

Table 1: Soil chemical analyze in the experimental area in the layer 0-0.20 m

	P	O.M	K	Ca	Mg	Al	H+Al	CEC	
pH	(mg dm^{-3})	(g kg^{-1})	----------------		cmol$_c$ dm^{-3}		-----------------		V (%)
6.1	44.4	1.4	0.25	2.0	0.3	0.1	2.7	5.25	49

pH: CaCl, P: Mehlich. O.M.: Organic matter, CEC: Cation exchange capacity

In the central rows of each plot, the following characters were evaluated: beginning of flowering (FL), beginning of maturation (MAT), first Pod Height (PH), number of pods per plant (NP), number of seeds per pod (NS), mass of one hundred grains (MHG) and grain yield (YIE), as performed by Correa *et al*. (2003).

Initially, to verify the existence of variability among the genotypes, the data were subjected to analysis of variance and F-test for each trait. The means were compared by the Scott and Knott (1974) test at 5% probability of occurrence of type I error. The following genetic parameters were estimated: environmental, phenotypic and genotypic variances, coefficients of experimental and genotypic variation, genotypic determination coefficient, b quotient, environmental, phenotypic and genotypic correlations, represented, respectively by the following estimators (Johnson *et al*., 1955):

$$\hat{\sigma}_E^2 = \frac{QM_r}{k} \tag{1}$$

$$\hat{\sigma}_F^2 = \frac{QM_g}{k} \tag{2}$$

$$\hat{\sigma}_G^2 = \frac{QM_g\text{-}QM_r}{k} \tag{3}$$

$$CV_g = \left(\frac{\sqrt{\hat{\sigma}_G^2}}{m}\right) \times 100 \tag{4}$$

$$CV_e = \left(\frac{\sqrt{QM_e}}{m}\right) \times 100 \tag{5}$$

$$\hat{R}^2 = \frac{\hat{\sigma}_G^2}{\hat{\sigma}_E^2} \tag{6}$$

$$b = \frac{CV_g}{CV_e} \tag{7}$$

$$r_E = \frac{COV_{E(xy)}}{\sqrt{\hat{\sigma}_{Ex}^2 \times \hat{\sigma}_{Ey}^2}} \tag{8}$$

$$r_F = \frac{COV_{F(xy)}}{\sqrt{\hat{\sigma}_{Fx}^2 \times \hat{\sigma}_{Fy}^2}} \tag{9}$$

$$r_G = \frac{COV_{G(xy)}}{\sqrt{\hat{\sigma}^2_{Gx} \times \hat{\sigma}^2_{Gy}}} \qquad (10)$$

All statistical analyzes GENES (Cruz, 2013) and followed the procedures recommended by Cruz *et al*. (2004).

RESULTS AND DISCUSSION

There were significant differences ($p<0.01$) among the genotypes for all traits (Table 2). Considering that the existence of genetic variability in a population is a decisive factor in any breeding program (Cruz *et al*., 2004; Lynch and Walsh, 1998; Falconer, 1987; Falconer and Mackay, 1996), germplasm under study is, in principle, promising to selection works or hybridizations aiming the improvement of the evaluated characteristics. Similar results were obtained in other studies with the common bean crop (Filho *et al*., 2010; Ribeiro *et al*., 2009; Filho *et al*., 2008; Ramos *et al*., 2005; Correa *et al*., 2003).

It was observed medium to high precision (Cruz *et al*., 2004) in environmental control, once the coefficients of experimental variation (CV_e) were less than 20%, except for the traits PH and YIE. Results in similar magnitude for the same traits were obtained by Carbonell *et al*. (2007). We realized that for all traits, the estimated values for the genetic variance ($\hat{\sigma}^2_G$) were similar to those obtained for the phenotypic variance ($\hat{\sigma}^2_F$) and higher than those observed for environmental variance ($\hat{\sigma}^2_E$). This indicates greater influence of genetic components regarding environmental components in the expression of the traits, resembling the results obtained by Correa *et al*. (2003).

According to Cruz *et al*. (2004) and Falconer (1987), estimates of the coefficient of genotypic determination ($\hat{R}^2$) were high ($\geq 75\%$) for the trials FL, MAT, NSP and MHS. Similar results were obtained by Correa *et al*. (2003), who report that high R^2 estimates may be due to genetic variability inherent in the tested genotypes, due to each contribute a distinct genetic identity. Lynch and Walsh (1998) and Falconer (1987) mention that R^2 higher may be associated with less environmental variance and less genotype x environment interaction. This allows inferring that the population under study is promising for selection of the above traits.

Coefficients of genetic variation (CV_g) ranged from 1.60% (MAT) to 28.12% (PH), similarly to values obtained by Ribeiro *et al*. (2009) and Correa *et al*. (2003). As well as R^2, this parameter allows to perform inferences about the variability of the different traits. High values of CV_g (more than 25%) are indicative that the population is promising for studied trait selection, should be expect significant gains in selection (Correa *et al*., 2003; Falconer and MacKay, 1996).

The b quotient is an auxiliary tool for the breeder. According to the interpretation of Vencovsky (1978) for this parameter, when it estimate is ≥ 1, the trait is favorable for selection. Thus, breeding programs can carry out the selection based on the traits FL, MAT, NSP and MHS, resembling the conclusions obtained by Ribeiro *et al*. (2009) and Correa *et al*. (2003).

Means obtained for traits FL and MAT (Table 3) allows classifying the genotypes as medium early (Araujo *et al*., 1996). Regarding to trait PH, it was observed that the genotypes BRS Pitanga, CNFC 10762, CNFP 10104, CNFP 10793, CNFP 10794, VR3 and IAPAR 81 obtained the highest values. According to Araujo *et al*. (1996), this trait, especially in cases of large-scale cultivation, is an important feature to be evaluated and taken into account during the choice of cultivar to be implanted. Plants with higher PH favor mechanical harvesting, reflecting mainly a lower percentage of lumps, because there is no need for the cutting deck working very close to the soil surface.

The genotypes CNFC 10762, CNFP 10104, CNFP 10793, CNFP 10794, VR3 and IAPAR 81 stood out for the highest

Table 2: Summary of analysis of variance, F test and estimates of genetic parameters for the traits evaluated in 24 common bean genotypes

SOV¹	FL	MAT	PH	NP	NSP	MHS	YIE
Mean square							
Blocks (DF = 2)	2.09	0.43	21.63	7.58	0.06	14.47	103,883.19
Genotypes (DF = 23)	10.57**	4.92**	13.10**	6.32**	0.68**	54.20**	29,009.22**
Residue (DF = 46)	1.41	1.03	5.57	2.11	0.14	1.84	8,803.08
Mean	46.86	70.73	5.63	8.05	4.85	20.70	325.47
CV_e (%)	2.53	1.44	41.89	18.06	7.91	6.56	28.82
Estimates of genetic parameters							
$\hat{\sigma}^2_F$	3.52	1.64	4.36	2.10	0.22	18.06	9,669.74
$\hat{\sigma}^2_E$	0.47	0.34	1.85	0.70	0.04	0.61	2,934.36
$\hat{\sigma}^2_G$	3.05	1.29	2.51	1.40	0.17	17.45	6,735.37
$\hat{R}^2$ (%)	86.61	78.90	57.48	66.49	78.48	96.59	69.65
CV_g (%)	3.72	1.60	28.12	14.69	8.72	20.17	25.21
b	1.46	1.11	0.67	0.81	1.10	3.07	0.87

[1]SV: Sources of variation, DF: Degrees of freedom, CV_e: Coefficient of experimental variation, $\hat{\sigma}^2_F$: Phenotypic variance, $\hat{\sigma}^2_G$: Genotypic variance, $\hat{\sigma}^2_E$: Environmental variance, $\hat{R}^2$: Genotypic determination coefficient, CV_g: Coefficient of genotypic variation, b: Quotient b, ns and **: Not significant and significant, respectively, at 1% by F-test. MAT: Maturation, PH: first pod height, NP: Number of pods per plant, NSP: Number of seeds per pod, MHS: Mass of one hundred seeds, YIE: Grain yield

Table 3: Average values for the maturation (MAT), first pod height (PH), number of pods per plant (NP), number of seeds per pod (NSP), mass of one hundred seeds (MHS) and grain yield (YIE) of 24 common bean genotypes

Genotype	FL	MAT	PH	NP	NSP	MHS	YIE
BRS Pitanga	48.0^{b}	71.3^{a}	8.7^{a}	9.6^{a}	4.3^{b}	16.5^{e}	228^{c}
BRS Radiante	43.3^{d}	67.3^{b}	3.9^{b}	7.6^{b}	3.9^{b}	32.1^{a}	403^{b}
BRS Requinte	47.0^{b}	72.0^{a}	1.5^{b}	6.3^{b}	4.9^{a}	17.1^{e}	177^{c}
BRS Pontal	46.7^{b}	71.7^{a}	4.4^{b}	7.5^{b}	5.6^{a}	18.6^{e}	347^{b}
BRS 9435cometa	47.0^{b}	71.0^{a}	4.9^{b}	7.8^{b}	4.2^{b}	19.9^{d}	237^{c}
BRS Estilo	49.7^{a}	72.3^{a}	7.3^{a}	7.9^{b}	4.5^{b}	18.8^{e}	207^{c}
VC3	45.7^{c}	70.3^{a}	1.4^{b}	8.4^{b}	4.9^{a}	21.0^{c}	353^{b}
VC6	46.3^{c}	71.0^{a}	8.0^{a}	7.0^{b}	4.8^{a}	21.8^{c}	348^{b}
BRS Campeiro	45.7^{c}	70.7^{a}	6.0^{a}	8.1^{b}	5.1^{a}	19.4^{d}	426^{b}
BRS 7762 Supremo	46.0^{c}	69.7^{a}	8.2^{a}	6.8^{b}	5.6^{a}	18.2^{e}	327^{b}
BRS Esplendor	47.3^{b}	70.7^{a}	8.4^{a}	6.3^{b}	4.9^{a}	14.3^{f}	211^{c}
BRS Valente	48.7^{a}	70.7^{a}	6.6^{a}	6.8^{b}	5.1^{a}	18.5^{e}	317^{b}
CNFC 10429	48.3^{a}	71.0^{a}	7.7^{a}	7.7^{b}	4.8^{a}	19.9^{d}	375^{b}
CNFC 10408	46.7^{b}	70.7^{a}	7.0^{a}	8.3^{b}	5.0^{a}	20.1^{d}	259^{c}
CNFC 10467	48.7^{a}	71.7^{a}	4.3^{b}	8.1^{b}	4.9^{a}	17.1^{e}	245^{c}
CNFC 10470	49.7^{a}	73.0^{a}	7.7^{a}	5.6^{b}	4.1^{b}	21.1^{c}	249^{c}
CNFC 10762	48.7^{a}	70.7^{a}	3.0^{b}	11.3^{a}	5.2^{a}	21.4^{c}	361^{b}
CNFP 10104	46.3^{c}	70.3^{a}	4.9^{b}	10.0^{a}	5.6^{a}	18.8^{e}	410^{b}
CNFP 10793	45.7^{c}	70.3^{a}	5.4^{b}	9.2^{a}	5.1^{a}	23.3^{c}	433^{b}
CNFP 10794	47.7^{b}	70.3^{a}	4.8^{b}	10.9^{a}	5.3^{a}	22.4^{c}	621^{a}
BJ4	44.7^{c}	70.7^{a}	3.6^{b}	7.8^{b}	4.5^{b}	29.6^{b}	396^{b}
CNFRJ 10556	41.7^{d}	67.3^{b}	6.2^{a}	6.5^{b}	4.1^{b}	29.4^{b}	338^{b}
VR3	46.7^{b}	71.7^{a}	7.0^{a}	9.4^{a}	5.1^{a}	17.6^{e}	283^{c}
IAPAR 81	47.7^{b}	71.3^{a}	4.4^{b}	8.8^{a}	5.0^{a}	20.0^{d}	259^{c}
Average	46.9	70.7	5.6	8.1	4.9	20.7	325

Means followed by the same letter in the column do not differ by Scott and Knott test at 5% probability

Table 4: Estimates of genotypic (r_g), phenotypic (r_p) and environmental (r_e) correlation coefficients among the traits maturation (MAT), first pod height (PH), number of pods per plant (NP), number of seeds per pod (NSP), mass of one hundred seeds (MHS) and grain yield (YIE) of 24 common bean genotypes

Traits	MAT	PH	NP	NSP	MHS	YIE
FL						
r_p	0.81**	0.23*	0.13^{ns}	0.17^{ns}	- 0.68**	- 0.34*
r_g	0.95**	0.36*	0.21^{ns}	0.22^{ns}	- 0.72**	- 0.34*
r_e	0.14^{ns}	$- 0.09^{ns}$	$- 0.11^{ns}$	$- 0.07^{ns}$	- 0.38*	- 0.38*
MAT						
r_p		0.10^{ns}	$- 0.01^{ns}$	0.17^{ns}	- 0.67**	- 0.43*
r_g		0.33*	$- 0.04^{ns}$	0.17^{ns}	- 0.76**	- 0.50*
r_e		- 0.39*	0.08^{ns}	0.13^{ns}	$- 0.13^{ns}$	$- 0.22^{ns}$
PH						
r_p			$- 0.24^{ns}$	$- 0.09^{ns}$	- 0.28*	$- 0.18^{ns}$
r_g			- 0.27*	$- 0.08^{ns}$	- 0.37*	- 0.29*
r_e			$- 0.21^{ns}$	$- 0.12^{ns}$	$- 0.05^{ns}$	0.00^{ns}
NP						
r_p				0.35*	$- 0.02^{ns}$	0.47*
r_g				0.33*	$- 0.06^{ns}$	0.55*
r_e				0.42*	0.24^{ns}	0.31*
NSP						
r_p					- 0.47*	0.28*
r_g					- 0.54*	0.35*
r_e					0.02^{ns}	0.09^{ns}
YIE						
r_p						0.47*
r_g						0.48*
r_e						0.72**

ns: Not significant, *'**: Significant at 5 and 1% by t-test, respectively

means of NP and NSP, while the genotypes BRS Radiante and CNFP 10794 obtained the highest mean of MHS and YIE, respectively.

There were positive and significant phenotypic correlations (r_p) among the traits FL×MAT, FL×PH, NP×NSP, NP×YIE, NSP×MHS, NSP×YIE and MHS×YIE (Table 4). Cruz *et al*. (2004), Falconer (1987), Goldenberg (1968) and Johnson *et al*. (1955) attribute this to the occurrence of pleiotropism or gene linkage disequilibrium among the pairs of traits and favor simultaneous selection of two or more traits, by selecting in only one of these. Furthermore, according to these authors, the selection of a trait can result in undesirable selecting another. In general, these results are in agreement with Correa *et al*. (2003) and Ramos *et al*. (2005), who claim that the NP, NSP and MHS are the main traits that influence the YIE.

The r_p negative and significant among the traits FL×MHG, FL×YIE, MAT×MHS, MAT×YIE, PH×MHS indicates antagonism among the same and allow to infer the earliest direct selection genotypes result in an increase of MHS and consequently of YIE. Significant environmental correlation (r_E) among MAT×PH indicates that the environment favors one trait over the other and that the causes of genetic and environmental variation show different physiological mechanisms, making the indirect selection.

The differences in magnitude and direction of the estimated phenotypic, genotypic and environment correlations among the various pairs of evaluated traits demonstrate the presence of distinct association trends. This shows that the correlation concept is similar to that of heritability and should be restricted to the evaluated genetic constitution and the environment under study (Lynch and Walsh, 1998; Falconer and MacKay, 1996). This disagreement may be attributed to environmental modifiers effects and to different physiological mechanisms controlling the traits expression (Falconer, 1987; Goldenberg, 1968; Johnson *et al*., 1955), as well as the differences in the combination capacity presented by the genitors (Cruz *et al*., 2004).

CONCLUSION

The genotype CNFP 10794 obtained better agronomic performance in Savanna-Pantanal ecotone region.

The population has a genetic variability and potential for selection in all evaluated traits.

Based on the evaluated genetic parameters, the number of seeds per pod and mass of one hundred seeds can be used in direct selection for more productive genotypes of common bean.

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