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Genetic diversity among bean landraces and cultivars for agronomy traits and selection of superior parents[1]

Diversidade genética entre variedades locais e cultivares de feijão para caracteres agronômicos e seleção de parentais superiores

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ABSTRACT - The characterization of genetic diversity in common bean genotypes for various agronomic traits enables the selection of promising parents and the identification of genotypes with high agronomic performance. The present study proposes to evaluate the genetic diversity of common bean landraces and cultivars for 14 agronomic traits; examine the correlations between these traits; define promising crosses; and select genotypes with high agronomic performance. A total of 49 common bean genotypes were evaluated in three growing seasons, consisting of 37 landraces and 12 common bean cultivars. Significant effects of genotype × environment interaction or genotype were observed for all agronomic traits, thereby allowing the study of genetic divergence. Several plant-architecture traits were correlated with each other, whereas grain yield was highly correlated with insertion of the last pod ($r = 0.74$), number of pods per plant ($r = 0.74$) and mass of 100 grains ($r = - 0.64$). The furthest-neighbor method separated the common bean genotypes into two groups, Mesoamerican and Andean, and mass of 100 grains showed the greatest contribution to the differentiation between the genotypes. Tocher's method was more informative and divided the common bean genotypes into 12 groups. The following crosses are recommended: Vagem Roxa × IPR Juriti, Vagem Roxa × Macanudo, Fepagro Triunfo × IPR Juriti, Fepagro Triunfo × Macanudo, Guapo Brilhante × IPR Juriti, and Guapo Brilhante × Macanudo. The common bean genotypes Fepagro Triunfo, IPR Juriti, Guapo Brilhante, BRS Campeiro and Vagem Roxa have high agronomic performance and should thus be selected by the breeding program.

Key words: *Phaseolus vulgaris* L. Genetic variability. Pearson's correlation. Cluster analysis. Selection index.

RESUMO - A caracterização da diversidade genética de genótipos de feijão para vários caracteres agronômicos permite selecionar parentais promissores e identificar genótipos de alto desempenho agronômico. Nesse contexto, foram objetivos desse trabalho avaliar a diversidade genética de variedades locais e cultivares de feijão para 14 caracteres agronômicos, estudar as correlações entre esses caracteres, definir cruzamentos promissores e selecionar genótipos com alto desempenho agronômico. Um total de 49 genótipos de feijão foram avaliados em três épocas de cultivo, sendo 37 variedades locais e 12 cultivares de feijão. Efeito significativo da interação genótipo x ambiente ou de genótipo foi observado para todos os caracteres agronômicos e isso possibilita o estudo da divergência genética. Vários caracteres da arquitetura de planta foram correlacionados, enquanto que a produtividade de grãos mostrou alta correlação com a inserção da última vagem ($r = 0{,}74$), o número de vagens por planta ($r = 0{,}74$) e a massa de 100 grãos ($r = - 0{,}64$). O método de agrupamento Vizinho mais Distante separou os genótipos de feijão em dois grupos Mesoamericano e Andino, pois a massa de 100 grãos apresentou a maior contribuição para a diferenciação entre os genótipos. O método de Tocher foi mais informativo e dividiu os genótipos de feijão em 12 grupos. Os seguintes cruzamentos são recomendados Vagem Roxa × IPR Juriti, Vagem Roxa × Macanudo, Fepagro Triunfo × IPR Juriti, Fepagro Triunfo × Macanudo, Guapo Brilhante × IPR Juriti e Guapo Brilhante × Macanudo. Os genótipos de feijão Fepagro Triunfo, IPR Juriti, Guapo Brilhante, BRS Campeiro e Vagem Roxa apresentam alto desempenho agronômico e deverão ser selecionados pelo programa de melhoramento.

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

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INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is reported to have two centers of origin: Mesoamerican and Andean, and grain size is one of the traits most commonly used to identify the origin of its genotypes (SINGH; GEPTS; DEBOUCK, 1991). As a result of domestication and the introduction of this species in several countries, great variability exists today in terms of grain size, color and shape.

Common bean production presents great nutritional importance due to the considerable amounts of protein, carbohydrates, minerals and vitamins found in its grains (CÂMARA; URREA; SCHLEGEL, 2013). In local gastronomy, common bean has been prepared in different ways, from simple menus to gourmet dishes, and many of these recipes use grains produced in family farming.

To preserve and multiply grains of common bean landraces - that is, local cultivars subjected to natural selection by farmers after years of cultivation, means to maintain the culture and identity of the people living in a given region. In addition, many of the common bean cultivars developed by research were obtained from crosses involving a very limited number of parents and, therefore, have a narrow genetic base. In other words, these cultivars possess less genetic variability than what is observed in landraces. Thus, characterizing the genetic diversity of common bean landraces and cultivars is of great importance for breeding programs. This information is essential to identify favorable traits found in genotypes and define more-promising cross combinations for common-bean breeding programs.

The genetic diversity found in common bean genotypes for agronomic traits, such as those related to phenology, plant architecture and yield components, has been evaluated in experiments conducted majorly in only one growing environment (CORREA; GONÇALVES, 2012; GONÇALVES *et al*., 2016; LIMA *et al*., 2012; YEKEN *et al*., 2019). However, agronomic traits in common bean are affected by the genotype × environment interaction (ARTEAGA *et al*., 2019; BOROS; WAWER; BORUCKA, 2014; CABRAL *et al*., 2011; COELHO *et al*., 2010; DELFINI *et al*., 2017). For this reason, the genetic diversity of common bean genotypes must be evaluated in various environments for the proper interpretation of results.

Genetic diversity for agronomic traits in common bean genotypes has also studied in two or more growing environments (ARTEAGA *et al*., 2019; BERTOLDO *et al*., 2014; BOROS; WAWER; BORUCKA, 2014; CABRAL *et al*., 2011; COELHO *et al*., 2010; DELFINI *et al*., 2017; MAZIERO; RIBEIRO; CASAGRANDE, 2017; PEREIRA *et al*., 2019; RANA *et al*., 2015). Nevertheless, in these studies, few agronomic traits were evaluated, especially those related to plant architecture. The analysis of genetic diversity involving a large number of agronomic traits evaluated in various environments is unprecedented for the common bean crop. This would allow into greater chances of success in forming groups of genotypes based on genetic dissimilarity; defining promising crosses to be made; and selecting common bean genotypes with high agronomic performance that can be grown in the region. On this basis, the present study was developed to evaluate the genetic diversity of common bean landraces and cultivars for 14 agronomic traits; examine the correlations between these traits; define promising crosses; and select common bean genotypes with high agronomic performance.

MATERIAL AND METHODS

Seed production from the evaluated genotypes

Seeds of the common bean landraces were acquired at Landrace Seed Fairs and from family farmers assisted by the Southern Association for Rural Credit and Assistance in the State of Rio Grande do Sul (RS), Brazil, in 2016. The seeds of common bean cultivars developed by research were provided by the Common Bean Germplasm Bank of the Federal University of Santa Maria (UFSM). All obtained seeds were multiplied in the experimental area of the Common Bean Breeding Program at UFSM, in Santa Maria, RS, Brazil (latitude 29º42′ S, longitude 53º43′ W and altitude 95 m), in the rainy-season crop of 2016. This procedure was necessary to standardize the physiological quality of the seeds of the common bean genotypes (landraces and cultivars).

Santa Maria has a humid subtropical climate with hot summers and without a clearly defined dry season. The soil at the Santa Maria mapping unit is characterized as a typic alitic Argisol, Hapludalf. Cultivation was carried out in a common bean/common bean/black oat succession system and the soil was prepared with plowing and harrowing operations.

The experiments to evaluate genetic diversity in common bean genotypes were installed during three growing seasons, namely, dry season of 2017, rainy season of 2017 and dry season of 2018, in the experimental area of the Common Bean Breeding Program at UFSM. The experiment was set up as a 7 × 7 simple lattice design with two replicates. The experimental plot consisted of four 3-m-long rows, spaced 0.5 m apart, a usable area of 3 m^2 and a density of 15 plants m^{-2}. A total of 49 common bean genotypes were evaluated, consisting of 37 landraces and 12 cultivars developed by research (Table 1). These genotypes characterize the diversity of common bean grains produced and consumed in Brazil, of both the Mesoamerican and Andean gene pools: carioca (beige seed coat with brown streaks), black, cranberry (cream seed coat with red streaks), red, white, yellow, pink, beige, mouro (gray seed coat with black streaks), brown, purple and green.

Table 1 - Name of genotypes, grain illustration, grain type and growth habit (GH) of common bean landraces and cultivars evaluated

Genotype	Grain	Type	GH	Genotype	Grain	Type	GH
Common bean landraces							
Inhoque		yellow	I	Vagem Roxa		black	II
Carioca		carioca	III	Folgado		black	II
Carioca (Vila Nova do Sul)		carioca	III	Banana		black	II
Trindade		carioca	III	Capixaba		black	II
Carioca (Ibarama)		carioca	III	Carioca Rosa		pink	II
Cavalo Claro		cranberry	I	Rosinha		pink	II
Bege Ibarama		beige	I	Milico		green	I
Pintadinho		beige	II	Verde 208		green	I
Preguiçoso		white	II	Tubiano		red	I
Rajado 319		brown	II	Amendoim Comprido		red	II
Mourinho (Claro)		brown	III	Fogo da Serra 322		red	I
Turrialba		black	II	Vermelho Graúdo		red	I
Paraná		black	II	Vermelho Rajado		red	I
Vagem Larga		black	I	Quero Quero		cranberry	II
Manteigão		black	I	Mouro		mouro	I
Argentino		black	II	Mouro 128		mouro	I
Azulão		black	II	Mouro Graúdo		mouro	II
Predominante 140		black	II	Guabiju Roxo		purple	I
Chumbinho		black	II				
Common bean cultivars							
SCS 205 Riqueza		carioca	III	IPR Uirapurú		black	II
BRS Estilo		carioca	III	BRS Campeiro		black	II
IPR Juriti		carioca	III	Macanudo		black	II
Pérola		carioca	III	Guapo Brilhante		black	II
BRS MG Realce		cranberry	I	Rio Tibagi		black	II
Iraí		cranberry	I	Fepagro Triunfo		black	II

GH*: growth habit - I: determinate; II: indeterminate with short guides; III: indeterminate with long guides

Sowing was done manually, using a hoe to open the lines. Fertilizers were applied within the sowing lines, with the amount calculated according to the results of soil chemical analysis. A light layer of soil was placed over the fertilizers to avoid phytotoxicity to the seeds. The seeds were treated with the fungicide Maxim XL (fludioxonil and metalaxyl−M) and the insecticide Cruiser (thiamethoxam), both at a dose of 200 mL 100 kg^{-1} of seeds.

The other management practices consisted of herbicide application in the pre-emergence phase, urea topdressing, mechanical control of weed plants and chemical control of insects. These were carried out according to the technical recommendations for the common bean crop in RS (COMISSÃO TÉCNICA SUL BRASILEIRA DE FEIJÃO, 2012). No fungicides were applied during plant development and irrigation was only used when strictly necessary for the establishment of the initial plant population.

Evaluation of agronomic traits

At the maturity stage (R9), that is, when the pods began to dry and acquired the typical color of each cultivar, the cycle and four qualitative traits of plant architecture (lodging, stay-green, general adaptation score and architecture) were evaluated in the usable plot area. The cycle was quantified as the number of days from emergence to harvest. The following score scales were used to determine the qualitative traits of plant architecture: lodging - (1) all upright plants to (9) all prostrated plants, touching the soil; stay-green - (1) plants exhibiting over 80% of their stem green with pods completely dry to (5) up to 20% of the stem green, i.e., no stay-green; general adaptation score - (1) upright plants, with a high number of pods per plant and absence of disease symptoms on the pods to (9) prostrated plants, with long internodes, few pods per plant and high severity of diseases on the pods; and architecture - (1) plants fully upright to (9) plants fully lodged.

Plant architecture was also analyzed by four quantitative traits that were determined in 10 plants collected at random in the usable area of the plots, at the R9 stage, namely, insertion of the first pod, insertion of the last pod, hypocotyl diameter and epicotyl diameter. Yield components (number of pods per plant, number of grains per plant, number of grains per pod and mass of 100 grains) were also quantified in this sample of 10 plants. Grain yield was calculated by summing the weights of the grains obtained in the usable plot area and in the 10 plants, with grain moisture standardized at 13%, and expressed in kg ha^{-1}.

Statistical analyses

Analysis of variance was performed individually for each experiment to check the homogeneity of residual variances by Hartley's maximum F test as described by Cruz, Regazzi and Carneiro (2012). The efficiency of the simple lattice design (Ef), compared to a randomized block design was determined by;

$$Ef = \frac{RM_S}{M_{EV}} \times 100 \qquad (1)$$

in which RM_S is the residue mean square of the lattice analysis as randomized blocks and M_{Ev} is the mean effective variance of the lattice analysis (RAMALHO; FERREIRA; OLIVEIRA, 2005).

In the combined analysis of variance the effects of genotype, environment and genotype × environment interaction were considered fixed and the other effects were analyzed as random. The significance level was evaluated by the F test (p-value < 0.05).

Multicollinearity diagnostics was carried out 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 established according to the classification proposed by Montgomery, Peck and Vining (2012). 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 × environment interaction were included in this analysis. The significance of the correlation coefficients was assessed by Student's t test (p value < 0.05).

The residual variance and covariance matrix was obtained from combined analysis of variance. These matrices were used to generate the genetic matrix of dissimilarity between common bean genotypes by Mahalanobis' generalized distance with standardized means. The Mahalanobis' generalized distance analysis were also applied to identify traits with the greatest relative contribution to genetic divergence. Cluster analyses were carried out using the complete-linkage hierarchical method, called furthest-neighbor, and Tocher's optimization method, described by Regazzi and Cruz (2020).

The index based on the rank-sum (MULAMBA; MOCK, 1978) was used to obtain selection gain estimates and select superior common bean genotypes. For this, the applied selection intensity was 10%, which resulted in the selection of five common bean genotypes. Selection was performed to obtain the lowest values of lodging, stay-green, general adaptation score and architecture and the highest values for the other traits. The following weights were attributed: three - grain yield; two - insertion of the last pod and number of pods per plant; and one - other agronomic traits. Analyses were performed using the spreadsheets of the Microsoft Office Excel and Genes software program (CRUZ, 2016).

RESULTS AND DISCUSSION

Overall results

The ratio between the highest and the lowest error mean square (EMS^+/EMS^-) in individual analysis of variance was less than seven for all evaluated traits, except for the cycle. Thus, the degrees of freedom of the error and of the genotype × environment interaction (G × E) obtained for the cycle were defined as described by Cruz, Regazzi and Carneiro (2012). In this way, it was possible to obtain homogeneous residual variances for all agronomic traits, as required for combined analysis of variance.

The use of the simple lattice design showed less than 100% efficiency for 23 of the 42 combinations (14 traits × 3 environments) tested in individual analysis of variance. Thus, its efficiency was low for most agronomic traits. For this reason, combined analysis of variance was performed following the randomized block design as recommended by Ramalho, Ferreira and Oliveira (2005).

A significant difference for genotype and environment effects was observed in the traits of epicotyl diameter, number of pods per plant and number of grains per plant (Table 2). For the other agronomic traits, a significant G × E interaction was detected. When common bean landraces were evaluated in different growing environments, a significant G × E interaction effect was also obtained for various agronomic traits (ARTEAGA *et al.*, 2019; BOROS; WAWER; BORUCKA, 2014; CABRAL *et al.*, 2011; COELHO *et al.*, 2010). In other words, the common bean genotypes showed variation for most traits related to phenology, plant architecture and yield components in response to changes in the growing environment. This reinforces the need to consider different growing environments in the analysis of genetic diversity and select superior parents for agronomic traits in common-bean breeding programs.

The coefficient of experimental variation (CEV) ranged from 6.24 (mass of 100 grains) to 28.18% (stay-green). A similar range of variation has been reported for CEV determined in agronomic traits in common bean landraces (CABRAL *et al*., 2011; COELHO *et al*., 2010; GONÇALVES *et al.*, 2016; ZILIO *et al*., 2013). Therefore, two classes of CEV were obtained for the traits evaluated in the present study: low experimental precision (CEV ≥ 23.41%) – stay-green, number of grains per plant and number of pods per plant; and high experimental precision (CEV ≤ 21.48%) - other agronomic traits. Nonetheless, when experimental precision was analyzed based on selective accuracy (SA), the traits were grouped into four classes, according to the classification of de Resende and Duarte (2007): low ($SA \leq 0.40$) - epicotyl diameter, number of pods per plant and number of grains per plant; moderate ($0.50 < SA < 0.65$) - stay-green and hypocotyl diameter; high ($0.70 < SA < 0.85$) - cycle, lodging, general adaptation score, architecture, insertion of the first pod, insertion of the last pod, number of grains per pod and grain yield; and very high ($SA \geq 0.90$) - mass of 100 grains. Ribeiro *et al*. (2019) also obtained four classes of experimental precision for agronomic traits evaluated in lines and cultivars of common bean. These results indicate that SA can be more informative than CEV to evaluate the experimental precision of agronomic traits in common bean.

Table 2 - Combined analysis of variance, considering the randomized block design, containing the degrees of freedom (DF), mean squares, mean, coefficient of experimental variation (CEV%) and selective accuracy (SA) for the following traits: cycle (days), lodging (LDG), stay-green (SG), general adaptation score (GAS), architecture (ARC), insertion of the first pod (IFP, cm), insertion of the last pod (ILP, cm), hypocotyl diameter (HD, cm), epicotyl diameter (ED, m), number of pods per plant (NPP), number of grains per plant (NGP), number of grains per pod (NGPod), mass of 100 grains (M100G, g), and grain yield (YIELD, kg ha^{-1}) of 49 common bean genotypes evaluated in the three growing seasons (dry season of 2017, rainy season of 2017 and dry season of 2018)

	DF	Mean square				
		CYCLE	LDG	SG	GAS	ARC
Block/environment	3	185.32	35.95	9.51	14.13	0.60
Genotype (G)	48	311.04*	4.28*	1.33*	2.95*	2.20*
Environment (E)	2	19,024.67*	3.31^{ns}	178.59*	25.07^{ns}	2.61^{ns}
G x E	96	126.16*	3.59*	1.51*	1.29*	1.64*
Error	144	40.99	1.02	0.91	0.64	0.82
Mean		92.67	6.20	3.38	6.59	5.78
CEV (%)		6.91	16.27	28.18	12.16	15.67
SA		0.82	0.85	0.63	0.71	0.71

Continuation Table 2

	DF	IFP	ILP	HD	ED	NPP
Block/environment	3	9.86	70.07	0.86	1.35	25.57
Genotype (G)	48	38.11*	273.05*	1.90*	1.72*	34.03*
Environment (E)	2	1,394.62*	12,617.67*	46.69*	54.00*	1,048.23*
G x E	96	18.53*	51.43*	0.33*	0.32^{ns}	5.35^{ns}
Error	144	4.77	22.91	0.22	0.26	5.09
Mean		15.19	34.64	5.04	5.01	9.75
CEV (%)		14.38	13.82	9.36	10.28	23.41
SA		0.86	0.74	0.56	0.43	0.22
	DF	NGP	NGPod	M100G	YELD	
Block/environment	3	208.08	0.47	6.49	667,047.37	
Genotype (G)	48	862.36*	1.61*	250.96*	913,927.36*	
Environment (E)	2	13,519.01*	0.65^{ns}	406.05*	27,127,494.26*	
G x E	96	100.06^{ns}	0.28*	24.45*	188,400.19*	
Error	144	90.21	0.12	3.50	95,776.97	
Mean		35.87	3.58	30.00	1,440.59	
CEV (%)		26.48	9.84	6.24	21.48	
SA		0.31	0.74	0.93	0.70	

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

Multicollinearity diagnostics revealed a CN of 2,951.15, characterizing severe collinearity according classes proposed by Montgomery, Peck and Vining (2012). After identifying the pairs of traits with the highest correlation and determining the less important traits for the differentiation between common bean genotypes, three traits (epicotyl diameter, number of grains per plant and number of grains per pod) were excluded, generating a CN = 79.15, i.e., weak collinearity. This procedure prevented that multicollinear variables from implicitly receiving greater weights in the correlation and cluster analyses, allowing the correct interpretation of the results obtained.

Correlations between agronomic traits

The cycle showed positive correlations of high magnitude with insertion of the last pod (r = 0.81) and of intermediate magnitude with insertion of the first pod, hypocotyl diameter, number of pods per plant, mass of 100 grains and grain yield (r = 0.55 to 0.68) (Table 3). Similarly, Yeken *et al.* (2019) observed a positive correlation between cycle and grain yield (r = 0.57), in a study with common bean landraces collected in Turkey. However, no correlation was found between the cycle and some traits of plant architecture and yield components in common bean genotypes (PEREIRA *et al*., 2019; RIBEIRO *et al*., 2018; SOFI *et al*., 2011). The genetic diversity between the common bean genotypes may explain the differences found. In the present study, were evaluated predominantly common bean landraces. Most of the evaluated landraces have an indeterminate growth habit with long guides, and intermediate to long cycles. These cultivars exhibit a longer flowering period, which provides greater fixation of pods per plant and greater grain yield, even in adverse growing conditions.

Some plant architecture traits were positively correlated (r ≥ 0.52): lodging - general adaptation score; lodging - architecture; stay-green - insertion of the last pod; general adaptation score - architecture; and insertion of the first pod - insertion of the last pod. General adaptation score and hypocotyl diameter were negatively correlated (r = -0.61). These correlations suggest that there is no need to use a large number of traits to evaluate plant architecture in common bean, considering that correlated traits provide similar information. Therefore, the plant architecture of common bean could very well be determined by one qualitative trait and one quantitative trait to be defined based on the ease, simplicity, speed and experimental precision obtained in these evaluations.

The following traits were highly correlated with grain yield: insertion of the last pod (r = 0.74), number of pods per plant (r = 0.74) and mass of 100 grains (r = -0.64). However, Ribeiro *et al*. (2018) did not observe a significant correlation between grain yield and the traits of insertion of the last pod and number of pods per plant, whereas grain yield was positively correlated with

Table 3 - Pearson’s phenotypic correlation coefficients obtained between the traits of cycle, lodging (LDG), stay-green (SG), general adaptation score (GAS), architecture (ARC), insertion of the first pod (IFP), insertion of the last pod (ILP), hypocotyl diameter (HD), number of pods per plant (NPP), mass of 100 grains (M100G), and grain yield (yield) obtained from 49 common bean genotypes evaluated in three experiments carried out between 2017 and 2018

	LDG	SG	GAS	ARC	IFP	ILP	HD	NPP	M100G	YIELD
CYCLE	0.12^{ns}	0.42*	-0.28*	-0.08^{ns}	0.68*	0.81*	0.58*	0.55*	0.55*	0.55*
LDG		0.32	0.68*	0.81*	0.35*	0.29*	-0.30*	0.06^{ns}	-0.22^{ns}	0.05^{ns}
SG			-0.12^{ns}	0.27^{ns}	0.43*	0.52*	0.22^{ns}	0.50*	-0.53*	0.45*
GAS				0.65*	-0.03^{ns}	-0.27^{ns}	-0.61*	-0.49*	0.24^{ns}	-0.56*
ARC					0.37*	0.27^{ns}	-0.40*	-0.09^{ns}	-0.18^{ns}	0.02^{ns}
IFP						0.82	0.23^{ns}	0.29*	-0.52*	0.44*
ILP							0.45*	0.61*	-0.70*	0.74*
HD								0.64*	-0.25ns	0.48*
NPP									-0.67*	0.74*
M100G										-0.64*

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

mass of 100 grains, in an experiment with lines and cultivars of common bean. In the present study, most of the evaluated common bean genotypes were landraces. The common bean landraces with the highest grain yield were those which also showed a higher insertion of the last pod, a higher number of pods per plant and lower mass of 100 grains. Common bean genotypes with a higher insertion of the last pod have a greater tendency to lodging, and small grains expand less after cooking. Therefore, common bean genotypes with these traits are less accepted for cultivation in commercial farming and for acquisition by bean-packaging companies. However, in family farming, these traits do not represent restrictions on the cultivation and consumption of these common bean genotypes, since many producers of this crop preserve and multiply genotypes based on criteria related to tradition, culture and affective memories associated with the flavor of the grains.

Cluster analysis

In any study of genetic diversity is important to evaluate which traits allow a better differentiation between common bean genotypes based on phenotype assessment. By using Mahalanobis’ generalized distance, it was possible to identify the two agronomic traits that would most contribute to the differentiation of common bean genotypes: mass of 100 grains (53.84%) and cycle (12.35%) (Table 4). In applying the same methodology, other authors also observed that mass of 100 grains was the trait of the greatest relative contribution to the differentiation of common bean genotypes (CABRAL *et al*., 2011; COELHO *et al*., 2010; CORREA; GONÇALVES, 2012).

Table 4 - Relative contribution (S.j) of the traits of cycle, lodging (LDG), stay-green (SG), general adaptation score (GAS), architecture (ARC), insertion of the first pod (IFP), insertion of the last pod (ILP), hypocotyl diameter (HD), number of pods per plant (NPP), mass of 100 grains (M100G), and grain yield (yield) for the genetic dissimilarity of 49 common bean genotypes obtained by Mahalanobis’ generalized distance

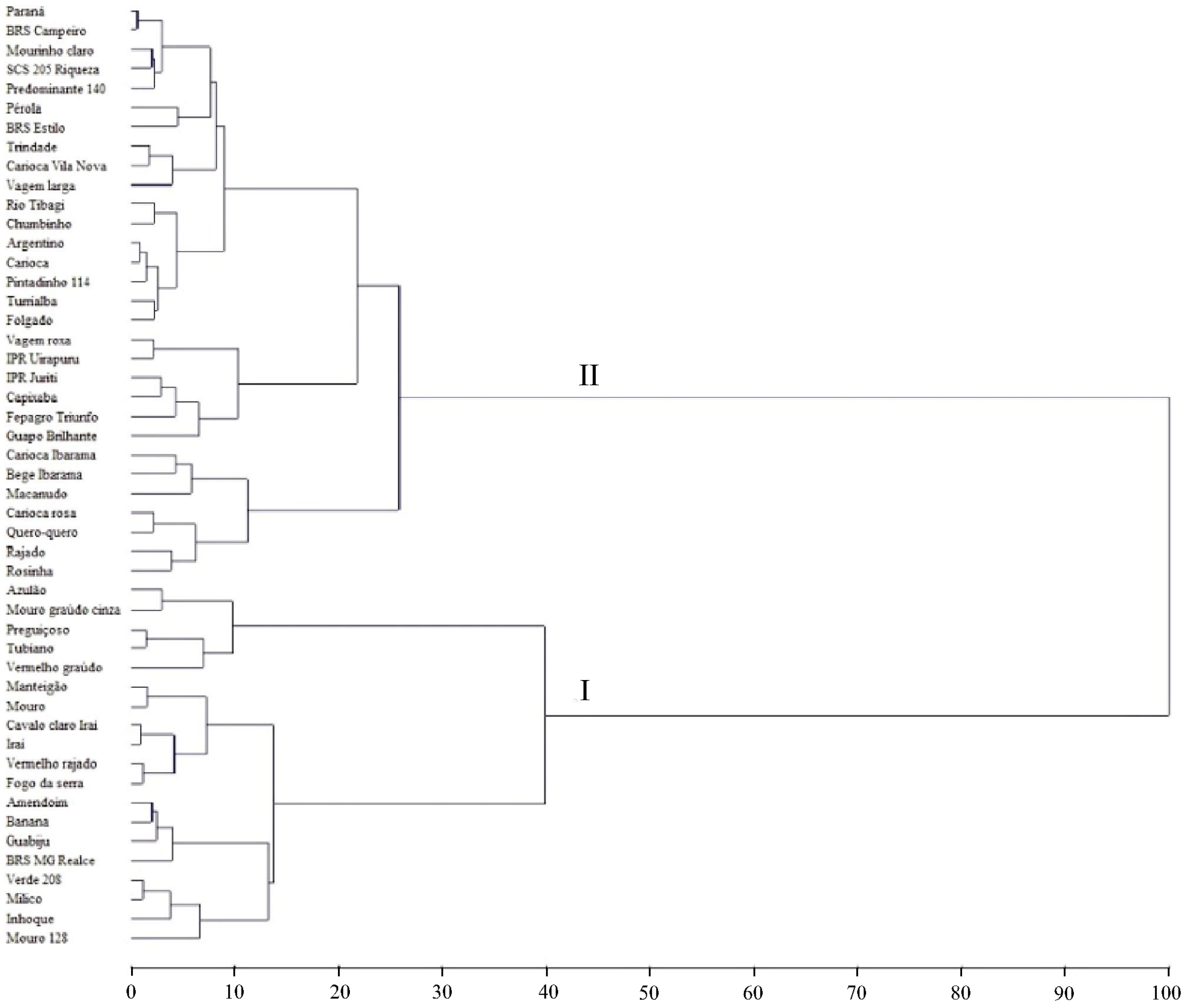
TRAIT	S.j	Value (%)
CYCLE	7,137.17	12.35
LDG	1,046.59	1.81
SG	592.70	1.02
GAS	1,661.44	2.87
ARC	960.13	1.66
IFP	1,688.71	2.92
ILP	3,090.96	5.35
HD	4,729.83	8.19
NPP	1,633.90	2.83
M100G	31,104.18	53.84
YELD	4,127.26	7.14

The complete-linkage hierarchical method - furthest neighbor, based on Mahalanobis’ generalized distance matrix, separated the common bean genotypes into two groups (Figure 1). Group 1 consisted of 19 common bean genotypes with medium to large grains (mass of 100 grains ≥ 30 g), namely, Azulão, Mouro Graúdo Cinza, Preguiçoso, Tubiano, Vermelho Graúdo, Manteigão, Mouro, Cavalo Claro Iraí, Iraí, Vermelho

Rajado, Fogo da Serra 322, Amendoim Comprido, Banana, Guabijú Roxo, BRS MG Realce, Verde 208, Milico, Inhoque, and Mouro 128. Group 2 consisted of the other 30 evaluated common bean genotypes which have small grains (mass of 100 grains < 30 g). Therefore, the generated dendrogram separated the common bean genotypes into two gene pools, namely, Andean (group 1, with 38.77% of the evaluated genotypes) and Mesoamerican (group 2, with 61.22% of the evaluated genotypes), according to the grain size classes. Guidoti *et al*. (2018) also observed that the size of common bean grains defined the two groups formed by the unweighted pair group method with arithmetic mean (UPGMA). In this study, the 17 common bean genotypes evaluated were also separated into two gene pools, namely, Andean, with 64.70% of the evaluated genotypes, and Mesoamerican, representing 35.30% of the genotypes.

The dendrogram generated by the furthest-neighbor method revealed high reliability in the cluster formation illustrated in Figure 1. This is because the obtained cophenetic correlation coefficient (CCC) was 0.77 and significant at 1% probability by the t test. High CCC values indicate high adjustment between the cophenetic matrix and the dissimilarity matrix based on Mahalanobis' generalized distance (CABRAL *et al*., 2011), and this contributed to the greater consistency of the clustering pattern. However, the clustering obtained using the furthest- neighbor method made it possible to differentiate the groups formed only by mass of 100 grains.

Figure 1 - Dendrogram representing genetic dissimilarity among the 49 common bean genotypes obtained by the complete-linkage (furthest-neighbor) hierarchical method, using Mahalanobis' generalized distance, based on agronomic traits evaluated in three experiments carried out between 2017 and 2018



When cluster analysis was performed via Tocher's optimization method, also using Mahalanobis' generalized distance matrix, 12 groups were formed (Table 5). Groups 1 and 2 comprised the largest number of common bean genotypes, 17 and 9, respectively. The other groups were composed of one to four common bean genotypes. Groups 1, 7 and 9 contained common bean genotypes with higher grain yield and small grains. The common bean genotypes with large grains (mass of 100 grains > 40 g) were clustered in groups 4, 11 and 12, and these genotypes showed lower (groups 4 and 12) or higher (group 11) grain yields than the overall mean obtained in the experiments (Table 2). Therefore, although a negative correlation was observed between grain yield and mass of 100 grains (Table 3), cultivar Mouro Graúdo Cinza (group 11) stood out for grain yield, despite having large grains (Table 5).

Groups 7 and 12 were formed by common bean genotypes with an upright plant architecture, characterized by the lowest lodging, general adaptation score and architecture values and the largest hypocotyl diameter. The common bean genotypes showed cycles ranging from 81.75 (group 3) to 103.00 days (group 10), which is an important trait in the differentiation between groups of common bean genotypes. Therefore, Tocher's method allowed for greater detail in relation to the

Table 5 - Cluster analysis formed by Tocher's optimization method, based on Mahalanobis' generalized distance, for the traits of cycle, lodging (LDG), stay-green (SG), general adaptation score (GAS), architecture (ARC), insertion of the first pod (IFP), insertion of the last pod (ILP), hypocotyl diameter (HD), number of pods per plant (NPP), mass of 100 grains (M100G), and grain yield (YIELD) determined in 49 common bean genotypes evaluated in three experiments carried out between 2017 and 2018 and means obtained in each group

Group	Number	Cultivars
1	17	Paraná, BRS Campeiro, SCS 205 Riqueza, Mourinho Claro, Predominante 140, Folgado, Argentino, Pintadinho 114, Carioca, Rio Tibagi, Turrialba, Chumbinho, BRS Estilo, IPR Uirapuru, Trindade, Vagem Larga and Capixaba
2	9	Cavalo Claro Iraí, Iraí, Vermelho Rajado, Fogo da Serra 322, Azulão, Mouro, Banana, Amendoim Comprido and Manteigão
3	4	Verde 208, Milico, Inhoque and Mouro 128
4	2	Preguiçoso and Tubiano
5	3	Carioca Rosa, Quero Quero and Carioca Vila Nova
6	4	Rajado 319, Rosinha, Carioca Ibarama and Bege Ibarama
7	3	Vagem Roxa, Fepagro Triunfo and Guapo Brilhante
8	2	Guabiju Roxo and BRSMG Realce
9	2	IPR Juriti and Macanudo
10	1	Pérola
11	1	Mouro Graúdo Cinza
12	1	Vermelho Graúdo

Means obtained in each group

Group	CYCLE	LDG	SG	GAS	ARC	IFP	ILP	HD	NPP	M100G	YIELD
1	98.10	6.31	3.59	6.29	5.81	16.73	39.63	5.33	10.96	26.29	1,707.23
2	84.09	5.93	3.06	6.91	5.80	13.27	27.26	4.61	7.74	37.03	1,057.67
3	81.75	6.25	3.00	7.33	5.75	11.46	24.08	4.34	6.75	31.44	1,040.88
4	94.42	6.25	3.00	7.08	5.42	13.10	29.41	5.05	7.17	42.75	933.08
5	99.89	7.33	3.89	7.39	6.50	19.51	43.33	4.72	10.57	25.24	1,643.31
6	90.46	6.71	3.63	6.71	6.13	16.43	35.50	4.45	10.73	22.32	1,462.49
7	97.11	4.39	3.56	5.11	4.56	14.14	37.08	6.10	12.41	24.76	1,892.91
8	92.50	6.42	3.42	7.33	5.92	15.49	30.78	5.07	7.34	34.34	799.38
9	93.25	6.92	3.50	6.42	6.17	13.85	38.87	5.85	15.32	26.15	1,882.78
10	103.00	6.00	2.83	6.50	6.00	17.36	43.10	5.25	8.50	29.11	1,506.79
11	83.33	6.00	3.33	6.17	6.00	15.34	32.60	4.47	5.72	43.63	1,503.40
12	89.83	5.00	2.50	5.83	4.67	12.54	25.02	5.64	9.10	45.67	1,184.14

differences observed for the agronomic traits between the groups formed, rendering it more informative than the furthest-neighbor method. Previous results also showed that Tocher's method allowed a better stratification of the dissimilarity observed between the groups and the similarity found between genotypes of the same group (COELHO *et al*., 2010; LIMA *et al*., 2012; MAZIERO; RIBEIRO; CASAGRANDE, 2017; PEREIRA *et al*., 2019). Additionally, it is important to highlight that the cluster analyses were performed based on results obtained in combined analysis of variance, thus using average data from three growing environments. Therefore, greater consistency and greater representativeness of the groups formed were obtained in the cluster analyses, providing a more accurate interpretation of the obtained results.

The greater knowledge of the dissimilarity between groups and the similarity of common bean genotypes of the same group allows a better planning of the crosses to be carried out by the breeding program. In the process of developing a new common bean cultivar, the most important trait to be evaluated is grain yield, followed by plant architecture and cycle. Therefore, to increase the chances of developing superior common bean cultivars, crosses must be carried out between high-grain-yield genotypes, which are not part of the same group, but which have complementary agronomic traits. The cross between the common bean genotypes of group 7 (Vagem Roxa, Fepagro Triunfo and Guapo Brilhante) and those of group 9 (IPR Juriti and Macanudo) meet these requirements, since they have high grain yield and are complementary to the traits of plant architecture and cycle. The following crosses should be made: Vagem Roxa × IPR Juriti, Vagem Roxa × Macanudo, Fepagro Triunfo × IPR Juriti, Fepagro Triunfo × Macanudo, Guapo Brilhante × IPR Juriti, and Guapo Brilhante × Macanudo. However, it is recommended to keep the other common bean genotypes in the Germplasm Bank and characterize them in terms of other morphological traits, of technological and nutritional quality, so that traits of importance for breeding programs can be identified.

Selection index

High heritability estimates were obtained for all traits ($h^2 \geq 62.74\%$), except stay-green ($h^2 = 31.86\%$) (Table 6). Therefore, genetic variability is present for most agronomic traits, indicating the possibility of selecting superior genotypes. Rana *et al.* (2015) also found high heritability values for agronomic traits evaluated in 4274 common bean accessions from the Germplasm Bank of India. Similarly, Ribeiro *et al.* (2019) observed high heritability values for grain yield and for 10 plant architecture traits analyzed in common bean lines and cultivars. High heritability estimates are useful for predicting the results obtained with the selection of superior common bean genotypes for agronomic performance.

The use of the rank-sum selection index allowed a total genetic gain of 30.16%, which can be considered high. However, the individual genetic gains obtained for the traits of stay-green, insertion of the first pod and mass of 100 grains were not favorable to the objectives of selection of common bean genotypes with high agronomic performance. Previous studies also showed that some agronomic traits exhibited signs of genetic gain unfavorable to the selection of common bean lines with high agronomic performance (RIBEIRO *et al*., 2018, 2019). For this reason, it is important to evaluate various agronomic traits, especially when selection is performed with the aim of increasing and reducing specific traits, as in the present study. Considering that the total genetic gain was positive and high (30.16%), ease is expected in the selection of common bean genotypes with high grain yield, upright plant architecture and longer cycle.

Table 6 - Average of the original population (Xo), average of selected genotypes (Xs), heritability (h^2), genetic gain (GG) and percentage of genetic gain (GG%) with simultaneous selection by the rank-sum index for the traits of cycle (days), lodging (LDG), stay-green (SG), general adaptation score (GAS), architecture (ARC), insertion of the first pod (IFP, cm), insertion of the last pod (ILP, cm), hypocotyl diameter (HD, cm), number of pods per plant (NPP), mass of 100 grains (M100G, g), and grain yield (YIELD, kg ha^{-1}) and the five common bean genotypes selected based on the evaluation of three experiments carried out between 2017 and 2018

TRAIT	Selection direction	Xo	Xs	h² %	GG	GG %
CYCLE	Highest value	92.67	95.73	93.78	2.87	3.10
LDG	Lowest value	6.20	5.00	76.19	-0.91	-14.75
SG	Lowest value	3.38	3.43	31.86	0.01	0.46
GAS	Lowest value	6.59	5.40	78.21	-0.93	-14.14
ARC	Lowest value	5.78	4.97	62.74	-0.51	-8.85
IFP	Highest value	15.19	14.61	87.47	-0.50	-3.32

Continuation Table 6

ILP	Highest value	34.64	38.21	91.61	3.26	9.43
HD	Highest value	5.04	5.92	88.26	0.77	15.33
NPP	Highest value	9.75	12.65	85.04	2.46	25.27
M100G	Highest value	30.00	25.80	98.60	-4.14	-13.82
YIELD	Highest value	1,440.59	1,946.67	89.52	453.05	31.45
Total gain					445.43	30.16

Selected genotypes

Cultivar	CYCLE	LDG	SG	GAS	ARC	IFP
Fepagro Triunfo	95.50	5.50	3.50	5.50	5.17	14.72
IPR Juriti	93.50	6.33	3.17	6.17	6.00	13.62
Guapo Brilhante	97.17	4.00	3.67	4.67	3.83	12.89
BRS Campeiro	93.83	5.50	3.33	5.50	5.17	17.04
Vagem Roxa	98.67	3.67	3.50	5.17	4.67	14.82

Cultivar	ILP	HD	NPP	M100G	YIELD
Fepagro Triunfo	38.55	6.63	13.53	25.78	1,918.62
IPR Juriti	40.22	6.09	15.18	27.76	2,189.25
Guapo Brilhante	33.33	5.64	12.91	24.67	2,090.54
BRS Campeiro	39.56	5.20	10.84	26.95	1,865.38
Vagem Roxa	39.38	6.03	10.78	23.83	1,669.57

The common bean cultivars Fepagro Triunfo, IPR Juriti, Guapo Brilhante and BRS Campeiro and the Vagem Roxa landrace showed superior agronomic traits and were selected by the rank-sum index. Therefore, of the 37 common bean landraces evaluated, only Vagem Roxa showed cycle, plant architecture and grain yield similar to the best common bean cultivars selected.

The analysis of the rank-sum selection index was consistent with Tocher's cluster analysis in the identification of four superior common bean genotypes for agronomic traits, namely, Fepagro Triunfo, IPR Juriti, Guapo Brilhante and Vagem Roxa. Therefore, Tocher's cluster analysis should be recommended to define promising crosses to be made for the development of common bean cultivars with high agronomic performance. The rank-sum selection index, in turn, defined which were the superior common bean genotypes for agronomic performance that can be grown in the region.

CONCLUSIONS

1. Common bean genotypes have genetic variability for traits of phenology, plant architecture and yield components. Grain yield is highly correlated with insertion of the last pod (r = 0.74), number of pods per plant (r = 0.74) and mass of 100 grains (r = -0.64);
2. The following crosses are recommended based on the analysis of the groups formed by Tocher's method and on the mean values obtained for the different agronomic traits: Vagem Roxa × IPR Juriti, Vagem Roxa × Macanudo, Fepagro Triunfo × IPR Juriti, Fepagro Triunfo × Macanudo, Guapo Brilhante × IPR Juriti, and Guapo Brilhante × Macanudo;
3. The common bean genotypes Fepagro Triunfo, IPR Juriti, Guapo Brilhante, BRS Campeiro and Vagem Roxa, selected by the rank-sum index, show high agronomic performance.

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