Genetic divergence and combined selection for traits that provide high agronomic performance in common bean lines[1]

Nerinéia Dalfollo Ribeiro[2*], Greice Godoy dos Santos[2], Henrique da Silva Argenta[2]

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ABSTRACT

The selection of common bean lines with intermediate cycle, upright plant architecture and high grain yield is an important goal of breeding programs. This study proposes to examine the genetic diversity of common bean genotypes for agronomic traits, select superior genotypes for traits that provide high agronomic performance and define promising crosses. Seventeen common bean genotypes were evaluated in two growing seasons in 2019. A total of 17 agronomic traits were determined, which comprised the cycle, 12 traits related to plant architecture and four traits related to production. All traits exhibited a significant genotype × environment interaction, except for lodging and insertion of the first pod. Tocher's and the unweighted pair group method with arithmetic mean (UPGMA) cluster analyses resulted in the formation of three groups of genotypes. Tocher and UPGMA analyses do not allow identifying differences between the superior genotypes of high agronomic performance. Cultivars Fepagro Triunfo and Fepagro Garapiá and lines SM 1510 and Linhagem 110, selected by the multiplicative index, stand out for different agronomic traits. The cross between cultivars Fepagro Triunfo and Fepagro Garapiá (superior agronomic traits) is recommended for the breeding program. Recombiants with high agronomic performance could be setected from the tested hybrid combinations.

Keywords: *Phaseolus vulgaris* L.; genotype × environment interaction; cluster analyses; selection index.

INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is grown in 120 countries (FAO, 2018). Brazil is one of the largest producers and consumers of this legume, having a cultivated area of 2,926,700 ha (Conab, 2020). The inclusion of common bean in the human diet is a healthy practice, given the high levels of protein, minerals, vitamins and dietary fiber and low fat content in this grain (Suárez-Martínez *et al*., 2016). For this reason, common bean has been used to replace animal protein by vegetarians, vegans and other consumers who seek to add high nutritional value to their diet.

However, for a common bean cultivar to be produced by farmers, its cycle must be suitable for cultivation with the other agricultural species in succession as well as have an upright plant architecture and exhibit high grain-yield potential. Many common-bean producers prefer early- or intermediate-cycle cultivars, that is, cultivars that can be harvested in up to 90 days, allowing the cultivation of other species in the same area. Plant architecture in common bean has been evaluated by lodging, insertion of the first pod, plant height, among other traits (Moura *et al*., 2013; Soltani *et al*., 2016; Ribeiro *et al*., 2018; Nadeem *et al*., 2020). Developing common bean cultivars with upright plant architecture offers a number of advantages, e.g., easier management practices, reduced incidence of some diseases, improved grain quality due to less contact of the pods with soil and reduced losses in mechanized harvest (Ramalho *et al*., 1998).

To increase the chances of success in the development process of a new common bean cultivar, the favorable agronomic traits of promising parents - such as new lines and cultivars - must be first characterized in great detail. In this respect, cluster analyses have shown good results

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[2] Universidade Federal de Santa Maria, Departamento de Fitotecnia, Santa Maria, Rio Grande do Sul, Brazil. nerineia@hotmail.com; godoy.greice@gmail.com; henriqueargenta@hotmail.com
*Corresponding author: nerineia@hotmail.com

in differentiating common bean genotypes for agronomic traits when Tocher's method (Lima *et al*., 2012; Gonçalves *et al*., 2016; Santos *et al*., 2019) and the UPGMA method (Cabral *et al*., 2011; Bertoldo *et al*., 2014) were used. However, no studies were found in the literature that evaluate genetic divergence considering a large number of traits related to plant architecture in common bean.

In addition, the use of a selection index can contribute to a better characterization of the genetic diversity available in superior genotypes for use in the common-bean breeding program. The multiplicative index was considered a good selection index to be used in the selection of common bean lines based on agronomic traits and mineral concentration, since high total genetic gain and individual gains favorable to the objectives of selection were achieved (Jost *et al*., 2012; Maziero *et al*., 2015). However, individual gains favorable to the objectives of selection were not obtained for all evaluated agronomic traits when the multiplicative index was used (Ribeiro *et al*., 2018). The evaluation of multicollinearity diagnostics before the selection index analyses are carried out would eliminate the multicollinear variables, allowing the proper interpretation of results.

The use of cluster analysis and the selection index may generate complementary and more in-depth information about the genetic diversity of promising parents for use in breeding programs. Therefore, the present study was undertaken to examine the genetic diversity of common bean genotypes for 17 agronomic traits, select superior genotypes for traits that provide high agronomic performance and define promising crosses.

MATERIAL AND METHODS

Description of experiments and evaluations

The two experiments were conducted in 2019 on the campus of the Federal University of Santa Maria, in Santa Maria, Rio Grande do Sul (RS), Brazil (29º42´ S latitude, 53º49´ W longitude and 95 m altitude). The first experiment was sown in February and the second in October, which is in agreement with the agroclimatic zoning for common bean growing in RS for the dry and rainy season crops, respectively. According to the Köppen classification, the climate in the region is humid subtropical (Alvares *et al*., 2013).

The experiment was carried out in a randomized-block design with three replicates. Each experimental unit was represented by four 4-m-long rows spaced 0.5 m apart, with only the two central rows considered usable area (4 m^2). The evaluated treatments were 17 common bean genotypes, consisting of four cultivars (Pérola, Fepagro Garapiá, BRS Intrépido and Fepagro Triunfo) and 13 lines obtained by different research institutions that participated of the Value of Cultivation and Use (VCU) experiment of Common-Bean Southern-Brazilian network in the 2018 and 2019 biennial (Table 1).The evaluated genotypes have different grain types, namely, carioca (beige seed coat with brown streaks), black, cranberry (cream seed coat with red streaks) and pink, typical of the Mesoamerican and Andean gene pools. These common bean genotypes are representative of the most produced grain types in Brazil.

The number of seeds used in sowing was variable to reach the plant population indicated for common bean genotypes with different growth habits (GH): type I (determinate GH): 300,000 plants ha^{-1}; type II (indeterminate GH with short guides): 250,000 plants ha^{-1}; and type III (indeterminate GH with long guides): 200,000 plants ha^{-1} (CTSBF, 2012).

The soil in the experimental area is classified as typic alitic Argisol, Hapludalf, in which the common bean, black oat and common bean crops were implemented in succession in 2019. The soil was prepared with two plowings and one harrowing, which corresponds to conventional cultivation. Soil analysis results indicated that there was no need for liming; however, the following fertilizers were incorporated into the soil: 180 kg ha^{-1} of the 05-20-20 formula (urea: 45% nitrogen, single super-phosphate: 18% P_2O_5 and potassium chloride: 60% K_2O) at sowing and 40 kg ha^{-1} of urea (45% nitrogen) in the first trifoliate leaf stage (V3).

As with fertilization, the other management practices were identical for the two experiments. Seed treatment was performed with the fungicide Maxim® (Fludioxonil and Metalaxyl-M) and the insecticide Cruiser® 350 FS Thiamethoxam), both at a dose of 200 mL 100 kg^{-1} of seeds. Weeds were eliminated by using the pre-emergence herbicide Dual Gold® (S-Metolachlor) at a dose of 1.25 L ha^{-1}, and also mechanically, after the emergence of the common bean plants. Insects were controlled by using the product Engeo™ Pleno (Thiamethoxam and Lambda-cyhalothrin) at a dose of 125 mL ha^{-1}, whenever 5% damage was observed in the leaf area. Irrigation was implemented after sowing, so that there was no reduction in the plant stand, and at flowering stage (R6), aiming at the fixation of the flowers.

The following evaluations were made in the usable area of the plots with the plants at the maturation stage (R9): cycle (number of days between emergence and R9), lodging and general adaptation score. The score scale used for lodging ranged from 1 (all plants upright) to 9 (all plants fallen); and for general adaptation score, from 1 (excellent plant architecture) to 9 (very poor plant architecture). Then, 10 plants were harvested at random from the usable area to evaluate the following traits: insertion of the first pod (cm), insertion of the last pod (cm), plant height (cm), epicotyl diameter (mm), hypocotyl diameter (mm), first-internode length (cm), second-internode length (cm), third-internode length (cm), fourth-internode length (cm), fifth-internode length (cm), number of pods per plant, number of grains per pod and mass of 100 grains (g). The traits measured in centimeters were obtained using a tape measure from the cotyledon node, except for the lengths of the second, third, fourth and fifth internodes, for which the length from the immediately previous internode was used as a reference. Epicotyl diameter was determined at 1 cm above the cotyledon node, whereas hypocotyl diameter was measured at 1 cm below the cotyledon node.

Mass of 100 grains and grain yield were analyzed at an average moisture content of 13%. To calculate the mass of 100 grains, three random 100-grain samples from each replicate were weighed. Grain yield was determined as the sum of the weights of the grains in the usable area and the 10 plants, whose result was converted to kg ha^{-1}.

Statistical analyses

The obtained data were subjected to combined analysis of variance, in which all effects were considered fixed, except for the error, which was analyzed as random. To evaluate the significance level, the F test was applied (p-value < 0.05). The homogeneity of the residual variances was checked by Hartley's maximum F test. For the traits for which the ratio between the highest and lowest residual mean square was greater than seven, it was necessary to correct the degrees of freedom of the error and of the genotype × experiment interaction (Cruz, 2016).

Multicollinearity diagnostics was performed with the phenotypic correlation matrix obtained from combined analysis of variance. Collinearity analysis was based on the classes established by Montgomery *et al.* (2012). If weak collinearity was not obtained, the exclusion of highly correlated traits with greater weight in the last eigenvectors was evaluated before the clustering and selection-index analyses were performed.

The genetic dissimilarity matrix was obtained from the residual variance and covariance matrices of combined of analysis variance. Two cluster analyses were applied: Tocher's optimization and the hierarchical unweighted pair group method with arithmetic mean (UPGMA). The two cluster analyses were based in the Mahalanobis´ generalized distance, using standardized means. The cophenetic correlation coefficient (CCC) was established from Pearson's linear correlation between the elements of the cophenetic matrix and the elements of the dissimilarity matrix to check the consistency of the clustering pattern.

The multiplicative index (Subandi *et al.*, 1973) was used for the combined selection of common bean lines with high agronomic performance. The applied selection intensity was 23.53%, which allowed the selection of the four superior common bean lines. For this, selection was carried out to obtain the lowest values for cycle, lodging, general adaptation score and insertion of the last pod; and the highest values for the other traits. All statistical analyses were performed using Genes software (Cruz, 2016).

Table 1: Common bean genotypes evaluated, breeding program, grain type, gene pool, and growth habit

Genotype	Breeding Program	Grain type	Gene pool	Growth habit
1. CHP 04-239-01	EPAGRI	Black	Mesoamerican	II
2. TB 17-02	EMBRAPA – TC	Black	Mesoamerican	II
3. Fepagro Garapiá	SAPDR	Carioca	Mesoamerican	III
4. Linhagem 110	IAC	Carioca	Mesoamerican	III
5. CHP 01-182-12	EPAGRI	Black	Mesoamerican	II
6. BRS Intrépido	EMBRAPA – TC	Black	Mesoamerican	II
7. CNFRS 15558	EMBRAPA – RB	Pink	Mesoamerican	II
8. CNFRJ 15411	EMBRAPA – RB	Cranberry	Andean	I
9. FAP-F3-2 SEL	IAC	Carioca	Mesoamerican	III
10. Pérola	EMBRAPA – RB	Carioca	Mesoamerican	III
11. LP 13-624	IAPAR	Black	Mesoamerican	II
12. SM 1510	SAPDR	Black	Mesoamerican	II
13. LEC 04-16	UEM	Carioca	Mesoamerican	III
14. UEM 266	UEM	Carioca	Mesoamerican	III
15. TB 17-03	EMBRAPA - TC	Black	Mesoamerican	II
16. Fepagro Triunfo	SAPDR	Black	Mesoamerican	II
17. LP 13-84	IAPAR	Carioca	Mesoamerican	III

Breeding Program: EPAGRI: Agricultural Research and Rural Extension Corporation; EMBRAPA – TC: Brazilian Agricultural Research Corporation – Temperate Climate; SAPDR: Secretariat of Agriculture, Livestock and Irrigation; Agronomic Institute of Campinas; EMBRAPA – RB: Brazilian Agricultural Research Corporation – Rice and Beans; Agronomic Institute of Campinas; UEM: State University of Maringá.

Growth habit: I: determinate; II: indeterminate with short guides; III: indeterminate with long guides.

Agronomic Institute of Campinas

RESULTS AND DISCUSSION

Analysis of variance and multicollinearity diagnostics

The ratio between the highest and lowest residual mean square of analysis of variance was less than seven for all the evaluated traits, except for insertion of the first pod. In this case, the degrees of freedom of the error and of the genotype × environment interaction for insertion of the first pod were corrected (Cruz, 2016) and, thus, homogeneous residual variances were obtained for all agronomic traits evaluated in common bean.

A significant genotype × environment interaction was detected for all traits, except for lodging and insertion of the first pod (Table 2). Previous studies have also found a significant genotype × environment interaction for most of the agronomic traits evaluated in common bean (Cabral *et al*., 2011; Moura *et al*., 2013; Boros *et al*., 2014; Soltani *et al*., 2016; Delfini *et al*., 2017; Arteaga *et al*., 2019; Nadeem *et al*., 2020), showing that the agronomic performance of common bean genotypes can be altered by their growing environment. There was a significant genotype effect for lodging; however, for insertion of the first pod, the genotype and genotype × environment interaction effects were not significant. Therefore, all agronomic traits possessed genetic variability, except for insertion of the first pod, which warranted the exclusion of this trait in the complementary analyses.

The coefficient of experimental variation (CEV) ranged from 4.66 to 29.19%, and selective accuracy (SA) ranged from 0.49 to 0.94. A similar variation amplitude was observed for agronomic traits evaluated in common bean

Table 2: Combined analysis of variance containing the degrees of freedom (DF), mean squares, mean, coefficient of experimental variation (CEV%) and selective accuracy (SA) for the traits of cycle (days), lodging (LDG), general adaptation score (GAS), insertion of the first pod (IFP, cm), insertion of the last pod (ILP, cm), plant height (PH, cm), epicotyl diameter (ED, mm), hypocotyl diameter (HD, mm), 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), number of pods per plant (NPP), number of grains per pod (NGP), mass of 100 grains (M100G, g), and grain yield (YIELD, kg ha^{-1}) of 17 common bean genotypes evaluated in the two growing seasons (dry season of 2019 and rainy season of 2019)

	DF	Mean square					
		CYCLE	**LDG**	**GAS**	**IFP**	**ILP**	**PH**
Block/environment	4	7.74	4.01	1.20	137.35	110.78	156.91
Genotype (G)	16	95.26^{*}	2.36^{*}	1.39^{ns}	29.61^{ns}	176.83^{*}	678.41^{*}
Environment (E)	1	15.69^{ns}	6.63^{ns}	22.59^{*}	4298.20^{*}	8408.81^{*}	5343.41^{*}
G x E	16	38.52^{*}	1.77^{ns}	1.69^{*}	20.27^{ns}	102.50^{*}	228.56^{*}
Error	64	17.41	1.20	0.89	17.68	31.90	58.11
Mean		89.49	4.84	5.31	18.12	48.48	63.66
CEV(%)		4.66	22.59	17.79	23.21	11.65	11.97
SA		0.61	0.82	0.61	0.94	0.49	0.84
		ED	**HD**	**1stIL**	**2ndIL**	**3rdIL**	**4thIL**
Block/environment	4	0.38	0.20	1.86	0.80	0.79	0.68
Genotype (G)	16	1.38^{*}	1.34^{*}	0.51^{*}	0.58^{*}	0.75^{*}	1.18^{ns}
Environment (E)	1	0.00^{ns}	0.21^{ns}	19.86^{*}	52.34^{*}	66.81^{*}	56.15^{*}
G x E	16	1.81^{*}	1.88^{*}	0.46^{*}	0.55^{*}	1.09^{*}	1.67^{*}
Error	64	0.39	0.46	0.23	0.29	0.37	0.74
Mean		6.28	6.34	2.84	4.23	5.62	7.30
CEV(%)		9.95	10.74	16.89	12.73	10.84	11.76
SA		0.86	0.85	0.85	0.70	0.85	0.78
		5thIL	**NPP**	**NGP**	**M100G**	**YIELD**	
Block/environment	4	0.35	39.56	0.10	5.56	106250.34	
Genotype (G)	16	3.38^{*}	35.65^{*}	0.65^{*}	42.65^{*}	703216.47^{*}	
Environment (E)	1	60.31^{*}	148.68^{ns}	0.00^{ns}	359.53^{*}	4428454.27^{*}	
G x E	16	3.85^{*}	53.31^{*}	0.54^{*}	8.50^{*}	311220.15^{*}	
Error	64	1.64	17.80	0.22	3.15	121113.75	
Mean		9.66	15.58	3.82	23.52	1192.10	
CEV(%)		13.25	27.08	12.44	7.55	29.19	
SA		0.70	0.89	0.61	0.73	0.92	

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

genotypes grown in different environments when experimental precision was determined by CEV (Cabral *et al*., 2011; Moura *et al*., 2013; Soltani *et al*., 2016; Delfini *et al*., 2017) and SA (Pereira *et al*., 2019; Ribeiro *et al*., 2019). Most of the traits analyzed in the present study showed a CEV ≤ 25.54% and SA ≥ 0.70, characterizing high experimental precision, according to the classes established by Oliveira *et al*. (2009) and Resende & Duarte (2007), respectively. This result suggests greater reliability in the selection of superior common bean cultivars.

Multicollinearity diagnostics revealed a condition number (CN) of 4,945.38, characterizing severe collinearity. To obtain weak collinearity (CN ≤ 100), it was necessary to exclude traits that were highly correlated and that had a greater weight in the last eigenvectors, namely, epicotyl diameter, hypocotyl diameter, plant height and second-, third- and fifth-internode lengths. These six traits were not included in the cluster and selection-index analyses to prevent multicollinear variables from being implicitly assigned a greater weight, which would result in errors in the interpretation of the results from these analyses.

Cluster analyses

Cluster analysis by Tocher’s optimization method, using the Mahalanobis´ generalized distance matrix, resulted in the generation of three groups (Table 3). Group 1 comprised all the evaluated black bean and most of the carioca bean genotypes, corresponding to 82.35% of the analyzed genotypes. Similarly, when agronomic traits were determined in common bean genotypes, the largest number of genotypes was present in the first group formed by Tocher’s method (Lima *et al*., 2012; Gonçalves *et al*., 2016; Pereira *et al*., 2019).

Tocher’s method was efficient in forming different groups, which allowed identifying favorable agronomic traits in common bean genotypes belonging to different groups. The genotypes from group 1 stood out for having an upright plant architecture, characterized by the lower lodging and general adaptation score values and higher first- and fourth-internode length values; intermediate cycle (89.87 days); small-sized grains (mass of 100 grains < 25 g; Blair *et al*., 2010); and the highest grain yield among the three groups formed. Group 2 consisted of lines CNFRS 15558 and CNFRJ 15411, whose grains are the pink and cranberry types, respectively. These lines had a medium grain size (25 to 40 g; Blair *et al*., 2010) and low grain yield. Group 3, on the other hand, was formed by the line UEM 266, of carioca beans, which differed from other common bean genotypes in its long cycle (96 days); prostrate plant architecture, as evidenced by the higher insertion of the last pod and lower first- and fourth-internode lengths; and the lowest grain yield among the evaluated common bean lines.

Nonetheless, Tocher’s method did not allow for differentiating carioca and black bean lines of high agronomic performance, as these were clustered into a single group. Pereira *et al*. (2019) evaluated the genetic divergence of common bean genotypes for 10 agronomic traits and did not obtain groups with grains exclusively of the carioca or black types, using Tocher’s method. This is explained by the fact that the carioca and black bean lines showed similar mass of 100 grains. In the present study, mass of 100 grains was the most efficient descriptor, identified by Mahalanobis´ generalized distance, for differentiate common bean genotypes of different grain types. Therefore, genotypes with similar mass of 100 grains were clustered in the same group.

Cluster analysis by the UPGMA hierarchical method, using the Mahalanobis´ generalized distance matrix, also resulted in three groups formed (Figure 1), adopting 57% similarity as a group definition criterion. The UPGMA method was considered promising for differentiating

Table 3: Cluster analysis formed by Tocher’s optimization method, based on Mahalanobis’ generalized distance, for the traits of cycle (days), lodging (LDG), general adaptation score (GAS), insertion of the last pod (ILP, cm), first-internode length (1stIL, cm), fourth-internode length (4thIL, cm), number of pods per plant (NPP), number of grains per pod (NGP), mass of 100 grains (M100G, g), and grain yield (YIELD, kg ha^{-1}) determined in 17 common bean genotypes evaluated in two experiments carried out in the year 2019 and means obtained in each group

Group	Number	Genotypes
1	14	FAP-F3-2 SEL, Pérola, Linhagem 110, CHP 04-239-01, TB 17-03, LP 13-624, Fepagro Triunfo, TB 17-02, BRS Intrépido, Fepagro Garapiá, CHP 01-182-12, LEC 04-16, SM 1510 and LP 13-84
2	2	CNFRS 15558 and CNFRJ 15411
3	1	UEM 266

Means obtained in each group

Group	CYCLE	LDG	GAS	ILP	1stIL	4thIL	NPP	NGP	M100G	YIELD
1	89.87	4.80	5.25	48.99	2.87	7.39	16.26	3.88	23.11	1310.52
2	83.58	5.17	5.67	42.55	2.82	7.09	11.33	3.25	28.68	695.98
3	96.00	4.83	5.50	53.18	2.49	6.52	14.45	4.08	18.87	526.45

common bean genotypes based on agronomic (Cabral *et al*., 2011; Bertoldo *et al*., 2014) and morphological traits (Grahić *et al*., 2013; Hegay *et al*., 2014; Guidoti *et al*., 2018; Savić *et al*., 2019). Recent studies have shown that the UPGMA method allowed the analysis of genetic dissimilarity between common bean genotypes of different grain types for agronomic and morphological traits (Arteaga *et al*., 2019; Long *et al*., 2020), which is important for characterizing the genetic diversity available in common-bean breeding programs.

However, the composition of the groups formed by Tocher's and the UPGMA cluster analyses was not identical (Table 3, Figure 1). By the UPGMA method, group 1 was formed by all black bean genotypes and a large part of the carioca bean genotypes. Group 2 contained carioca bean lines LEC 04-16 and UEM 266, and group 3 consisted of lines CNFRS 15558 (pink bean) and CNFRJ 15411 (cranberry bean). When the genetic divergence of common bean genotypes for agronomic traits was assessed by Tocher's and the UPGMA cluster analyses, the number of groups formed and the composition of each group was different (Gonçalves *et al*., 2016; Santos *et al*., 2019). In the present study, was obtained a CCC = 0.75 (significant at 1% probability by the t test), which is comparable to the CCC values described by Cabral *et al*. (2011), Veloso *et al*. (2015) and Arteaga *et al*. (2019) in cluster analysis performed using the UPGMA method for common bean genotypes. In this case, the dendrogram generated by the UPGMA method indicated high reliability in the clustering pattern, since CCC values close to unity represent a high adjustment between the cophenetic matrix and the dissimilarity matrix based on Mahalanobis´ generalized distance (Cabral *et al*., 2011).

In the present study, Tocher's and the UPGMA cluster analyses identified three groups of common bean genotypes based on agronomic traits. However, these methods were not consistent in the composition of two groups formed. This is explained by the fact that in the development process of new carioca and black bean cultivars, crosses were performed between parents of both grain types, resulting in genetic similarity (Veloso *et al*., 2015). For this reason, lines and cultivars of carioca and black beans have a narrow genetic base, which makes it difficult to differentiate common bean genotypes of these grain types for agronomic traits when cluster analysis is applied (Delfini *et al*., 2017; Pereira *et al*., 2019). Moreover, the use of a selection index can contribute to a better characterization of the genetic diversity of superior genotypes for use in the common-bean breeding program.

Selection index

Heritability estimates of intermediate ($30 < h^2 > 60\%$) to high ($h^2 > 60\%$) magnitude were obtained for the different agronomic traits (Table 4), considering the classes presented by Soltani *et al.* (2016). A wide variation amplitude for heritability has been described for phenological traits, plant architecture and yield determined in common bean genotypes (Soltani *et al*., 2016; Ribeiro *et al*., 2018), indicating that the magnitude of the heritability estimates varies with the agronomic trait. In the present study, high herdability ($\geq$ 60.00%) were observed for cycle, insertion of the last pod, number of

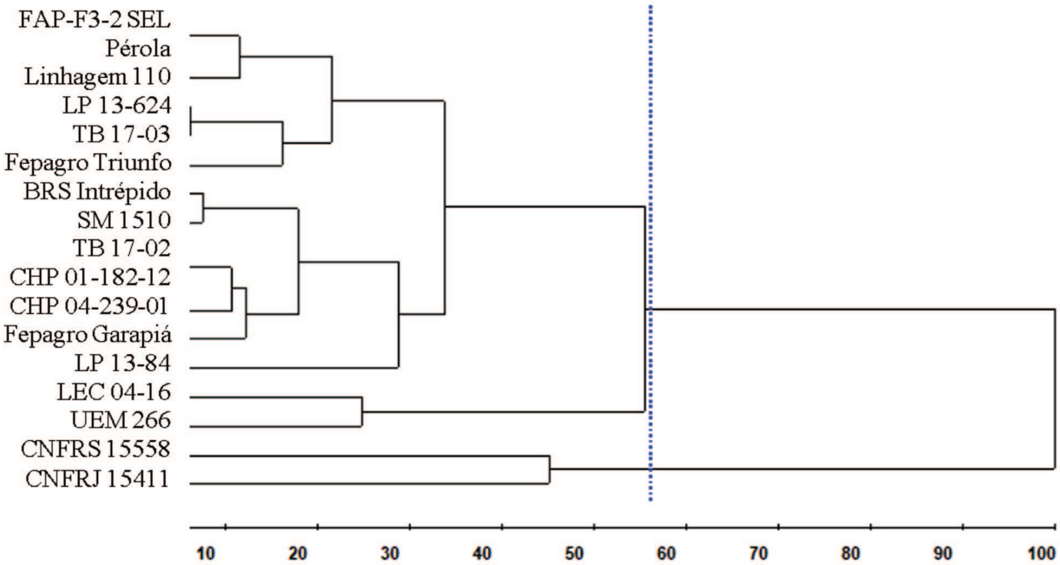

Figure 1: Dendrogram representing genetic dissimilarity among the 17 common bean genotypes obtained by the unweighted pair group method with arithmetic mean (UPGMA), using Mahalanobis' generalized distance, based on agronomic traits evaluated in two experiments carried out in the year 2019.

grains per pod, mass of 100 grains and grain yield. High herdability estimates are associated with greater genetic variability and with greater gains with selection, i.e., increase chances of success in the selection of superior common bean genotypes for agronomic performance.

The multiplicative index indicated a total genetic gain of 19.39%, which is comparable to genetic gain values previously described in combined selection for agronomic traits determined in common bean (Ribeiro *et al*., 2018). For all traits, the genetic gain estimates were favorable to the selection common bean genotypes with intermediate cycle, upright plant architecture and higher values of production-related traits, except for insertion of the last pod. However, the use of the multiplicative index provided a high estimate of total genetic gain and individual genetic gains, with magnitude and sign favorable to the selection of superior common bean lines for agronomic traits and mineral concentration (Jost *et al*., 2012: Maziero *et al*., 2015). In the present study, the greater number of traits related to plant architecture and production may explain the observed differences.

By applying the multiplicative index, it was possible to select the four common bean genotypes that stood out for different agronomic traits, namely, Fepagro Triunfo, SM 1510, Fepagro Garapiá and Linhagem 110. These genotypes had small-sized grains, two of which were of the black beans (Fepagro Triunfo and SM 1510) and the other two of the carioca beans (Fepagro Garapiá and Linhagem 110). Cultivar Fepagro Triunfo and line SM 1510 showed an upright plant architecture, i.e., lower lodging and greater first- and fourth-internode lengths, but its grain yield was considered low. Cultivar Fepagro Garapiá and line Linhagem 110, in turn, exhibited a prostrate plant architecture, characterized by greater lodging and lower first- and fourth-internode lengths; and the highest grain yield values (≥ 1668.71 kg ha^{-1}).

A current goal of breeding programs is to develop new common bean cultivars with upright plant architecture and high grain yield. To increase the chances of success under this demand, the favorable agronomic traits of promising parents must be characterized in great detail. Tocher's and the UPGMA cluster analyses were efficient in differentiating groups of common bean genotypes for agronomic traits, but did not allow identifying differences between the superior genotypes of high agronomic performance. The multiplicative index allowed the

Table 4: Average of the original population (X_0), average of selected genotypes (Xs), heritability (h^2), genetic gain (GG) and percentage of genetic gain (GG%) with simultaneous selection by the multiplicative index for the traits of cycle (days), lodging (LDG), general adaptation score (GAS), insertion of the last pod (ILP, cm), first-internode length (1stIL, cm), fourth-internode length (4thIL, cm), number of pods per plant (NPP), number of grains per pod (NGP), mass of 100 grains (M100G, g), and grain yield (YIELD, kg ha^{-1}) and the four common bean genotypes selected based on the evaluation of two experiments carried out in the year 2019

TRAIT	Selection direction	X_0	Xs	h^2 %	GG	GG %
CYCLE	Lowest value	89.49	88.50	81.72	-0.81	-0.90
LDG	Lowest value	4.84	4.25	49.35	-0.29	-6.04
GAS	Lowest value	5.31	4.83	35.84	-0.17	-3.24
ILP	Lowest value	48.48	49.86	81.96	1.13	2.34
1stIL	Highest value	2.84	2.93	54.96	0.05	1.79
4thIL	Highest value	7.30	7.57	37.53	0.10	1.41
NPP	Highest value	15.58	15.91	50.07	0.16	1.06
NGP	Highest value	3.82	3.96	65.55	0.10	2.54
M100G	Highest value	23.52	23.76	92.61	0.23	0.97
YIELD	Highest value	1192.10	1472.29	82.78	231.94	19.46
Total gain					232.44	19.39

Selected genotypes

Genotype	CYCLE	LDG	GAS	ILP	1stIL	4thIL
Fepagro Triunfo	94.50	3.50	4.33	55.29	3.20	8.21
SM 1510	84.50	3.83	5.00	41.33	3.08	7.51
Fepagro Garapiá	85.33	5.17	5.33	49.13	2.84	7.35
Linhagem 110	89.67	4.50	4.67	53.69	2.63	7.23

	NPP	NGP	M100G	YIELD
Fepagro Triunfo	18.49	3.70	24.67	1099.46
SM 1510	13.70	4.01	22.80	1258.71
Fepagro Garapiá	15.82	4.10	23.35	1862.29
Linhagem 110	15.62	4.05	24.23	1668.71

selection of the four superior genotypes of carioca and black beans for agronomic traits: Fepagro Triunfo, SM 1510, Fepagro Garapiá and Linhagem 110. These common bean genotypes stood out for one or more agronomic traits in the 2019 dry and rainy growing seasons in Santa Maria, RS.

Based on results obtained by multiplicative index, the cross between cultivars Fepagro Triunfo (greater number of traits that provide an upright plant architecture) and Fepagro Garapiá (higher grain yield) is recommended for the breeding program. The selection of recombinants obtained from this cross may result in the development of new carioca and black bean cultivars and with upright plant architecture and high grain yield for cultivation in regions to which they showed adaptation.

CONCLUSIONS

Tocher's and the unweighted pair group method with arithmetic mean cluster analyses distinguish three groups of common bean genotypes; however, do not allow identifying differences between the superior genotypes of high agronomic performance.

Cultivars Fepagro Triunfo and Fepagro Garapiá and lines SM 1510 and Linhagem 110, selected by the multiplicative index, stand out for different agronomic traits.

The cross between cultivars Fepagro Triunfo and Fepagro Garapiá (superior agronomic traits) is recommended for the breeding program. Recombinants with high agronomic performance could be selected from the hybrid combinations assessed.

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