Rev. FCA UNCuyo. 2020. 52(2): 1-11. ISSN (en línea) 1853-8665.

Genetic parameters and association between agronomic traits in special-grain common bean (*Phaseolus vulgaris* L.) genotypes

Parámetros genéticos y asociación entre caracteres agronómicos en genotipos de frijoles (*Phaseolus vulgaris* L.) de grano especial

Carla Medianeira Giroletta dos Santos [1]; Jeferson Antonio dos Santos Silva [1]; Denise Prevedel Capristo [3]; Agenor Matinho Correa [2]; Larissa Pereira Ribeiro [3]

Originales: Recepción: 15/02/2020 - Aceptación: 05/05/2020

Abstract

Estimates of genetic parameters allow to determine the genetic variability present in a population, constituting one of the initial steps in a breeding program. The objectives of this study were to estimate genetic parameters and identify agronomic traits directly and indirectly correlated with grain yield (GY), as well as to estimate their direct and indirect effects on the yield of special-grain common bean genotypes. The experiment was carried out in the 2016/2017 season, in a complete blocks design, with three repetitions. The evaluated traits were days to flowering, days to maturity, first pod height, plant height, number of pods per plant, number of grains per pod, mass of hundred grains, and grain yield. Data were subjected to analysis of variance, and genetic parameters were estimated followed by phenotypic and genotypic correlations. Phenotypic and genotypic correlations were split into direct and indirect effects by path analysis. The studied population seemed promising for breeding purposes considering most traits. Correlation and path analyses indicated that there was a positive direct effect of days to maturity on grain yield. The traits days to maturity and mass of hundred grains can be used in indirect selection aiming at higher grain yield. Path analysis also revealed that the indirect effects of number of pods per plant and number of grains per pod should be taken into consideration in the genetic breeding of the common bean for the increased grain yield.

Keywords
plant breeding • genetic correlation • path analysis • grain yield

---

1 Universidade Federal da Grande Dourados.
2 Universidade Estadual de Mato Grosso do Sul.
3 Universidade Federal de Mato Grosso do Sul. Campus de Chapadão do Sul, Mato Grosso do Sul, Brasil.
larissa_ribeiro@ufms.br

RESUMEN

Las estimaciones de los parámetros genéticos permiten determinar la variabilidad genética presente en una población y constituyen uno de los pasos iniciales de un programa de mejoramiento genético. El objetivo de este trabajo fue estimar los parámetros genéticos, identificar los caracteres agronómicos que se correlacionan directa e indirectamente con la productividad del grano, así como estimar sus efectos directos e indirectos sobre la productividad de diez genotipos de frijol común de grano especial. El experimento se realizó en la campaña agrícola 2016/2017 en diseño de bloques aleatorios, con tres repeticiones. Los caracteres evaluados fueron: días hasta la floración, días hasta la maduración, altura de inserción de la primera vaina, altura de la planta, número de vainas por planta, número de granos por vaina, masa de cien granos y rendimiento de granos. Los datos obtenidos se sometieron al análisis de varianza y se estimaron los parámetros genéticos seguidos de correlaciones fenotípicas y genotípicas. La población estudiada ha demostrado ser prometedora para la mejora de la mayoría de los caracteres evaluados. Hubo un efecto directo positivo de los días hasta la maduración en el rendimiento de granos. Los caracteres días hasta la maduración y masa de cien granos pueden ser utilizados en la selección indirecta con el fin de obtener un mayor rendimiento de granos.

Palabras clave
mejoramiento vegetal • correlación genética • análisis de ruta • rendimiento de granos

INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is one of the most important components of the Brazilian diet. Its grain is an excellent source of protein, besides being rich in carbohydrates, vitamins, minerals, fibers and phenolic compounds with antioxidant action that can reduce the incidence of diseases (9). Due to its adaptation to different climatic conditions, it is grown practically all year round in all Brazilian States, making possible to have a constant supply in the market (2).

Brazil is one of the world's largest common bean producers along with Myanmar and India, having in the 2018/2019 season a cultivated area of 2.9 million ha, where 3.02 million tons of grains were harvested, resulting in an average yield of 1,439 kg ha^{-1} (6). Production, consumption and imports have remained stable over the last 10 years. However, exports have increased from 4.5 t in the 2009/2010 season to 106.3 t in 2018/2019 (6, 20). One of the reasons why the export of common beans is not expressive is the low international demand of the main types of common beans produced in our country.

New common bean varieties with medium to large-size grain, and different tegument color (such as white, red, and cream), called "special-grain type" (1), have been launched in the last years and have become an alternative for the commercialization in the world market. This reveals the need for uninterrupted investments in research for the development of special-grain cultivars which are resistant to diseases, adapted to climatic conditions, productive, and with grain quality that meet the requirements of importing countries. In this group, the Andean beans of Jalo, brindle, red, white, among other types, present very incipient production in Brazil due to the lack of adapted and productive cultivars. This is due to the fact that the number of breeding programs that develop special common bean cultivars is still very restricted in Brazil (27).

In breeding programs, throughout the selection process, the goal is to improve a main trait in addition to maintaining or enhancing the expression of other traits simultaneously (18, 25). Thus, the understanding of the relationships between traits, as estimated by correlations, has been of key importance to plant breeding, providing essential data to assist the selection process. According to correlation estimates, to conduct indirect selection for a low heritability and/or difficult to evaluate trait, may be possible. This practice allows the obtention of faster genetic gains in relation to the use of direct selection (8).

The quantification and interpretation of the magnitude of a correlation may, however, result in misunderstandings in the selection strategy, since high correlation between two traits may be the result of the effect of a third trait or group of traits on the one of interest (8). Wright (1921), in order to better understand the causes involved in the associations between traits, proposed a method called path analysis. This method unfolds the estimated correlations in direct and indirect effects of traits on a basic variable.

Considering the above, the objectives of this study were to estimate genetic parameters and identify agronomic traits that directly and indirectly correlated with grain yield of special-grain common bean genotypes.

Material and methods

Experimental data

The experiment was carried out at the experimental area of the State University of Mato Grosso do Sul, Unit of Aquidauana, located at 20°27'00" S latitude and 55°48'00" W, with altitude of 170 meters, in the period May to August 2017. The region climate according to Köppen classification is Tropical hot-humid with dry winter season (Aw). Annual rainfall values range from 1200 to 1300 mm, and the average annual temperature is 26 °C, with daily maximum of 36 °C during the spring and minimum of 12 °C in the winter.

The soil is classified as Argissolo Vermelho-Distrófico, with a sandy loam texture, moderately deep, with restricted drainage (30), with the following chemical properties in the depth 0-20 cm: pH (H_2O) = 5.85; organic matter = 16.03 mg dm^{-3}; P =26.68 mg dm^{-3}; K = 0.0012 $cmol_c$ dm^{-3}; Ca = 0.016 $cmol_c$ dm^{-3}; Mg = 0.68 $cmol_c$ dm^{-3}; Al= 0.00 $cmol_c$ dm^{-3}; Al + H = 3.29 $cmol_c$ dm^{-3}. The total rainfall was 296.70 mm, which is considered sufficient to supply all the water needs of the crop, since according to Kay (1979) the common bean water requirements is between 300 mm and 400 mm per vegetative cycle.

The experimental design was a randomized block with ten treatments and three replicates, each plot was composed of four rows of 4 m long, spaced 0.5 m apart. The evaluated genotypes consisted of five advanced lines and five control cultivars from the Emprapa - National Rice and Bean Research Center germplasm bank (and are part of the National VCU Testing of special-grain common bean developed by that institution. The description of the genotypes evaluated are shown in table 1.

Table 1. Description of special-grain common bean genotypes, evaluated in the experiment.

Tabla 1. Descripción de los genotipos de frijoles de grano especial evaluados en el experimento.

Genotype	Cultivar/Line	Commercial group
CF 250007	Line	Big Dark Red – DRK
CF 200059	Line	Mulatto
CF 840732	Line	Big Dark Red – DRK
CF 240050	Line	Big Dark Red – DRK
CNFRX 15446	Line	Big Dark Red – DRK
IPR Garça	Cultivar	White
BRS Artico	Cultivar	White
BRS Antares	Cultivar	Striped
BRS Executivo	Cultivar	Striped
BRS Embaixador	Cultivar	Big Dark Red - DRK

Source/Fuente:
Embrapa (2007, 2018);
IAPAR (2018); and
Kappes (2008).

The soil preparation consisted of harrowing for the destruction weeds and to stimulate the germination of the seed bank of weeds in the soil by its revolving. Approximately 20 days after the harrowing, with weed sowing already emerged and in vegetative growth, the application in tank mix of the herbicides Glyphosate (480 g de a.i. L^{-1}) + 2, 4-D (806 g de a.i L^{-1}) was performed at total area using the rates 1440 and 670 g of a.i. ha^{-1}, respectively. One week after the application, two harrowing were sequentially performed followed by the mechanical opening of the grooves at a depth of 5 to 10 cm.

Cover fertilization was carried out at the phenological stage V4, at a rate of 60 kg ha^{-1} of Nitrogen, using urea fertilizer (45% of N), which was distributed in continuous fillet beside the plant lines. Three additional irrigations were carried out by means of a conventional sprinkler irrigation system. Irrigations were carried out at the stage where the crop was in fruiting and pod filling, corresponding to R7 and R8 stages, respectively (14), spaced from seven days, with a blade of approximately 25 mm being applied to each one. All crop management performed in the experiment followed the recommendations for common bean cultivation in Brazil provided by Fancelli and Dourado Neto (1999).

At flowering, the traits days to flowering (DFL), and plant height (PH), evaluated in cm, were measured. Subsequently, at maturity, the following traits were randomly evaluated in the plots: first pod height (FPH), days to maturation (DMT), number of pods per plant (NPP), number of grains per pod (NGP). The harvest was performed on the two central rows of each plot between August 10 and 20, 2017, when the plants presented with completely dry leaves, 90 to 95% of the dried pods and the grains with 13 to 15% moisture. The production of each plot was conditioned in paper bags and taken to the laboratories for weighing and determination of humidity. At this time, the traits mass of hundred grains (MHG, g), and grain yield (GY) were measured, in which GY was estimated by extrapolating the production obtained in the area to kg ha^{-1} and adjusting the values found for the 13% moisture.

Statistical analysis

The following genetic parameters and their estimators were analyzed for each trait: phenotypic variance (σ^2_F); environmental variance (σ^2_E), genotypic variance (σ^2_G), genotypic determination coefficient (H^2), genotypic coefficient of variation (CV_g), coefficient of experimental variation (CV_e), and b quotient (CV_g / CV_e). We also estimate the following correlations: phenotypic correlation (r_F), genotypic correlation (r_G), and environmental correlation (r_E). All genetic parameters were estimated according to the expressions described in Cruz *et al*. (2012), while the correlation estimates were obtained according to Falconer (1996) and Cruz *et al.* (2012).

To graphically express the functional relationship between the estimates of the coefficients of genetic correlations among variables, the correlation network was used, where the proximity of nodes (traits) is proportional to the absolute value of the correlation between these nodes. Only $|r_{ij}| \geq 0.40$ had their edges highlighted, in which positive correlations were highlighted in green, while negative correlations were represented in red.

Subsequently, r_F were deployed by the path analysis into direct and indirect effects considering the following model : $Y = p_1X_1 + p_2X_2 +... + p_nX_n + p\mathcal{E}u$, where Y is the principal dependent variable; $X_1, X_2, ..., X_n$ are the explanatory independent variables; $p_1, p_2, ..., p_n$: are the coefficients of the path analysis. Coefficient of determination was calculated by expression: $R^2 = p_1y_2 + p_2y_2 + ..., 2p_2yp_2nR^2n$.

The degree of multicollinearity of the singular matrix X'X was established based on the condition number (NC), which is the relation between the largest and the smallest eigenvalue of the matrix (21). If NC<100, multicollinearity is weak and is not a problem for analysis; if 100≤NC<1000, multicollinearity is considered moderate to strong; and if NC≥1000 is severe. Lastly, path analysis was performed considering grain yield (GY) as principal dependent variable and the other variables as explanatory.

Data were submitted to analysis of variance using the F test and considering the following model: $Y_{ij} = \mu + G_i + B_j + \varepsilon_{ij}$ = , wherein: Y_{ij} = effect of the i-th genotype on the j-th block; μ = overall mean; G_i = random effect of the i-th genotype (i = 1, 2,..., 10); B_j = effect of the j-th block (j=1, 2, 3); and ε_{ij} = effect of experimental error associated with observation Y_{ij}, ε_{ij} ~ NID (0, σ^2). In the correlations, the Student test (t) at 5% of probability was applied. All analyses were performed with the Genes software (7).

RESULTS AND DISCUSSION

Analysis of variance and genetic parameters

The results of analysis of variance and estimates of genetic parameters are shown in table 2 (page 5). It can be observed that the population has variability only for the PH, DMT, NPP and NGP, in which significant treatment effects were observed ($p < 0.05$), showing, at first, that the population is promising for the selection of these traits in breeding programs.

The coefficient of variation (CV), which indicates the degree of experimental accuracy and, therefore, the reliability of the data obtained in the experiment, was below 20% for all traits, except for the NPP. According to Pimentel-Gomes (2009), CV values obtained in agricultural tests below 10% are considered low, and medium between 10 and 20%, indicating, respectively, high and medium experimental precision. The nature of the trait interferes with the magnitude of the coefficient of variation (3), so that those more influenced by the environment tend to have greater magnitude, as observed for NPP (20.96%), PH (17.69%) and FPH (15.16%).

Variance components are crucial in a plant breeding program, since the population and the breeding method to be used depend on the results of these componentes (25). In the decomposition of the phenotypic variance (σ_P^2) in its genetic and environmental components it is observed a greater participation of the environmental variance (σ_G^2) for the traits DFL and GY, indicating that these traits are strongly influenced by the environment in their phenotypic expressions, similar participation of both variances for the FPH and MHG traits and greater participation of the genetic variance for the FPH, NGP, NPP and DMT traits, allowing to infer greater possibility of genetic gains in the early selection cycles for these traits.

Table 2. Summary of the analysis of variance and estimates of genetic parameters for days to flowering (DFL), first pod height (FPH, cm), plant height (PH, cm), days to maturity (DMT), number of pods per plant (NPP), number of grains per pod (NGP), mass of hundred grains (MHG, g), and grain yield (GY, kg ha^{-1}), evaluated in 10 special-grain common bean genotypes.

Tabla 2. Resumen del análisis de varianza y estimaciones de parámetros genéticos para días hasta la floración (DFL), altura de inserción de la primera vaina (FPH, cm), altura de la planta (PH, cm), días hasta la maduración (DMT), número de vainas por planta (NPP), número de granos por vaina (NGP), masa de cien granos (MHG, g) y rendimiento de granos (GY, kg ha^{-1}) evaluados en 10 genotipos de frijoles de grano especial.

F.V.	DF	DFL	FPH	PH	DMT	NPP	NGP	GY	MHG
Mean squares									
Block	2	0.30	1.50	83.59	0.23	7.03	0.17	197455.53	200.60
Genotype	9	30.40^{ns}	10.39^{ns}	0.03*	3.81*	3.46*	0.24*	29.14^{ns}	10.30^{ns}
Error	18	0.41	8.37	96.01	4.05	3.50	0.12	23181.05	46.66
Mean		30.80	19.09	55.37	64.46	8.92	3.87	1308.88	52.17
CV(%)		2.08	15.16	17.69	3.12	20.96	9.12	11.63	13.09
Genetic parameters									
σ_P^2		0.17	5.53	215.19	3.56	3.15	0.20	10236.32	30.88
σ_E^2		0.14	2.79	32.00	1.35	1.16	0.04	7727.02	15.55
σ_G^2		0.03	2.74	183.19	2.21	1.99	0.15	2509.30	15.33
H^2 (%)		23.53	49.55	85.13	62.08	63.17	75.00	24.51	49.64
CV_g (%)		0.65	8.67	24.44	2.31	15.79	10.19	3.83	7.50
b quotient		0.31	0.57	1.38	0.79	0.79	1.11	0.33	0.70

σ_P^2 = phenotypic variance; σ_E^2 = environmental variance; σ_G^2 = genotypic variance; H^2 (%) = genotypic coefficient of determination; b quotient = (CV_g/ CV_e), wherein CV_g(%) = genotypic coefficient of variation, and CV_e(%) = coefficient of variation; * and ^{ns} = significant and not significant at 5% probability level by F test, respectively.

σ_P^2 = varianza fenotípica; σ_E^2 = varianza ambiental; σ_G^2 = varianza genotípica; H^2 (%) = coeficiente de determinación; cociente b = (CV_g/ CV_e), donde CV_g(%) = coeficiente de variación genotípica, y CV_e(%) = coeficiente de variación; * y ^{ns} = significativo y no significativo al nivel de probabilidad del 5% por la prueba F, respectivamente.

Heritability (h^2), parameter that gives the proportion of the genetic variance present in the total phenotypic variance is one of the parameters that most contributes to the breeder's work by its predictive role, allowing to estimate the genetic gains in selection cycles, being, therefore, essential to the choice of methods to be applied (12). Yokomizo and Vello (2000) state that when the treatments are considered fixed, as in the present study, the heritability becomes called the genotypic determination coefficient (H^2).

For most traits, it is considered that estimates of H^2 above 70% are considered high and indicate that the population is promising for trait selection. Estimates of H^2 above 70% were observed only for the PH (85.13%) and NGP (75%), allowing to infer that these traits are the most easily selected in a breeding program.

Estimates of H^2 between 50 and 70% indicate greater difficulties in trait selection due to the greater influence of the environment on its expression, in this sense, the population is only moderately promising for the selection of DMT trait (62.08%) and NPP (63.17%), due to the difficulty of obtaining expressive gains in earlier generations. Estimates of H^2 below 50% indicate that population is unpromising for trait selection. The data in table 3 allow us to infer that the study population is unpromising for the selection of FPH (49.55%) and MHG (49.64%) and non-promising traits for selection of DFL (23.53%) and GY (24.51%).

An explanation for the low heritability that is generally observed in the grain yield, and the consequent difficulty of selection gains may be the fact that this trait is controlled by several genes of small effect on the phenotype determining strong influence of the environment on its expression (12).

Table 3. Phenotypic, genotypic and environmental correlation estimates (r_F, r_G and r_E, respectively) for days to flowering (DFL), first pod height (FPH), plant height (PH), days to maturity (DMT), number of pods per plant (NPP), number of grains per pod (NGP), mass of hundred grains (MHG), and grain yield (GY), evaluated in 10 special-grain common bean genotypes.

Tabla 3. Estimaciones de correlaciones fenotípicas, genotípicas y ambientales (r_F, r_G y r_E, respectivamente) para días hasta la floración (DFL), altura de inserción de la primera vaina (FPH), altura de la planta (PH), días hasta la maduración (DMT), número de vainas por planta (NPP), número de granos por vaina (NGP), masa de cien granos (MHG) y rendimiento de granos (GY) evaluados en 10 genotipos de frijoles de grano especial.

Traits	**DFL**	**FPH**	**PH**	**DMT**	**NPP**	**NGP**	**GY**	**MHG**
r_F	1.00^{*}	-0.236^{*}	0.267^{*}	0.146^{ns}	0.020^{ns}	0.053^{ns}	-0.368^{*}	0.155^{ns}
DFL r_G	1.00^{*}	0.092^{ns}	0.714^{*}	0.568^{*}	-0.169^{ns}	-0.217^{*}	-0.279^{ns}	-0.117^{ns}
r_E	1.00^{*}	-0.428^{*}	-0.142^{ns}	-0.126^{ns}	0.159^{ns}	0.360^{*}	-0.085^{ns}	0.311^{ns}
r_F		1.00^{*}	0.075^{ns}	0.207^{*}	-0.483^{*}	-0.224^{*}	-0.166^{ns}	0.109^{ns}
FPH r_G		1.00^{*}	0.336^{*}	0.151^{ns}	-0.793^{*}	-0.547^{*}	0.194^{ns}	0.526^{*}
r_E		1.00^{*}	-0.519^{*}	0.282^{*}	-0.091^{ns}	0.361^{*}	-0.378^{*}	-0.300^{*}
r_F			1.00^{*}	0.691^{*}	-0.311^{*}	0.449^{*}	0.132^{ns}	0.814^{*}
PH r_G			1.00^{*}	0.981^{*}	-0.522^{*}	0.624^{*}	0.151^{ns}	0.250^{*}
$,r_E$			1.00^{*}	-0.095^{ns}	0.305^{*}	-0.354^{*}	0.188^{ns}	0.005^{ns}
r_F				1.00^{*}	-0.234^{ns}	0.488^{*}	0.566^{*}	0.772^{*}
DMT r_G				1.00^{*}	-0.479^{*}	0.664^{*}	-0.241^{ns}	0.104^{ns}
r_E				1.00^{*}	0.175^{*}	0.080^{ns}	0.299^{ns}	0.364^{ns}
r_F					1.00^{*}	-0.086^{ns}	-0.086^{ns}	-0.200^{ns}
NPP r_G					1.00^{*}	-0.105^{ns}	0.940^{*}	-0.573^{*}
r_E					1.00^{*}	-0.043^{ns}	0.296^{ns}	0.279^{ns}
r_F						1.00^{*}	0.267^{ns}	0.105^{ns}
NGP r_G						1.00^{*}	0.693^{*}	0.055^{ns}
r_E						1.00^{**}	-0.096^{ns}	0.217^{ns}
r_F							1.00^{*}	0.373^{ns}
GY r_G							1.00^{*}	-0.011^{ns}
r_E							1.00^{*}	0.611^{*}
r_F								1.00^{*}
MHG r_G								1.00^{*}
r_E								1.00^{*}

* and ^{ns} = significant and not significant at 5% probability level by F test, respectively.

* y ^{ns} = significativo y no significativo al nivel de probabilidad del 5% por la prueba F, respectivamente.

The estimates of H^2 are specific for a given population in a specific environment and the comparisons are not valid. However, the estimates of H^2 obtained in this work were similar to those obtained by Oliveira (2018) studying in the same environment for the traits NGP (73.5%) and GY (27.7%), differing in relation to the others. Santos *et al.* (2015) working with common bean from several groups, in the same place and time, but in a different year, also obtained an estimate of H^2 similar to that found in this work for the NGP trait (76.07%).

The high CVg may be a positive factor considering its use in the CVg/CVe ratio, which assists the selection. It should be used together with the heritability (H^2) to compare the genetic variability of different populations and different traits, as well as to have an idea of the expected gain with selection. The highest CVg values were obtained for PH (24.44%), NPP (15.75%) and NGP (10.19%), confirming the fact that the population is more promising for the selection of these trait as a function of their genetic variability for them. The lowest CVg estimates were for DFL (0.65%), DMT (2.31%) and GY (3.83%).

The b quotient expresses the relationship between CVg and CVe and makes it possible to infer about the chances of success of breeding in the study population. According to Vencovsky (1978), the quotient b constitutes an additional information for the breeder, because, when it reaches value ≥1.0 indicates a situation very favorable to the selection, allowing the selection of genotypes with superior performance. Estimates of $b \geq 1$ were only observed for the PH (1.38) and NGP (1.11), which confirms the possibility of greater success for selecting these traits.

Correlation estimates

Phenotypic (r_F), genotypic (r_G), and environmental (r_E) correlation estimates between the traits are shown in table 3 (page 6). In order to graphically express the phenotypic correlations among the traits, a correlation network was created (figure 1). It can be observed that there was a general disagreement in magnitude and direction, and the genotypic correlation coefficients are mostly higher than the phenotypic and environmental correlation coefficients, which shows greater contribution of the genetic factors than the environmental factors in the expression of these traits. Signal and magnitude mismatches between correlations for the same pair of traits can be attributed to environment-modifying effects and different physiological mechanisms controlling the expression of the traits involved (4, 12).

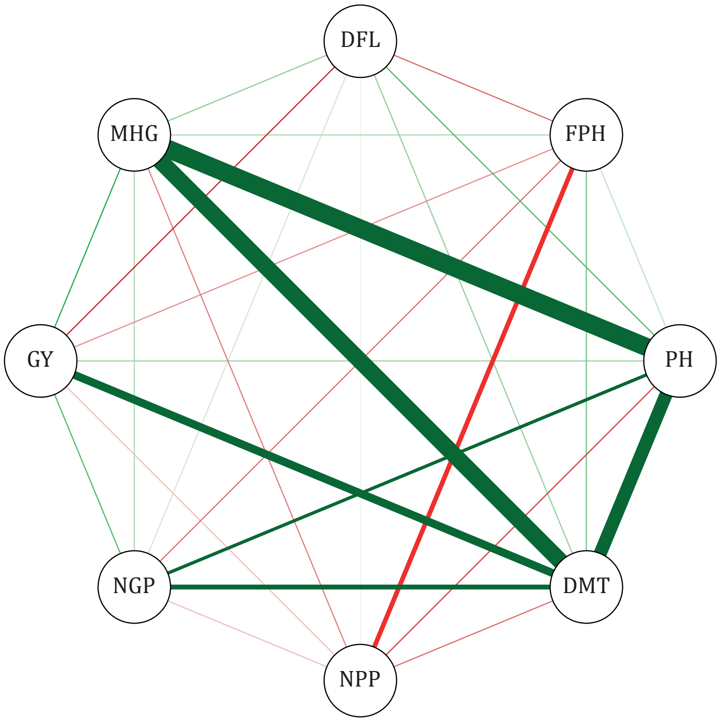

Figure 1. Correlation network between the traits days to flowering (DFL), first pod height (FPH), plant height (PH), days to maturity (DMT), number of pods per plant (NPP), number of grains per pod (NGP), mass of hundred grains (MHG), and grain yield (GY), evaluated in 10 special-grain common bean genotypes.

Figura 1. Red de correlación entre los caracteres días hasta la floración (DFL), altura de inserción de la primera vaina (FPH), altura de la planta (PH), días hasta la maduración (DMT), número de vainas por planta (NPP), número de granos por vaina (NGP), masa de cien granos (MHG) y rendimiento de granos (GY) evaluados en 10 genotipos de frijoles de grano especial.

The highest positive phenotypic correlations occurred between PH x MHG (0.814), DMT x MHG (0.772) and PH x DMT (0.691) pairs of traits, allowing us to infer that taller and later cycle plants tend to accumulate more photosynthesized content in the grains making them heavier, in the same way that later maturing plants tend to be taller. The most expressive negative phenotypic correlation, although of medium magnitude occurred between FPH x NPP (-0.483), indicating that the higher the first pod insertion height, smaller the number of pods per plant, an aspect that should be considered when selecting for increased pod height as a function of the mechanical harvest. Positive phenotypic correlation between phenological traits and PH was also found by Morais *et al.* (2001), when evaluating grain yield and development of four common bean cultivars under three spacings between plants.

Genotypic correlations are the most important because they involve an association of inheritable nature and can be used to guide breeding programs (8, 25). When positive, it indicates that the selection aiming gain in one trait will have the same effect on the other and, if negative, that the improvement in one trait will cause damage in another, being this a situation undesirable to the breeder.

The highest positive genotypic correlations were observed between the DMT x PH (0.981), NPP x GY (0.940) and DFL x PH (0.714), indicating that later cycle selection will imply taller plants and that NPP followed by NGP (NGP x GY = 0.693) is the primary production component that most influences grain yield in common bean. Santos *et al.* (2011 y 2015), Sousa *et al.* (2016), and Oliveira (2018), when studying common bean also observed that NPP trait is the one that most influences the grain yield, which allows to infer about the possibility of indirect selection for GY via NPP.

Negative genotypic correlation of high magnitude was observed between the PH x NPP (-0.793) and medium magnitude between FPH x NGP (-0.547) and PH x NPP (-0.522). These results confirm the need for care when selecting plants with high pod insertion height for mechanical harvesting, because grain yield via number of pods per plant may be impaired, a fact observed by Oliveira *et al.* (2018), although not confirmed in this study (the ALV *vs.* PRD correlation was not significant) and also in the studies developed by Moura *et al.* (2013) and Mambrim *et al.* (2015).

Negative genotypic correlation observed between the production components NPP x MHG (-0.573) can be explained by the need for compensation among the production components, such that an increase in the NPP will induce a decrease in grain mass (MHG) and vice versa (5).

The existence of significant environmental correlation indicates that the two traits are influenced by the environmental conditions, when positive, as for GY x MHG (0.611) and DFL x NGP (0.360). This means that the variation effect is favorable to both traits and, when negative, as observed for FPH x PH (-0.519) and DFL x FPH (-0.428), indicates that the environment favored one over another trait (8).

Path analysis

In the unfolding of phenotypic correlation, we considered the study on the influence of the phenological (DFL and DMT), morphological (FPH and PH) and primary production components traits (NPP, NGP and MHG), denominated explanatory variables, on grain yield (GY), considered a dependent variable (table 4, page 9), taking care that the that the presence of collinearity would not impair the reliability of the results. Thus, we proceeded to the multicollinearity diagnosis proposed by Montgomery and Peck (1981), which indicated the presence of severe multicollinearity (CN>1000). For this reason, path analysis was performed using a constant k = 0.15 in the diagonal of the phenotypic correlation matrix.

According to Vencovsky and Barriga (1992), with the unfolding of the correlation coefficient, some situations and conclusions emerge, such as: a) the similar correlation in sign and magnitude with direct effect shows that the trait determine variations on the basic trait; b) if the correlation is positive, but its direct effect is negative or small, indirect effects should be considered in the selection; and c) negative correlation associated with positive and high direct effect indicates that the variable should not be discarded in common bean breeding.

The path coefficient (direct effect), positive and of greater magnitude was obtained by DMT (= 0.503), however, the genotypic correlation coefficient for DMT x GY pair was negative (-0.241) (table 4, page 9), this fact indicates that the DMT variable should not be discarded in common bean breeding. The positive genotypic correlations between the NPP x GY (0.940) and NGP x GY (0.693) pairs associated with the direct effects expressed by the negative path coefficients -0.269 (for the NPP trait) and -0.003 (for the NGP trait), allow to infer that the indirect effects of these traits (NPP and NGP) should be taken into consideration in the genetic breeding of the common bean for the increased grain yield (GY).

The genotypic correlation DFL x GY (-0.279), equal in sign and of magnitude not so different from the direct effect of the explanatory variable DFL on GY (-0,408), indicates that this variable is determinant in the variations of the GY in common bean. It is possible to observe the relevant importance of the MHG, PH and NGP, via DMT (table 4) on GY. The analysis of the coefficient of determination (R^2) indicates that the variables used partially explain (69.5%) the behavior of the basic variable GY and that other variables not considered here also influence the behavior of this trait.

Table 4. Estimates of direct and indirect effects of the explanatory traits days to flowering (DFL), first pod height (FPH), plant height (PH), days to maturation (DMT), number of pods per plant (NPP), number of grains per pod (NGP) and mass of hundred grains (MHG) on the grain yield (GY), evaluated in 10 special-grain common bean genotypes.

Tabla 4. Estimaciones de los efectos directos e indirectos de los caracteres explicativos días hasta la floración (DFL), altura de inserción de la primera vaina (FPH), altura de la planta (PH), días hasta la maduración (DMT), número de vainas por planta (NPP), número de granos por vaina (NGP), masa de cien granos (MHG) sobre el rendimiento de granos (GY), evaluados en 10 genotipos de frijoles de grano especial.

Effect	**DFL**	**FPH**	**PH**	**DMT**	**NPP**	**NGP**	**MHG**
Direct on GY	-0.408	-0.421	-0.296	0.503	-0.269	-0.003	0.174
Indirect via FL	--	0.096	-0.109	-0.059	-0.008	-0.022	-0.063
Indirect via FPH	0.099	--	-0.031	-0.087	0.203	0.094	-0.046
Indirect via PH	-0.079	-0.022	--	-0.205	0.092	-0.133	-0.242
Indirect via DMT	0.086	0.122	0.409	--	-0.139	0.289	0.458
Indirect via NPP	-0.005	0.129	0.083	0.063	--	0.023	0.054
Indirect via NGP	-0.002	0.008	-0.001	-0.002	0.003	--	-0.004
Indirect via MHG	0.027	0.019	0.142	0.135	-0.035	0.018	--
Total	-0.368	-0.166	0.131	0.566	-0.213	0.266	0.373
Coefficient of determination (R^2) = 0.695							

CONCLUSIONS

Days to maturity have a positive direct effect on grain yield in special-grain common bean.

The traits days to maturity and mass of hundred grain can be used in the indirect selection aiming at higher grains yield.

REFERENCES

1. Blair, M. W; González, L. F.; Kimani, P. M.; Butare, L. 2010. Genetic diversity, inter-gene pool introgression and nutritional quality of common beans (*Phaseolus vulgaris* L.) from Central Africa. Theor. Appl. Genet. 121: 237-248.
2. Bonett, L. P.; Gonçalves-Vidigal, M. C.; Schuelter A. R.; Vidigal Filho, P. S.; Gonela, A.; Lacanalho, G, F. 2006. Divergência genética em germoplasma de feijoeiro comum coletado no estado do Paraná, Brasil. Semina Cien. Agr 27: 547-560.
3. Carvalho, C. G. P.; Arias, C. A. A.; Toledo, J. F. F.; Almeida, L. A.; Kihil, R. A. de S.; Oliveira, M. F. de; Hiromoto, D. M.; Takeda, C. 2003. Proposta de classificação dos coeficientes de variação em relação à produtividade e altura da planta de soja. Pesq. Agropec. Bras. 38: 187-193.
4. Carvalho, F. I. F; Lorencetti, C.; Benin, G. 2004. Estimativas e implicações da correlação no melhoramento vegetal. Pelotas. Ed. UFPel. 142 p.
5. Castoldi, F. L. 1991. Análises das interpretações entre rendimentos e diversas características agronômicas do feijoeiro (*Phaseolus vulgaris* L.). Master Thesis in Genetics and Breeding. Universidade Federal de Viçosa, 73 p.
6. CONAB - Companhia Nacional de Abastecimento. 2020. Acompanhamento da safra brasileira de grãos: safra 2019/2020, n. 6, sexto levantamento. Brasília. Conab. 154 p.
7. Cruz, C. D. 2013. GENES - a software package for analysis in experimental statistics and quantitative genetics. Acta Scie. Agron. 35: 271-276.
8. Cruz, C. D.; Carneiro, P. C. S; Regazzi, A. J. 2012. Modelos biométricos aplicados ao melhoramento genético. Viçosa. Ed. UFV. 668 p.
9. Embrapa. 2005. Cultivo do feijão da primeira e segunda safras na Região Sul de Minas Gerais. Santo Antônio de Goiás: Embrapa Arroz. Sistemas de Produção. 6.
10. Embrapa. 2007. BRS Embaixador. Cultivar de feijão comum com tipo de grão para exportação. https://www.infoteca.cnptia.embrapa.br/bitstream/doc/193059/brsembaixador.pdf.2007> (accessed on: 06/20/2018).
11. Embrapa. 2018. Catálogo de Cultivares de Feijão Comum Safra 2016-2017. https://ainfo.cnptio.embrapa.br/digita/bitstream/item/154713/catalogoF.eijão.2017> (accessed on: 06/25/2018).
12. Falconer, D. S.; Mackay, T. F. C. 1996. Introduction to quantitative genetics. London. Longman Group. 464 p.
13. Fancelli, A. L.; Dourado Neto, D. 1999. Estresse de água e temperatura na cultura do feijão. In: Fancelli, A. L.; Dourado Neto (Eds). Feijão irrigado: estratégias básicas de manejo. Piracicaba. Ed. Publique. 155-159.
14. Fehr, W. R.; Caviness, C. E. 1977. Stages of soybean development. Ames. lowa State University of Science and Technology. 11 p.
15. IAPAR-Instituto Agronômico do Paraná. 2018. Principais características dos cultivares de feijão com sementes disponíveis no mercado, 2018. www.iapar.br/pagina-1363 2018> (accessed on: 07/22/2018).
16. Kappes, C.; Wruck, F. J.; Carvalho, M.A.C de.; Amashit, O. M. 2008. Feijão comum: características morfo-agronômicas de cultivares. Campinas. Instituto Agronômico. 85: 506- 509.
17. Kay, D. E. 1979. Food legumes. London. Tropical Products Institute. 435 p.
18. Lopes, A. C. A.; Vello, N. A.; Pandini, F.; Rocha, M. M,; Tsutsumi, C. Y. 2002. Variabilidade e correlações entre caracteres em cruzamentos de soja. Scie Agric. 59: 341-348.
19. Mambrin, R. B.; Ribeiro, N. D.; Storck, L.; Silva, L. 2015. Seleção de linhagens de feijão (*Phaseolus vulgaris* L.) baseada em caracteres morfológicos, fenológicos e de produção. Rev. Agric. 90: 141-155.
20. MAPA - Ministério Da Agricultura, Pecuária e Abastecimento. 2018. Plano nacional de desenvolvimento da cadeia do feijão e pulses. Brasília. MAPA. 40 p.
21. Montgomery, D. C.; Peck, E. A. 1981. Introduction to linear regression analysis. New York. J. Wiley. 504 p.
22. Morais, L. K.; Carbonel, S. A. M.; Pinheiro, J. B.; Fonseca Júnior, N da S.; Brasil, E. M. 2001. Avaliação de cultivares de feijoeiro, *Phaseolus vulgaris* L., sob diferentes espaçamentos. Acta Sci. Agron. 23: 1199-1203.
23. Moura, M. M.; Carneiro, P. C. S.; Carneiro, J. E. de S.; Cruz, C. D. 2013. Potencial de caracteres na avaliação da arquitetura de plantas de feijão. Pesq. Agropec. Bras. 48: 417-425.
24. Oliveira, V. Q. 2018. Avaliação do potencial para melhoramento genético de uma população de genótipos de feijoeiro comum do tipo carioca. Graduate thesis in Agronomy. Universidade Estadual de Mato Grosso do Sul. Aquidauana. Brazil. 18 p.
25. Oliveira de Souza, N.; Silva Alves, R.; Teodoro, P. E.; Silva, L. A.; Dessaune Tardin, F.; Baldoni Tardin, A.; Vilela de Resende, M. D.; Lopes Bhering, L. 2019. Single- and multiple-trait BLUP in genetic selection of parents and hybrids of grain sorghum. Revista de la Facultad de Ciencias Agrarias. Universidad Nacional de Cuyo. Mendoza. Argentina. 51(2): 1-12.
26. Pimentel-Gomes, F. 2009. Curso de estatística experimental. Piracicaba. Fealq. 451 p.
27. Ribeiro, N. D.; Domingues, L. S.; Gruhn, E. M.; Zemollin, A. E. M.; Rodrigues, J. A. 2014. Desempenho agronômico e qualidade de cozimento de linhagens de feijão de grãos especiais. Rev. Cien. Agron. 45: 92-100.

28. Santos, A.; Correa, A. M.; Melo, C. L. P. de.; Durente, L. G. Y.; Carneiro, T.; Oliveira, R. 2011. Desempenho agronômico de genótipos de feijão comum cultivados no período “da seca” em Aquidauana-MS. Agrarian 4: 33-42.
29. Santos, A.; Braga, D. C.; Correa, A. M.; Melo, C. L. P de.; Silva, J.; A.; dos S.; Lima, A. R. de S.; Rodrigues, E. V. 2015. Escolha de genitores de feijão-comum baseado na divergência genética. Agrarian 8: 235-245.
30. Schiavo, J. A.; Pereira, M. G.; Miranda, L. P. M.; Dias Neto, A. H.; Fontana, A. 2010. Caracterização e classificação de solos desenvolvidos de arenitos da formação Aquidauana. Rev. Bras. Cien. Solo 34: 881-889.
31. Sousa, S. A. de.; Tavares, T. C de O.; Ramos, D. P.; Barros, H. B.; Fidelis, R. R. 2016. Comportamento de genótipos de feijão comum sob estresse de nitrogênio no Cerrado. Appl. Res. Agrotec. 9: 53-62.
32. Vencovsky, R. 1978. Herança quantitativa. In: Patterniani, E. (Ed). Melhoramento e produção de milho no Brasil. Piracicaba. Marprint. p.122-201.
33. Vencovsky, R.; Barriga, P. 1992. Genética biométrica no fitomelhoramento. Ribeirão Preto. Sociedade Brasileira de Genética. 496p.
34. Yokomizo, G. K. I.; Vello, N. A. 2000. Coeficiente de determinação genotípica e de diversidade genética em topocruzamentos de soja tipo alimento com tipo grão. Pesq. Agropec. Bras. 35: 2223-2228.
35. Wright, S. 1921. Theory of path coefficients. Genetics. 8: 239-285.

Acknowledgements

This study was financed in part by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brasil (CAPES) - Finance Code 001 and Universidade Federal de Mato Grosso do Sul (UFMS).