

GENETIC DIVERGENCE AND SELECTION OF COMMON BEAN CULTIVARS BASED ON PLANT ARCHITECTURE AND GRAIN YIELD¹

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ABSTRACT - The characterization of genetic divergence in common bean cultivars for various traits related to plant architecture and grain yield is unprecedented. This study proposes to determine whether common bean cultivars of different grain types differ for 12 traits of plant architecture and grain yield; examine the correlations between these traits; analyze the genetic divergence of these cultivars; and select superior cultivars for these traits. A total of 22 common bean cultivars with the grains types most produced in Brazil were evaluated in two growing seasons. Plant architecture was analyzed based on 12 traits, and grain yield was determined at maturity. Significant genotype and genotype × environment interaction effects were obtained, indicating the existence of genetic variability for all evaluated traits. Several plant architecture traits were correlated, but none was highly correlated with grain yield. First- and second-internode lengths are more important in differentiating common bean cultivars. Principal component and Tocher's analyses resulted in the formation of four and seven groups of cultivars, respectively. Both methods are efficient in analyzing genetic divergence; however, Tocher's method is more informative. Cultivars BRS Campeiro, SCS 205 – Riqueza, BRS Esteio, IAC Imperador and Guapo Brilhante have a high grain yield potential, but only BRS Campeiro, BRS Esteio and Guapo Brilhante have upright plant architecture.

Keywords: *Phaseolus vulgaris*. Genetic variability. Pearson's correlation. Cluster analysis. Selection index.

DIVERGÊNCIA GENÉTICA E SELEÇÃO DE CULTIVARES DE FEIJÃO BASEADA EM ARQUITETURA DE PLANTA E PRODUTIVIDADE

RESUMO - A caracterização da divergência genética de cultivares de feijão para vários caracteres relacionados a arquitetura de planta e produtividade de grãos é inédita. Os objetivos desse estudo foram avaliar se cultivares de feijão de diferentes tipos de grãos diferem para 12 caracteres da arquitetura de planta e para produtividade de grãos, estudar as correlações entre esses caracteres, analisar a divergência genética dessas cultivares e selecionar as cultivares superiores para esses caracteres. Um total de 22 cultivares de feijão com os tipos de grãos mais produzidos no Brasil foram avaliadas em duas épocas de cultivo. A arquitetura de planta foi analisada por 12 caracteres e a produtividade de grãos foi determinada na maturação. Efeitos significativos de genótipo e de interação genótipo x ambiente foram obtidos, portanto há variabilidade genética para todos os caracteres avaliados. Vários caracteres da arquitetura de planta foram correlacionados, entretanto nenhum foi altamente correlacionado com a produtividade de grãos. Os comprimentos do primeiro e do segundo entrenós apresentam maior importância na diferenciação entre as cultivares de feijão. As análises de componentes principais e de Tocher resultaram na formação de quatro e de sete grupos de cultivares, respectivamente. Os dois métodos são eficientes na análise da divergência genética, no entanto o método de Tocher é mais informativo. As cultivares de feijão BRS Campeiro, SCS 205 – Riqueza, BRS Esteio, IAC Imperador e Guapo Brilhante apresentam um alto potencial de produtividade de grãos, mas apenas as cultivares BRS Campeiro, BRS Esteio e Guapo Brilhante têm arquitetura de planta ereta.

Palavras-chave: *Phaseolus vulgaris*. Variabilidade genética. Correlação de Pearson. Análise de agrupamento. Índice de seleção.

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INTRODUCTION

The common bean (*Phaseolus vulgaris* L.) is a legume largely produced and consumed by people of the most varied social classes, ethnicities and ages, in different regions of the planet. However, plant and production characteristics more widely accepted by farmers may vary according to growing conditions.

In the southern region of Brazil, the development of high-grain-yielding common bean cultivars with upright plant architecture meets the demand of less capitalized producers, who harvest the plants manually by pulling, and highly capitalized producers, who use modern harvesters to harvest the grains. This is because, in common bean plants with upright plant architecture, pods have less contact with the soil, which results in better quality of the produced grains (MENDES; RAMALHO; ABREU, 2009; MOURA et al., 2013).

Plant architecture in common bean has been evaluated through qualitative traits using score scales, such as lodging (JOST et al., 2013; RIBEIRO et al., 2018a; SOLTANI et al., 2016) and general adaptation score (RIBEIRO et al., 2018a). Quantitative traits also have been used to differentiate genotypes with upright plant architecture, e.g. insertion of the first pod, plant height and length and number of internodes (JOST et al., 2013; MOURA et al., 2013; PEREIRA et al., 2019; RIBEIRO et al., 2018a,b, 2019; SILVA et al., 2013). These studies also analyzed the correlation between plant architecture traits and grain yield, aiming at the indirect selection of high-grain-yielding common bean lines. Nonetheless, the analysis of genetic divergence using different traits related to plant architecture and grain yield is unprecedented for common bean cultivars.

The characterization of genetic divergence in common bean cultivars of different grain types helps to exploit the genotypic variation that can be effectively used by breeding programs for the development of new cultivars with upright plant architecture and high grain yield potential. This will provide greater efficiency in the planning of crosses that will be implemented to generate new common bean cultivars with the grain types most produced and consumed in Brazil, namely, carioca (beige seed coat with brown streaks), black, red and cranberry (cream seed coat with red streaks and spots) (LEMOS; MINGOTTE; FARINELLI, 2015). In addition, combined selection for different traits related to upright plant architecture and high grain yield potential will allow the selection of common bean cultivars with high agronomic performance that can be indicated for cultivation in the most varied production systems.

Therefore, this study was conducted to determine whether common bean cultivars of

different grain types differ for 12 traits of plant architecture and grain yield; examine the correlations between these traits; analyze the genetic divergence of these cultivars; and select high-grain-yielding common bean cultivars with upright plant architecture.

MATERIALS AND METHODS

Experimental layout and data collection

Both experiments were conducted in the area of the Department of Plant Science at the Federal University of Santa Maria, located in the municipality of Santa Maria, Rio Grande do Sul, Brazil (29°42' S latitude, 53°49' W longitude and 95 m altitude). The climate of the region is a humid subtropical type with hot summers, without a clearly defined dry season. The two experiments were performed in the dry- and rainy-season crops. The dry-season crop was implemented from February to May of 2019, whereas the rainy-season crop covered the months from October of 2019 to January of 2020, which corresponds to the two traditional common bean growing seasons in the southern region of Brazil.

The soil of the experimental area is classified as a typic alitic Argisol, Hapludalf, which was prepared conventionally, by two plowings and one harrowing operation. Based on the result of soil chemical analysis, there was no need for soil acidity correction. However, application of the following fertilizers was required: 160 kg ha⁻¹ of the 05-20-20 formula (urea: 45% nitrogen, single superphosphate: 18% P₂O₅ and potassium chloride: 60% K₂O) at sowing; and 40 kg ha⁻¹ urea (45% nitrogen), which were divided into two doses and distributed in the stages of first trifoliolate leaf (V3) and third trifoliolate leaf (V4).

The experiment was carried out in a randomized-block design with three replicates, with the experimental unit consisting of two 4-m rows, spaced 0.5 m apart, and a usable area of 4 m². A sowing density of 15 seeds m⁻¹ was adopted. The evaluated treatments were 22 common bean cultivars of different grain types, namely, carioca, black, red and cranberry (Figure 1). The selection of these cultivars was based on grain morphology, that is, different grain colors, sizes and shapes, without previously considering their agronomic performance in the growing region. These cultivars represent the common bean grain types most produced in Brazil, namely, Mesoamerican (BRSMG Madrepérola, SCS 205 - Riqueza, IAC Imperador, Pérola, IPR Siriri, BRS Esteio, BRS Campeiro, IPR Tiziu, IAC Netuno, Guapo Brilhante, Macanudo, BRS Pitanga and Ouro Vermelho) and Andean (others cultivars evaluated) gene pools.

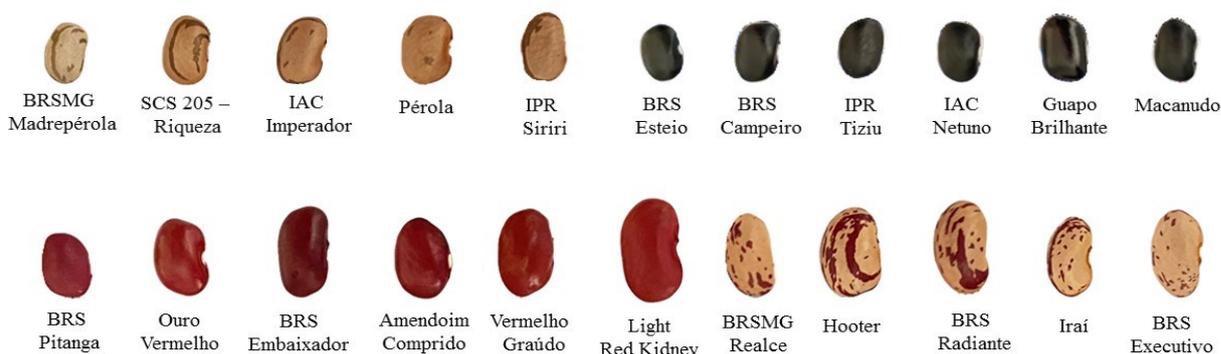


Figure 1. Common bean cultivars of different grain types evaluated in the study.

Similar management practices were used in the experiments, which consisted of phytosanitary treatments, mechanical control of weed plants and irrigation. The fungicide Maxim[®] (Fludioxonil and Metalaxil-M) and the insecticide Cruiser[®] 350 FS (Thiamethoxam) were applied in the form of seed treatment, both at the dose of 200 mL 100 kg⁻¹ of seeds. Weed plants were controlled by using the pre-emergent herbicide Dual Gold[®] (S-Metolachlor), at the dose of 1.25 L ha⁻¹, and by weeding after the emergence of the common bean plants. The insecticide Engeo[™] Pleno (Thiamethoxam and Lambda-cyhalothrin) was applied at the dose of 125 mL ha⁻¹ whenever insect infestation caused 5% damage to the leaf area. Sprinkler irrigation was carried out before water deficit was observed, that is, when the evapotranspiration rate was higher than the absorption rate. The average irrigation volume was 3 mm day⁻¹ in the vegetative stage and 5 mm day⁻¹ during the reproductive stage, which is equivalent to 350 to 400 mm depending on the length of the crop cycle.

At the maturity stage (R9), which is characterized by the presence of dry pods and grains exhibiting the typical color of each cultivar, qualitative assessments of plant architecture (lodging and general adaptation score) were carried out on the plants in the usable area of the plots. Lodging was determined by using a score scale ranging from 1 to 9, in which score 1 corresponded to all plants upright and score 9 indicated all plants fallen and touching the soil. General adaptation score was also analyzed using a score scale ranging from 1 to 9; on this scale, score 1 referred to plants upright, with one stem, a greater number of pods per plant and no disease symptoms in the pods, and score 9 was assigned to plants with long internodes, very prostrate, with a lower number of pods per plant and high severity of disease symptoms in the pods.

Plant architecture was also evaluated based on 10 quantitative traits measured in 10 plants collected at random in the usable area of the plots, at the R9

stage. The following traits were measured using a tape measure: insertion of first pod; insertion of last pod; plant height; and first-, second-, third-, fourth- and fifth-internode lengths. Epicotyl and hypocotyl diameters were obtained using a digital caliper.

Grain yield was determined by extrapolating the weight of the product obtained in the usable area per hectare, after correcting grain moisture to 13%. Due to the heterogeneity in the final plant stand obtained in both growing environments, grain yield was corrected using the Covariance – ideal stand method proposed by Vencovsky and Cruz (1991). Corrected grain yield (Z_{ij}) was estimated as $Z_{ij} = Y_{ij} - b(X_{ij} - H)$, where Y_{ij} is the grain yield observed in the plot; b is the residual regression coefficient of Y_{ij} due to X_{ij} ; X_{ij} is the plant stand observed in the plot; and H represents the stand considered ideal, which, in this case, was 120 plants.

Statistical analyses

The data were subjected to individual and combined analyses of variance. The homogeneity of residual variance was checked using Hartley's maximum F test. In combined analysis of variance, the effects of genotype, environment and genotype × environment interaction were analyzed as fixed, whereas the experimental error was considered random. The genotype effect was decomposed into grain types (carioca, black, red and cranberry beans) by the hierarchical method. The F test was used at a probability level of 5% to evaluate the significance level for all traits.

Multicollinearity diagnostics was performed with the phenotypic correlation matrix obtained in combined analysis of variance. The condition number (CN), which corresponds to the ratio between the highest and lowest eigenvalue of the matrix, was determined according to the classification proposed by Montgomery and Peck (1981). Traits that showed high correlation and

greater weight in the last eigenvectors were excluded until weak multicollinearity ($CN \leq 100$) was obtained.

Pearson's linear correlation coefficients were estimated from the genotype mean matrix of combined analysis of variance. Only the traits in which a significant difference was observed for the sources of variation of genotype and/or genotype \times environment interaction were included. The significance of correlation coefficients was assessed by Student's *t* test (p value < 0.05).

Residual variance and covariance matrices were obtained from combined analysis of variance. These matrices were used to generate the genetic dissimilarity matrix between common bean cultivars by generalized Mahalanobis distance. The traits with the highest and lowest contribution to the total variation were evaluated by principal component analysis (PCA), using standardized means. The following cluster analyses were implemented: PCA and Tocher's optimization method. For PCA, a scatter plot was generated from the first two principal components, allowing the visualization of the formed groups. Tocher's method included the means obtained for each trait, considering the groups of cultivars formed.

The index based on the rank sum (MULAMBA; MOCK, 1978) was used to obtain estimates of heritability and selection gain and to select the five superior common bean cultivars, which corresponded to an intensity of 22.73%. Narrow-sense heritability (%) was estimated considering the mean of the genotypes, using the following formula: $h^2 = \frac{\sigma^2G}{\sigma^2P}$, where h^2 is the heritability, σ^2G is the genetic variance and σ^2P is the phenotypic variance. Selection gain (%) was estimated by the following expression:

$SG = \{[(X_s - X_a)h^2]100\}/X_a$, where SG is the selection gain (%), X_s is the average of the selected cultivars, X_a is the average of all cultivars and h^2 is the heritability.

Selection was carried out to obtain the lowest lodging and general adaptation score values and the highest values for the other traits. The following weights were assigned: 4 for grain yield and 1 for the other evaluated traits. The analyses were performed using the Office Excel spreadsheet and Genes software (CRUZ, 2016).

RESULTS AND DISCUSSION

Overall results

The experimental error variance was homogeneous (p value > 0.05) for all traits evaluated in the two growing seasons, which allowed the execution of combined analysis of variance. In this

analysis, a significant genotype effect ($p < 0.05$) was observed for all traits (Table 1). However, in the evaluation of grain type, there were no significant differences for first-internode length and epicotyl diameter. Therefore, there was genetic variability for the plant architecture traits and grain yield, with differences found between common bean cultivars of different grain types.

The carioca bean cultivars differed for insertion of the first pod, insertion of the last pod and plant height. For the black bean cultivars, a significant effect was observed for insertion of the last pod, plant height, epicotyl diameter, hypocotyl diameter and grain yield. However, in experiments with carioca and black bean cultivars, Delfini et al. (2017) detected a significant difference for insertion of the first pod in common bean cultivars of both grain types, although only the carioca bean cultivars differed for grain yield. The observed differences can be explained by the quantity and genetic diversity of the carioca and black bean cultivars analyzed and by variations inherent to the growing environment.

For the red bean cultivars, significant differences were obtained for all traits related to plant architecture, but there was no significant effect for grain yield. The cranberry bean cultivars did not differ only for general adaptation score, fourth-internode length, fifth-internode length and grain yield. Ribeiro et al. (2014) described genetic variability for insertion of the first pod and grain yield in red and cranberry bean cultivars. In the present study, the red and cranberry bean cultivars showed greater genetic variability for the plant architecture traits, allowing the selection of cultivars with upright architecture. However, the selection of red and cranberry bean cultivars with high grain yield potential may be difficult due to the greater homogeneity found for this trait in common bean cultivars with these grain types.

All traits exhibited a significant genotype \times environment interaction effect, except lodging and the length of all evaluated internodes. Experiments evaluating common bean genotypes have frequently described the occurrence of a significant genotype \times environment interaction for plant architecture traits and grain yield (ARTEAGA et al., 2019; MAZIERO; RIBEIRO; CASAGRANDE, 2017; MOURA et al., 2013; NADEEM et al., 2020; RIBEIRO et al., 2018b). However, Ribeiro et al. (2019) also reported a non-significant genotype \times environment interaction for the length of different internodes measured in common bean genotypes, confirming the present results. Thus, most of the traits related to plant architecture and grain yield in common bean varied in response to the change in growing environment. On this basis, cluster analyses performed only in a growing season can provide incorrect information when a significant genotype \times environment interaction is observed for the evaluated traits, as they do not consider the environment

variability between years and growing seasons, within the same location (CARGNELUTTI FILHO; RIBEIRO; JOST, 2009). The data obtained in the two growing seasons provided highly repeatable and

more accurate information in the cluster and selection index analyses. Therefore, these analyses were carried out to select superior common bean cultivars for plant architecture and grain yield.

Table 1. Combined analysis of variance containing the degrees of freedom (DF), mean squares, mean, coefficient of experimental variation (CEV%) and selective accuracy (SA) for the following traits: lodging (LDG), general adaptation score (GAS), insertion of the first pod (IFP, cm), insertion of the last pod (ILP, cm), plant height (PH, cm), first-internode length (1stIL, cm), second-internode length (2ndIL, cm), third-internode length (3rdIL, cm), fourth-internode length (4thIL, cm), fifth-internode length (5thIL, cm), epicotyl diameter (ED, mm), hypocotyl diameter (HD, mm) and grain yield (YIELD, kg ha⁻¹) of 22 common bean cultivars evaluated in the two growing seasons (dry season of 2019 and rainy season of 2019).

Source of variation	DF	Mean square						
		LDG	GAS	IFP	ILP	PH	1 st IL	2 nd IL
Block/environment	4	0.26	0.88	3.71	71.05	107.98	0.32	0.35
Genotype (G)	21	7.49 *	1.09 *	86.08 *	746.03 *	1418.57 *	0.54 *	1.26 *
Grain type (T)	3	12.14 *	2.57 *	80.65 *	1981.01 *	3852.46 *	0.21 ^{ns}	1.92 *
G/Type	18	6.72 *	0.84 ^{ns}	86.93 *	540.02 *	1016.09 *	0.59 *	1.17 *
T/Carioca	4	1.95 ^{ns}	0.20 ^{ns}	39.92 *	167.15 *	200.72 *	0.16 ^{ns}	0.18 ^{ns}
T/Black	5	1.24 ^{ns}	0.38 ^{ns}	15.94 ^{ns}	139.78 *	292.52 *	0.28 ^{ns}	0.39 ^{ns}
T/Red	5	18.49 *	1.91 *	83.05 *	882.12 *	1617.00 *	1.00 *	3.01 *
T/Cranberry	4	3.62 *	0.72 ^{ns}	227.51 *	985.59 *	1984.78 *	0.89 *	0.83 *
Environment (E)	1	1.48 ^{ns}	36.07 *	2795.88 *	6120.01 *	5773.70 *	4.81 *	0.61 ^{ns}
G x E	21	1.20 ^{ns}	1.40 *	44.40 *	63.76 *	51.74 *	0.34 ^{ns}	0.41 ^{ns}
Error	84	0.75	0.47	4.50	18.47	27.41	0.25	0.29
Mean		4.88	5.01	18.45	49.41	57.06	3.55	5.46
CEV (%)		17.75	13.63	11.49	8.70	9.17	14.23	9.86
SA		0.95	0.76	0.97	0.99	0.99	0.73	0.88

		3 rd IL	4 th IL	5 th IL	ED	HD	YIELD
Block/environment	4	0.29	0.27	0.18	1.39	1.34	35414.39
Genotype (G)	21	1.30 *	1.26 *	2.08 *	2.47 *	2.60 *	1233498.85 *
Grain type (T)	3	1.59 *	1.82 *	3.32 *	0.84 ^{ns}	1.85 *	7021201.81 *
G/Type	18	1.24 *	1.19 *	1.87 *	2.71 *	2.71 *	231621.06 *
T/Carioca	4	0.07 ^{ns}	0.13 ^{ns}	0.52 ^{ns}	0.48 ^{ns}	0.48 ^{ns}	248825.30 ^{ns}
T/Black	5	0.33 ^{ns}	0.33 ^{ns}	0.48 ^{ns}	1.31 *	1.35 *	310082.17 *
T/Red	5	3.25 *	3.35 *	4.79 *	6.00 *	4.95 *	105849.22 ^{ns}
T/Cranberry	4	1.04 *	0.62 ^{ns}	1.30 ^{ns}	2.60 *	3.82 *	273555.21 ^{ns}
Environment (E)	1	1.00 ^{ns}	5.16 *	15.48 *	74.94 *	94.52 *	713241.07 *
G x E	21	0.35 ^{ns}	0.39 ^{ns}	1.01 ^{ns}	1.06 *	1.11 *	348473.46 *
Error	84	0.28	0.43	0.81	0.23	0.24	57826.09
Mean		6.85	8.44	10.48	6.19	6.13	1093.76
CEV (%)		7.70	7.82	8.59	7.74	7.96	21.98
SA		0.89	0.81	0.78	0.95	0.95	0.98

*: Significant by the F test at 0.05 probability. ^{ns}: non-significant.

Coefficients of variation $\leq 21.98\%$ were obtained for the evaluated traits. These values are similar to those described for plant architecture traits and grain yield evaluated in common bean genotypes (CABRAL et al., 2011; DELFINI et al., 2017; MAZIERO; RIBEIRO; CASAGRANDE, 2017; MOURA et al., 2013; RIBEIRO et al., 2018b, 2019). When the experimental precision was analyzed based on selective accuracy, values ≥ 0.73 were observed, which are similar to those previously reported by Pereira et al. (2019) and by Ribeiro et al. (2019) for plant architecture traits and grain yield in common

bean genotypes. Low coefficients of variation and high selective accuracy values, as observed in the present study, indicate greater experimental precision in the assessments of different traits. High experimental precision in the evaluation of plant architecture traits and grain yield contributes to greater efficiency in the selection of superior common bean cultivars.

Multicollinearity diagnostic revealed a CN of 4,273.81, characterizing severe collinearity. To obtain weak collinearity (CN ≤ 100), it was necessary to exclude the traits of insertion of the last

pod, plant height, third-internode length, epicotyl diameter, and fourth-internode length. These five traits were not included in the correlation, cluster or selection-index analyses to prevent multicollinear variables from implicitly receiving a greater weight, which would lead to errors in the interpretation of results.

Correlation between traits related to plant architecture and grain yield

Table 2. Pearson's phenotypic correlation coefficients obtained between the traits of lodging (LDG), general adaptation score (GAS), insertion of the first pod (IFP), first-internode length (1stIL), second-internode length (2ndIL), fifth-internode length (5thIL), hypocotyl diameter (HD) and grain yield (YIELD) obtained from 22 common bean cultivars evaluated in two experiments carried out in the year 2019.

	GAS	IFP	1 st IL	2 nd IL	5 th IL	HD	YIELD
LDG	0.633*	0.638*	-0.385	-0.440*	-0.133	-0.521*	0.421*
GAS		0.485*	-0.461*	-0.552*	-0.360	-0.116	0.196
IFP			-0.644*	-0.475*	-0.011	-0.283	0.151
1 st IL				0.859*	0.518*	0.061	-0.232
2 nd IL					0.737*	-0.039	-0.396
5 th IL						-0.388	-0.590*
HD							0.027

* Significant by the t test at 0.05 probability.

Among the other traits related to plant architecture, the following correlations are noteworthy: insertion of the first pod and first-internode length ($r = -0.644$), first-internode length and second-internode length ($r = 0.859$) and second-internode length and fifth-internode length ($r = 0.737$). Previous studies also described a high correlation between the lengths of different internodes determined in black and carioca bean lines (RIBEIRO et al., 2018a, 2019). The observed correlations between the plant architecture traits suggest that it is not necessary to evaluate a large number of traits, since correlated traits provide similar information. Therefore, plant architecture in common bean could perfectly be determined only by a qualitative trait and a quantitative trait to be defined based on the ease, simplicity, speed and experimental precision obtained in these evaluations. Lodging and insertion of the first pod meet these requirements; thus, these traits are recommended for evaluating plant architecture in common bean genotypes.

Correlation estimates for the other evaluated plant architecture traits were low or non-significant. None of the plant architecture traits correlated highly with grain yield, confirming the descriptions of other authors for common bean genotypes (MOURA et al., 2013; PEREIRA et al., 2019; RIBEIRO et al., 2018a, 2019; SILVA et al., 2013). According to Balestre et al. (2013), a lack of correlation between two traits

Several traits showed significant positive and negative correlations, but only values ≥ 0.600 were considered relevant and included in the discussion. Lodging correlated positively with general adaptation score ($r = 0.633$) and with insertion of the first pod ($r = 0.638$) (Table 2). Ribeiro et al. (2019) found a similar response in the evaluation of carioca and black bean lines. Therefore, common bean cultivars that were more lodged showed a higher general adaptation score, which characterizes inferior adaptability, and a higher insertion of the first pod, i.e., a prostrate plant architecture.

indicates that there are no linked genes or pleiotropic effects. As a consequence, the absence of a correlation has been related to independence between traits, so selection for a given trait is not expected to negatively interfere with another trait. Therefore, it is possible to select common bean cultivars with upright plant architecture and high grain yield potential, as these traits have proven to be independent.

Analysis of genetic divergence for plant architecture traits and grain yield

The first three principal components explained 82.32% of the variation contained in the data (46.83%, 23.22% and 12.26% for the first, second and third components, respectively) (Table 3). This percentage exceeds those previously found in evaluations of different morphological traits (GRAHIC et al., 2013; HEGAY et al., 2014) and in the determination of morphological and production traits (ARTEAGA et al., 2019; FREITAS et al., 2011; SOFI et al., 2014; YEKEN et al., 2019) in common bean genotypes using PCA. Therefore, there was greater consistency in the clustering pattern in the present study. This can be explained by the better discriminatory capacity of the evaluated descriptors and by the greater genetic diversity between the analyzed common bean cultivars.

Table 3. Estimation of eigenvalues (root and % cumulative [cumul.]) and relative importance of the traits of lodging (LDG), general adaptation score (GAS), insertion of the first pod (IFP), first-internode length (1stIL), second-internode length (2ndIL), fifth-internode length (5thIL), hypocotyl diameter (HD) and grain yield (YIELD) obtained in each principal component (PC) to estimate genetic dissimilarity among 22 common bean cultivars evaluated in two experiments carried out in the year 2019.

PC	ROOT (%)	CUMUL (%)	LDG	GAS	IFP	1 st IL	2 nd IL	5 th IL	HD	YIELD
PC1	46.83	46.83	-0.38	-0.38	-0.36	0.43	0.46	0.32	0.08	-0.27
PC2	23.22	70.05	-0.37	-0.11	-0.33	-0.06	-0.20	-0.53	0.60	0.22
PC3	12.26	82.32	0.33	-0.07	-0.28	0.41	0.19	-0.13	-0.25	0.73
PC4	7.84	90.15	0.18	0.79	-0.17	0.38	0.15	-0.03	0.31	-0.22
PC5	6.08	96.24	0.08	-0.12	0.63	0.10	0.27	0.25	0.58	0.31
PC6	1.87	98.10	0.68	-0.43	-0.12	0.21	-0.29	-0.07	0.27	-0.35
PC7	1.02	99.13	0.15	0.09	-0.48	-0.44	-0.11	0.64	0.24	0.24
PC8	0.87	100.00	0.29	-0.05	-0.12	-0.50	0.72	-0.33	0.04	-0.13

Second-internode length (0.46) and first-internode length (0.43) were the traits that most contributed to differentiating the common bean cultivars, according to PC1 of PCA. However, hypocotyl diameter (0.60) was the most important descriptor for PC2 of PCA. No studies were found in the literature including the measurement of different internode lengths and hypocotyl diameter in the analysis of genetic divergence between common bean cultivars, using PCA or other cluster analyses. However, previous studies identified the following agronomic traits as making the greatest contribution to genetic dissimilarity between common bean cultivars: grain yield and grain dimensions (ARTEAGA et al., 2019) and the phenological stages of pod-filling and maturation, along with plant height (YEKEN et al., 2019), using PCA. These results reinforce the need to evaluate the genetic divergence of common bean cultivars considering traits related to plant architecture, as the present study showed that the first- and second-internode lengths and hypocotyl diameter were efficient to differentiate common bean cultivars of different grain types.

The first two principal components separated the common bean cultivars into four groups (Figure 2). Group 1 was formed by cultivar Ouro Vermelho, which exhibited the lowest first- and second-internode length values and the third lowest hypocotyl diameter. Group 2 consisted of cultivar Light Red Kidney, which has the highest first- and second-internode length values and lowest hypocotyl diameter among the evaluated cultivars. Group 3 contained cultivars BRS Radiante, Irai and Hooter, which had lower first- and second-internode length values than that observed in group 2, but higher than those found in groups 1 and 4, and higher hypocotyl diameter values than those observed in the groups 1 and 2. Group 4 comprised the other common bean cultivars. Determining first- and second-internode lengths and hypocotyl diameter made it possible to cluster common bean cultivars with similar measurements for these traits in the same group. However, the clustering obtained using PCA was not very informative regarding the other traits related to plant architecture and grain yield that differentiate common bean cultivars.

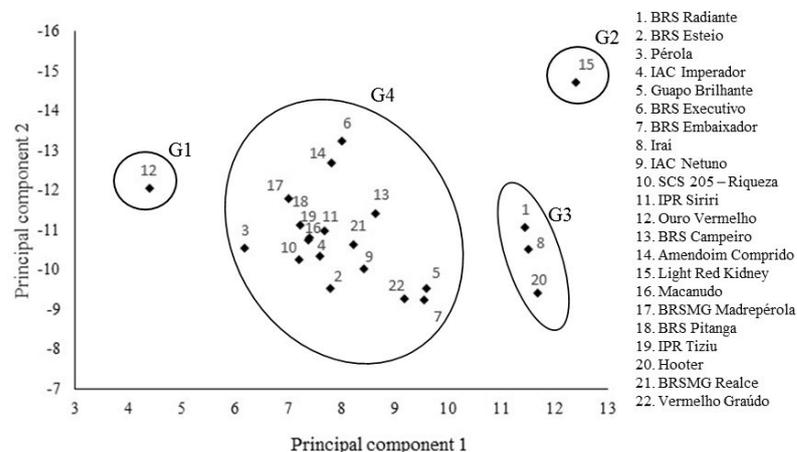


Figure 2. Scatter plot obtained from the plant architecture traits and grain yield of 22 common bean cultivars for the first two principal components.

When cluster analysis was performed by Tocher's optimization method, based on the generalized Mahalanobis distance matrix, seven groups were formed (Table 4). The number of common bean cultivars contained in each group ranged from one (groups 6 and 7) to seven (groups 1 and 2). Groups 1 and 2 included a higher number of cultivars, confirming a trend frequently reported in the literature of a higher number of common bean

cultivars being concentrated in the first two groups when genetic divergence is analyzed by Tocher's method (GONÇALVES et al., 2016; LIMA et al., 2012; MAZIERO; RIBEIRO; CASAGRANDE, 2017; PEREIRA et al., 2019; SANTOS et al., 2019). However, in all of these studies, Tocher's method showed to be efficient in the formation of homogeneous groups in relation to the evaluated agronomic traits.

Table 4. Cluster analysis formed by Tocher's optimization method, based on Mahalanobis' generalized distance, for the traits of lodging (LDG), general adaptation score (GAS), insertion of the first pod (IFP, cm), first-internode length (1stIL, cm), second-internode length (2ndIL, cm), fifth-internode length (5thIL, cm), hypocotyl diameter (HD, mm) and grain yield (YIELD, kg ha⁻¹) determined in 22 common bean cultivars evaluated in two experiments carried out in the year 2019 and means obtained in each group.

Group	Cultivars							
1	BRS Embaixador, Vermelho Graúdo, Hooter, Guapo Brilhante, BRSMG Realce, IAC Netuno and IPR Tiziu							
2	SCS 205 - Riqueza, BRS Campeiro, IAC Imperador, IPR Siriri, BRS Esteio, Pérola and Macanudo							
3	BRS Radiante and Irai							
4	Amendoim Comprido and BRSMG Madrepérola							
5	Ouro Vermelho and BRS Pitanga							
6	BRS Executivo							
7	Light Red Kidney							
Means obtained in each group								
Group	LDG	GAS	IFP	1 st IL	2 nd IL	5 th IL	HD	YIELD
1	4.05	5.00	16.39	3.61	5.48	10.34	6.76	955.52
2	5.31	5.00	19.14	3.45	5.34	10.18	6.06	1634.86
3	3.50	4.25	12.84	3.83	5.89	10.82	5.90	538.14
4	6.08	5.33	18.98	3.49	5.24	10.56	5.27	990.60
5	6.25	5.67	24.34	3.23	4.93	10.19	6.12	941.68
6	5.33	4.83	26.93	3.13	5.47	11.52	5.80	427.42
7	4.83	4.83	17.98	4.33	6.82	12.42	4.85	561.89

Group 1 comprised the cultivars with the largest hypocotyl diameter (a trait that can give upright architecture to the plant), namely, BRS Embaixador, Vermelho Graúdo, Hooter, Guapo Brilhante, BRSMG Realce, IAC Netuno and IPR Tiziu. Group 2 consisted of the highest-grain-yielding cultivars: SCS 205 - Riqueza, BRS Campeiro, IAC Imperador, IPR Siriri, BRS Esteio, Pérola and Macanudo. Group 3 contained the cultivars with the lowest lodging and general adaptation scores, namely, BRS Radiante and Irai, which were the least prostrate cultivars. Group 4 was formed by the other cultivars that did not show favorable upright architecture traits (highest lodging and general adaptation scores) for the selection of superior cultivars. Groups 5 and 6 comprised cultivars with the highest insertion of the first pod, that is, with desirable upright plant architecture traits: Ouro Vermelho, BRS Pitanga and BRS Executivo. Group 7 consisted of cultivar Light Red Kidney, which showed the highest first-, second- and fifth-

internode length values. The use of Tocher's method provided greater detail in relation to the differences observed between the formed groups based on the evaluated traits when compared with PCA, agreeing with previous results obtained by Kumar et al. (2009) and Maziero, Ribeiro and Casagrande (2017).

Greater knowledge of the dissimilarity between groups and the similarity of common bean cultivars from the same group allows a better planning of the crosses to be carried out by the breeding program. Based on results obtained with Tocher's method, the following crosses are recommended: SCS 205 - Riqueza × Light Red Kidney, BRS Campeiro × Light Red Kidney, IAC Imperador × Light Red Kidney, IPR Siriri × Light Red Kidney, BRS Esteio × Light Red Kidney, Pérola × Light Red Kidney and Macanudo × Light Red Kidney. These crosses use combinations of parents from group 2 and group 7, and hence they are promising for obtaining recombinants with high grain yield potential and a higher number of upright

plant architecture traits. However, crosses between Mesoamerican and Andean common bean cultivars may result incompatibility, making it difficult to obtain hybrids.

Selection of superior common bean cultivars for plant architecture and grain yield

All traits showed high narrow-sense heritability ($h^2 \geq 61.03\%$), except general adaptation score and first-internode length, which showed intermediate heritability (Table 5), according to the classes proposed by Soltani et al. (2016). Similarly, Jost et al. (2013) obtained heritability estimates of intermediate to high magnitude for plant architecture traits and grain yield in carioca and black bean genotypes. However, all plant architecture traits and grain yield determined in common bean genotypes exhibited high heritability (RIBEIRO et al., 2018b, 2019). These higher heritability values are related to greater genetic variability in the plant architecture

and grain yield traits, which is favorable to the selection of superior common bean cultivars.

All traits showed individual genetic gain estimates favorable to the selection of high-grain-yielding common bean cultivars with upright plant architecture, except lodging, insertion of the first pod and fifth-internode length, which showed a negative gain sign. Negative genetic gains for insertion of the first pod were also described in the selection of common bean genotypes of higher agronomic performance (RIBEIRO et al., 2018a,b, 2019). Therefore, common bean cultivars with a lower insertion of the first pod have been selected in breeding programs, which may make manual and mechanized harvesting operations difficult due to the closer proximity of the pods to the soil. However, all cultivars selected in the present study showed an insertion of the first pod ≥ 12 cm, which characterizes upright plant architecture in common bean.

Table 5. Average of the original population (X_0), average of selected cultivars (X_S), heritability (h^2), genetic gain (GG) and percentage of genetic gain (GG%) with simultaneous selection by the rank-sum index for the traits of lodging (LDG), general adaptation score (GAS), insertion of the first pod (IFP, cm), first-internode length (1stIL, cm), second-internode length (2ndIL, cm), fifth-internode length (5thIL, cm), hypocotyl diameter (HD, mm) and grain yield (YIELD, kg ha⁻¹) and the five common bean cultivars selected based on the evaluation of two experiments carried out in the year 2019.

Trait	X_0	X_S	$h^2\%$	GS	GS%
LDG	4.88	4.93	90.00	0.05	1.01
GAS	5.01	4.93	57.12	-0.04	-0.85
IFP	18.45	18.34	94.77	-0.10	-0.57
1 st IL	3.55	3.61	52.91	0.03	0.94
2 nd IL	5.46	5.49	77.09	0.02	0.35
5 th IL	10.48	10.16	61.03	-0.20	-1.91
HD	6.13	6.30	90.86	0.15	2.41
YIELD	1093.76	1615.01	95.31	496.81	45.42
Total gain				496.81	46.80
Selected cultivars					
Trait	BRS Campeiro	SCS 205 - Riqueza	BRS Esteio	IAC Imperador	Guapo Brillhante
LDG	5.50	5.00	4.83	5.00	4.33
GAS	4.83	5.00	5.17	5.00	4.67
IFP	19.98	20.02	18.18	18.25	15.28
1 st IL	3.72	3.42	3.52	3.57	3.83
2 nd IL	5.83	5.35	5.47	5.22	5.57
5 th IL	10.73	9.87	9.97	10.03	10.18
HD	6.05	5.97	6.82	5.87	6.78
YIELD	1695.12	1788.07	1643.51	1710.42	1237.93

Cultivars BRS Campeiro, SCS 205 - Riqueza, BRS Esteio, IAC Imperador and Guapo Brillhante were highlighted for plant architecture and/or grain yield and were selected by the rank-sum index. Similarly, Ribeiro et al. (2019) selected high-grain-yielding common bean lines with upright plant architecture using the rank-sum index. Cultivars BRS Campeiro, BRS Esteio and Guapo Brillhante

have black grains and stood out with the highest second-internode length (≥ 5.47 cm) and hypocotyl diameter values (≥ 6.05 cm), characterizing upright plant architecture. Cultivars SCS 205 - Riqueza and IAC Imperador have carioca grains and stood out with the highest grain yield values (≥ 1710.42 kg ha⁻¹).

Because the black- and carioca-bean growing

area in Brazil is larger than those used for other grain types, it is to be expected that breeding programs have devoted more time to the development of black- and carioca-bean cultivars adapted to the growing conditions. The three black bean cultivars selected (BRS Campeiro, Guapo Brilhante and BRS Esteio) have a type-II growth habit, i.e., indeterminate with short guides, which explains the upright plant architecture. In contrast, the carioca bean cultivars SCS 205 – Riqueza and IAC Imperador have a type-III growth habit, i.e., indeterminate with long guides and with a tendency to prostrate. The five common bean cultivars selected by the rank-sum index exhibited high grain yield potential in the evaluated environments, indicating greater adaptation to the growing conditions. The other cultivars evaluated showed low grain yield in the dry and rainy seasons of 2019.

CONCLUSIONS

Common bean cultivars of different grain types have genetic variability for plant architecture traits and grain yield. Several plant architecture traits are correlated; however, none is highly correlated with grain yield.

First and second internode lengths and hypocotyl diameter are more important in differentiating common bean cultivars. The number of groups formed and the composition of these groups of cultivars differ by principal component and Tocher's analyses, the latter of which is more informative.

Common bean cultivars BRS Campeiro, SCS 205 – Riqueza, BRS Esteio, IAC Imperador and Guapo Brilhante, selected by the rank-sum index, have high grain yield potential. Only BRS Campeiro, BRS Esteio and Guapo Brilhante have upright plant architecture.

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REFERENCES

ARTEAGA, S. et al. Morphological and agronomic characterization of Spanish landraces of *Phaseolus vulgaris* L. **Agriculture**, 9: 1-16, 2019.

BALESTRE, M. et al. Applications of multi-trait

selection in common bean using real and simulated experiments. **Euphytica**, 189: 225-238, 2013.

CABRAL, P. D. S. et al. Diversidade genética de acessos de feijão comum por caracteres agrônomicos. **Revista Ciência Agrônômica**, 42: 898-905, 2011.

CARGNELUTTI FILHO, A.; RIBEIRO, N. D.; JOST, E. Number of necessary experiments for the cluster analysis in common bean cultivars. **Ciência Rural**, 39: 371-379, 2009.

CRUZ, C. D. Genes Software - extended and integrated with the R, Matlab and Selegen. **Acta Scientiarum. Agronomy**, 38: 547-552, 2016.

DELFINI, J. et al. Distinctness of Brazilian common bean cultivars with carioca and black grain by means of morphoagronomic and molecular descriptors. **Plots One**, 30: 1-22, 2017.

FREITAS, G. et al. Morphological evaluation of common bean diversity on the Island of Madeira. **Genetic Resources and Crop Evolution**, 58: 861-874, 2011.

GONÇALVES, D. L. et al. Variabilidade genética de germoplasma tradicional de feijoeiro comum na região de Cáceres-MT. **Ciência Rural**, 46: 100-107, 2016.

GRAHIC, J. et al. Morphological evaluation of common bean diversity in Bosnia and Herzegovina using the discriminant analysis of principal components (DAPC) multivariate method. **Genetika**, 45: 963-977, 2013.

HEGAY, S. et al. Genetic diversity analysis in *Phaseolus vulgaris* L. using morphological traits. **Genetic Resources and Crop Evolution**, 61: 555-566, 2014.

JOST, E. et al. Comparison among direct, indirect and index selections on agronomic traits and nutritional quality traits in common bean. **Journal of the Science of Food and Agriculture**, 93: 1097-1104, 2013.

KUMAR, V. et al. Comparative analysis of diversity based on morpho-agronomic traits and microsatellite markers in common bean. **Euphytica**, 170: 249-262, 2009.

LEMOS, L. B.; MINGOTTE, F. L. C.; FARINELLI, R. Cultivares. In: ARF, O. et al. (Eds.). **Aspectos gerais da cultura do feijão** (*Phaseolus vulgaris* L.). Botucatu, SP: Fundação de Estudos e Pesquisas Agrícolas e Florestais, 2015, cap. 10, p. 181-207.

- LIMA, M. S. et al. Characterization of genetic variability among common bean genotypes by morphological descriptors. **Crop Breeding and Applied Biotechnology**, 12: 76-84, 2012.
- MAZIERO, S. M.; RIBEIRO, N. D.; CASAGRANDE, C. R. Genetic dissimilarity of common bean lines for agronomic and biofortification traits. **Genetics and Molecular Research**, 16: 1-13, 2017.
- MENDES, F. F.; RAMALHO, M. A. P.; ABREU, A. F. B. Índice de seleção para escolha de populações segregantes de feijoeiro-comum. **Pesquisa Agropecuária Brasileira**, 44: 1312-1318, 2009.
- MONTGOMERY, D. C.; PECK, E. A. **Introduction to linear regression analysis**. New York: John Wiley & Sons, 1981. 504 p.
- MOURA, M. M. et al. Potencial de caracteres na avaliação da arquitetura de plantas de feijão. **Pesquisa Agropecuária Brasileira**, 48: 417-425, 2013.
- MULAMBA, N. N.; MOCK, J. J. Improvement of yield potential of the ETO blanco maize (*Zea mays* L.) population by breeding for plant traits. **Egyptian Journal of Genetics and Cytology**, 7: 40-51, 1978.
- NADEEM, M. A. et al. Phenotypic characterization of 183 Turkish common bean accessions for agronomic, trading, and consumer-preferred plant characteristics for breeding purposes. **Agronomy**, 10: 1-20, 2020.
- PEREIRA, H. S. et al. Genetic diversity among common bean cultivars based on agronomic traits and molecular markers and application to recommendation of parent lines. **Euphytica**, 215: 1-16, 2019.
- RIBEIRO, N. D. et al. Desempenho agrônomo e qualidade de cozimento de linhagens de feijão de grãos especiais. **Revista Ciência Agronômica**, 45: 92-100, 2014.
- RIBEIRO, N. D. et al. Phenological, plant architecture, and grain yield traits on common bean lines selection. **Revista Caatinga**, 31: 657-666, 2018a.
- RIBEIRO, N. D. et al. Combined selection in beans for cycle, plant architecture and grain yield. **Bioscience Journal**, 34: 108-119, 2018b.
- RIBEIRO, N. D. et al. Upright plant architecture traits and their relationship with grain yield in the selection of Mesoamerican common bean lines cultivated at low altitude. **Genetics and Molecular Research**, 18: 1-13, 2019.
- SANTOS, P. R. J. et al. Genetic divergence among landraces and improved common bean genotypes in the central-southern region of Mato Grosso state in Brazil. **Genetics and Molecular Research**, 18: 1-14, 2019.
- SILVA, V. M. P. et al. Genetic potential of common bean parents for plant architecture improvement. **Scientia Agricola**, 70: 167-175, 2013.
- SOFI, P. A. et al. Genetic variability and factor analysis in common bean (*Phaseolus vulgaris* L.) germplasm collection for yield related traits. **Electronic Journal of Plant Breeding**, 5: 254-259, 2014.
- SOLTANI, A. et al. Targeted analysis of dry bean growth habit: interrelationship among architectural, phenological, and yield components. **Crop Science**, 56: 3005-3015, 2016.
- VENCOVSKY, R.; CRUZ, C. D. Comparação de métodos de correção do rendimento de parcelas com estandes variados: I. Dados simulados. **Pesquisa Agropecuária Brasileira**, 26: 647-657, 1991.
- YEKEN, M. Z. et al. Determination of Turkish common bean germplasm for morpho-agronomic and mineral variations for breeding perspectives in Turkey. **KSU Journal of Agriculture and Nature**, 22: 38-50, 2019.